

Jarrell, Noble

From: Jiang, Dong
Sent: Tuesday, February 28, 2006 11:52 AM
To: Jarrell, Noble
Subject: 10/616,788

Please search 1) SEQ ID NO:1 (nt)
2) SEQ ID NO:2 (aa) - standard & against nt
databases.

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail
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Thank you very much.

Dong

Dong Jiang

AU1646
REM - 4D70
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Noble 2NA
1AA
Jan 31/2/06
SPR computer
SONC

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 07:09:08 ; Search time 1261 Seconds
(without alignments)
4839.652 Million cell updates/sec

Title: US-10-616-788-2
Perfect score: 3948
Sequence: 1 MAPWLOCSVFTYNACNG.....SCRADLCGRSTDLHAVAP 738

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA Main -QFMT=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
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-Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database: Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3948	100.0	3083	3	US-09-809-567-1 Sequence 1, Appli
2	3948	100.0	3083	5	US-10-216-156-1 Sequence 1, Appli
3	3948	100.0	3083	7	US-10-616-788-1 Sequence 1, Appli
4	3948	100.0	3083	8	US-10-842-006-3 Sequence 3, Appli
5	3918	99.2	2341	3	US-09-912-157-7 Sequence 7, Appli
6	3918	99.2	2341	7	US-10-717-282-7 Sequence 7, Appli
7	3908	99.0	4477	8	US-10-842-006-1 Sequence 1, Appli

8	3908	99.0	4477	8	US-10-608-449-1	Sequence 1, Appli
9	3901	98.8	2383	3	US-09-912-157-1	Sequence 1, Appli
10	3901	98.8	2383	7	US-10-717-282-1	Sequence 1, Appli
11	3891	98.6	2383	3	US-09-912-157-4	Sequence 4, Appli
12	3891	98.6	2383	7	US-10-717-282-4	Sequence 4, Appli
13	3857	97.7	4392	7	US-10-343-348-15	Sequence 15, Appli
14	3835.5	97.2	2786	3	US-09-863-818A-9	Sequence 9, Appli
15	3835.5	97.2	2786	8	US-10-749-144-9	Sequence 9, Appli
16	3835.5	97.2	2786	8	US-10-924-667-9	Sequence 9, Appli
17	3706	93.9	4508	8	US-10-104-047-1429	Sequence 1429, Ap
18	3706	93.9	4508	8	US-10-608-449-3	Sequence 3, Appli
19	3690	93.5	2319	3	US-09-874-503-17	Sequence 17, Appli
20	3690	93.5	2319	3	US-09-747-259-17	Sequence 17, Appli
21	3690	93.5	2319	5	US-09-908-827-17	Sequence 17, Appli
22	3690	93.5	2319	5	US-10-000-157-17	Sequence 17, Appli
23	3690	93.5	2319	6	US-10-410-927-17	Sequence 17, Appli
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26	3690	93.5	2319	6	US-10-458-442-17	Sequence 17, Appli
27	3690	93.5	2319	7	US-10-408-385-17	Sequence 17, Appli
28	3594	91.0	4450	8	US-10-477-714-42	Sequence 42, Appli
29	3382	85.7	2443	3	US-09-912-157-11	Sequence 11, Appli
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31	3248	82.3	3948	7	US-10-302-172-125	Sequence 125, App
32	3085	78.1	2217	3	US-09-912-157-9	Sequence 9, Appli
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34	3069	77.7	2259	7	US-09-912-157-3	Sequence 3, Appli
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38	2649	67.1	2217	3	US-09-912-157-13	Sequence 13, Appli
39	2649	67.1	2217	7	US-10-717-282-13	Sequence 13, Appli
40	1345.5	34.1	1723	7	US-10-616-788-18	Sequence 18, Appli
41	670	17.0	453	3	US-09-918-995-26425	Sequence 26425, A
42	325	8.2	612	4	US-09-925-065A-50990	Sequence 50990, A
43	325	8.2	612	4	US-09-925-065A-50991	Sequence 50991, A
44	325	8.2	2387	4	US-09-925-065A-672368	Sequence 672368,
45	321.5	8.1	3120	5	US-10-207-655-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-09-809-567-1
; Sequence 1, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (22)..(2235)
US-09-809-567-1

Alignment Scores:
Pred. No.: 0
Score: 3948.00
Percent Similarity: 100.0%
Best local Similarity: 100.0%
Query Match: 100.0%

Length: 3083
Matches: 738
Conservative: 0
Mismatch: 0
Indels: 0

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QY	1	MetAlaProTbPLeuGlnLeuCySeSerValPhePheThrValAenAlaCySeLeuAenGly	20
Db	22	ATGGCCCGTGGCTGGACCTGCTCCGTCTTTCAGGTCAACGGCTCCCTCAACGGC	81
QY	21	SerGlnLeuAlaValAlaAlaGlyGlySerGlyValArgAlaTbPglValAaPbThrCySeGly	40
Db	82	TGGAGCTGGCTGTGGCGCGGTGGCGGGGTCCGGCCGGCGGTGGGGCGTGCACCTGTGGG	141
QY	41	TbPbArgGlyValGlyProAlaSerArgAenSerGlyLeuTybAenIleThrPheTybTyb	60
Db	142	TGGAGGGAGTGGGGGCCGACGACGAGAAACGTGGGGCTGTACCAACATCACCTTCAATAT	201
QY	61	AaPbAenCybThrThrTybLeuAaPbProValGlyTybSHIbValIleAlaAaPbAlaGlnAaPb	80
Db	202	GACAAATTTACCACTTACTTAAATCCAGTGGGAGAAAGCATGTAAATGCTGACGCCCAAGAT	261
QY	81	IleThrIleSerGlnTybAlaCySeSHIbAaPbGlnAlaValAlaThrIleLeuTybSerPro	100
Db	262	ATCACCAATCACCAAGTAACTGTGGCAATGACCAACAAATGGCAATGCACCAATTTGGTCCCA	321
QY	101	GlyAlaLeuGlyIleGlyPheLeuLeuGlyPheArgValIleLeuGlnGlyLeuTybSer	120
Db	322	GGGGCCCTCGGCATCGAATTCCTGAAAGATTTCTGGGTAACTGTGGAGAGCTGAAGTGG	381
QY	121	GlyGlyArgGlnCySeGlnGlnLeuIleLeuTybAaPbProValGlnLeuAaenSerPhe	140
Db	382	GAGGGAACAGTGCACCAACATATCTTAAGATTCGAAAGCACTGCAACAGTCAACAGTAGCTTC	441
QY	141	LybAaPbThrGlyMetGluSerGlnProPheLeuAaenMetLybPbGlnThrAaPbTybPhe	160
Db	442	AAAAGAACTGGAGATGGAAATGCACACCTTCTCTGAATGAATTTGAAACGATTTATTTTC	501
QY	161	ValTybValValProPheProSerIleTybAaGlnSerAaenTybIleProPhePhePhe	180
Db	502	GTAAGAAGTTGTCCCTTTTCTTCCATTAATAAAGCAATTAACACCCCTTTCTTCTTT	561
QY	181	ArgbThrAaGlnAlaCybAaPbLeuLeuGlnProAaPbAenLeuAlaCybValProPheThr	200
Db	562	AGAACCCGAGCTGTGACCTGTGTATACAGCCGACAAATCTAGCTGTATAAACCTTCTGG	621
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Db	622	AAGCTCGGAACCTGAACATCAGCCAGATAGCTCGGACATGCAAGGTGCTCTTGCACAC	681
QY	221	AlaProSHIbAaenPheGlyPheArgPhePheTybLeuHIbTybTybLeuTybSHIbGlyGly	240
Db	682	GCAACGACCACTTCGGGCTTCGTTTCTTCACTTCACTTAACAGCTCAAGCTCAAGACGAAAGG	741
QY	241	ProPheLybAaGlybThrCybLybGlnGlnGlnIleThrThrGlnThrThrSerCybLeuLeu	260
Db	742	CCTTTCAAGCCAAAGAACTGTGAACAGAGAGAAACTCAAGAGACCACTGCTCTT	801
QY	261	GlnAaenValSerProGlyAaPbTybIleIleGlyLeuValAaPbAaPbThrAaenThrArg	280
Db	802	CAAAATGTTTCTCCAGGGGATTAATTAATTAAGCTGTGGATGACATTAACACAAACAA	861
QY	281	LybValMetSHIbTybAlaLeuLybProValHIbSerProTbPbAlaGlyProIleArgAla	300
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QY	301	MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet	320
Db	922	ATGGCCATCACAGGCGCACTGTGTGCTATACCGGCATTTCCGAGAGCTTTCACCTGGATG	981
QY	321	CyAaPbGlybLybGlnGlnGlnAlaSHIbTybSerSHIbAaenPbGlnGlnGlnSerGlnSer	340
Db	982	TGCCGACGAAGACCAACAAAGAAATATATATTTACATTTAGATGAAGAGAGCTGTAGCTT	104
QY	341	SebThrTybThrAlaAlaLeuProArgGlybArgLeuArgProArgProValPheLeu	360

Dd	1042	TCACATTCACATTCGACGACTCCCAAGAGAGAGCTCCGGCCGGCCGAGAGCTCTTTCTC	1102
Qy	361	CySTyTSerSerLyVaAPgLyGlnAspHisMetAsnValValGlnCyAPheAlaTPhe	380
Dd	1102	TGCTATTTCAGTAAGAAGANTGGCCAGATTCAGATGATGTCGTCAGATGTTTGGCTTACTTC	1162
Qy	381	LeuGlnAspPheCyAGLyCyAGLValAlaLeuAspLeuTPGJLAspPheSerLeuCyA	400
Dd	1162	CTCCAGGACTCTCTGGCTGTGAGGTGGCTCTGCACTCTGGGAAAGACTTCAGCTCTCTGT	1222
Qy	401	ArgGlnGlyGlnAspGlnTPValLLeGlnLyLLeHisGlnSerGlnPheGLeLeVal	420
Dd	1222	AGAGAGGGGCAAGAGAAATGGGTACTTCAGAAAGATTCACGAGTCCAGTCAATCATGTG	1282
Qy	421	ValCySerSerLyAGLyMetLyTPheValAspLyLysAsnTPLyHisLeLyAGLy	440
Dd	1282	GTTTGTTCCAAAGGATGAAATGATCTTTGTGGCAAGAAAGACTCAAAACAAAGAGAGT	1342
Qy	441	GlyAPrgLySerGlyLyAGLyGlnLeuPheLeuValAlaValSerAlaLeaGlnLyA	460
Dd	1342	GGCGGAGGCTCGGGGAAAGAGAGACTCTCTCTGGTGGGGGTGTGACGACTTGGCCGAAAG	1402
Qy	461	LeuAPrgGlnAlaLyGlnSerSerSerAlaAlaLeuSerLyAPheLeaValTPhe	480
Dd	1402	CTCCGCGCACGCAAGACAGATTTGTCGGGGGGCTCAGCAAGATTATTCGGCTTACTTT	1462
Qy	481	AspTPyTSerCyAGGlnGlyAspValProGlyLLeLeuAspLeuSerTPheTPArgLeu	500
Dd	1462	GATTATTCCTCCGAGGAGAGAGCTCCCGCGTATCTCAAGCTCAAGTACCAATGACAGATC	1522
Qy	501	MetAspAsnLeuProGlnLeuCySerSerHisLeuHisSerArgAspHisAGLyLeuGlnGlu	520
Dd	1522	ATGGACAAATCTTCTCGACTGTGTTCACCTCGACTCCGAGACACAGGGCTCCAGAG	1582
Qy	521	ProGlyGlnHisTPheTPArgGlnGlySerTPArgTPArgAsnTPPheAspSerLySerGlyAPrg	540
Dd	1582	CCGGGGGACGACGCGCACAGGAGGAGGAGCAAGAACTACTTCCGAGAGAACTCAAGCCGG	1642
Qy	541	SerLeuTPValAlaLeaLeCyAspMetHisAGlnPheLeaAspGlnGluTPAspTPPhe	560
Dd	1642	TCCCTATACGTCCGCAATTGGCAATGCAACAGATTATGACAGAGAGCCGACTGTTC	1702
Qy	561	GlnLyAGlnPheValProPheHisProProProLeuAspTPArgGluProValLeuGln	580
Dd	1702	GAAAAGCAGTTGCTTCCCTCCATCTCTCCATCGCGCTACCGGAGGCCAGTCTTGAG	1762
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Qy	601	PheCySerLeuLyVaLLeuAlaProValLeuGlyAlaTPArgLyProAlaAspSerGlnHis	620
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Dd	1882	GAGAGTCAAGATGGGGGCTGTGACCAAGACGGGAGGCGCGCTTGACGGTGTAC	1942
Qy	641	AlaAlaLeuGlnProLeuLeuHisTPheValLyValAGLySerProSerAspMetProArg	660
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Qy	661	AspSerGlyLyTPArgAspSerValProSerSerGlnLeuSerLeuProLeuMetGlu	680
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Qy	681	GlyLeuSerTPheAspGlnTPArgLHisSerSerLeuTPArgLHisSerValSerSerSerSer	700
Dd	2062	GGACTCTGAGACGACAGAAACGATTCCTCCGACGAGAGGTGTCTCTCTCTCA	2122
Qy	701	GlyLeuGlyGlnGlnGluProProAlaLeuProSerLyLysLeuSerSerGlySerCyA	720

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 RESULT 2
 US-10-216-156-1
 ; Sequence 1, Application US/10216156
 ; Publication No. US20030099980A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jinq, Shuguan
 ; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/36916A
 ; CURRENT APPLICATION NUMBER: US/10/216,156
 ; CURRENT FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: US/09/809,567
 ; PRIOR FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: 09/724,460
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 60/189,816
 ; PRIOR FILING DATE: 2000-03-16
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3083
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (22)..(2235)
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 Score: 3948.00 Matches: 738
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
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 Db 82 TCGGAGCTGGCTGGCGCGCTGGCGGGGTCGGCGCGCGCGTGGGCGTGCACCTGTGGC 141
 Qy 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuGlyTrpAlaIleThrPheLeuTyr 60
 Db 142 TGGAGGGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGTACACATCACCCTTCAATAT 201
 Qy 61 AspAsnCysThrThrTyrLeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAsn 80
 Db 202 GACAAATGTGACCACTACTTGAATCCAGTGGGGAAGCATGTGATGCTGACGCCCAAAAT 261
 Qy 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
 Db 262 ATCCACCAATCCAGCGATAGCTTCCATGACCAACAGTGCAGTCACTTTGGTCCCA 321
 Qy 101 GlyAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGlnGluLeuLeuSer 120
 Db 322 GGGGCGCTCGGCATCGAATTCCTGAAAGGATTTGGGTAAATCTGAGAGAGCTGAAGTCG 381
 Qy 121 GluGlyArgGlnCysGlnGlnLeuIleLeuLeuAspProGlySerGlnLeuAsnSerPhe 140
 Db 382 GAGGGAAGACAGTCCCAACAATGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTC 441
 Qy 141 LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLeuSerPheGlnTrpAspTyrPhe 160

Db 442 AAGAACGTGAATGAATCTCAACTTTCGTGAATATGAATTTGAACGATTAATTC 501
 Qy 161 ValIysValValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhe 180
 Db 502 GTAAAGGTTCCTTTTCTTCCATTTAAAGAAAGAAATTAACACCTTTCTTCTT 561
 Qy 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
 Db 562 AGAACCCGAGCTGTGACCTGTTTTRACCCGAGCAATCTAGCTTTAAACCTTCTGG 621
 Qy 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 Db 622 AAGCTCGAAGCTGAACATCAGCAGCATGGCTCGGACATGCAAGTGTCTTGACACAC 681
 Qy 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrTyrLeuLeuGlnGly 240
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 Db 742 CTTTCAGGGAAGACCTGTAGAGAGCAACATACAGAGACAGCAGCTGCTCTT 801
 Qy 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrThrArg 280
 Db 802 CAATATCTTCTCAGGCGATTTATATATAGCTGTGTGATGACATTAACAACAAGA 861
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 Qy 321 CysArgLysGlnGlnGlnGlnLeuIleTyrSerHisLeuAspGlnGlnSerGlnSer 340
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 Qy 341 SerThrTyrThrAlaAlaLeuProArgGlnArgLeuArgProArgProLysValPheLeu 360
 Db 1042 TCCACATACACTGACAGACTCCCAAGAGAGAGCTCCGCGCGCGGAGGTCTTCTC 1101
 Qy 361 CysTyrSerSerLysAspGlnGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
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QY	521	ProGlyGlnHieThrArgGlnGlySerArgArgAntYrPheArgSerIysSerGlyArg	540
Db	1582	CCGGGGGACGACACCCGACAGGGGACGAGAAAGAACTCTCCGAGCAATCAAGCCGG	1641
QY	541	SeIeuYrValAlaIleCyabamethieGlnPheIleapGlnGluProAspTrpPhe	560
Db	1642	TCCCTATACGTGCGCATTTGGCAACTGACCAAGTTATTTGACGAGAGACCCGACGTTC	1701
QY	561	GluYrGlnPheValProPheHieProProProIeuArgTyArgGluProValIeuGlu	580
Db	1702	GAAAAGCAgTTCGTTCCCTTCATCTCTCCACAGCGGCTACCGGAGCCAGTCTTGAG	1761
QY	581	LysPheAspSerGlyLeuValIleuAnaAspValMetCyblyrProGlyProGluSerAsp	600
Db	1762	AAATTGGATTCCGGGCTTGGTTTAAATGATGATCATGTCAACACAGGGCCGAGAGTGAC	1821
QY	601	PheCybLeuLysValGluAlaProValIeuGlyAlaThrGlyProAlaAspSerGlnHie	620
Db	1822	TTCTGCTTAAAGTGAAGAGCGCTCTTCTTGAGGACCGGACAGCCGACTCCAGAC	1881
QY	621	GluSerGlnHieGlyGlyLeuAspGlnAspGlyGluAlaArgProAlaIeuAspGlySer	640
Db	1882	GAGACTACGATGGGGGCGCTGGACCAAGACGGGAGGCGCCGGCTTGACGGTAC	1941
QY	641	AlaAlaLeuGlnProLeuLeuHieThrValIysAlaGlySerProSerAspMetProArg	660
Db	1942	GCCGGCTCGAACCCCTCGCTGACACGGTGAAGCGCGGACGCCCTCGAGATGCCCGG	2001
QY	661	AspSerGlyIleYrAspSerSerValProSerSerGlyLeuSerLeuProLeuMetGlu	680
Db	2002	GACTAGGCATCTTAAGACTCGTGTGTGCCCTCATCCGAGCGTCTCTCCACTAGTGA	2061
QY	681	GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSerSer	700
Db	2062	GGACTCTCGACGGACCAAGCAAGAAACGTCTTCCCGAGGAGAGGCTCTCTCTTCA	2121
QY	701	GlyLeuGlyGluGluGluProProAlaLeuProSerIysLeuLeuSerSerGlySerCys	720
Db	2122	GGCCCTGGGTGAGAGAACTCTCTCCCTTCCCTTCCAAAGCTCTCTCTTCTGGGTCATGC	2181
QY	721	LysAlaAspLeuGlyCysArgSerYrThrAspGluLeuHieAlaValAlaPro	738
Db	2182	AAAGCAATCTTGTTGCCGCGACTACCTAGTAAGATCCACGCGGTGCCCCCT	2235
RESULT 3			
US-10-616-788-1			
; Sequence 1, Application US/10616788			
; Publication No. US20040048338A1			
; GENERAL INFORMATION:			
; APPLICANT: Jinq, Shudjan			
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof			
; FILE REFERENCE: 01017739525			
; CURRENT APPLICATION NUMBER: US/10/616,788			
; CURRENT FILING DATE: 2003-07-10			
; PRIOR APPLICATION NUMBER: 09/809,567			
; PRIOR FILING DATE: 2001-03-15			
; PRIOR APPLICATION NUMBER: 09/724,460			
; PRIOR FILING DATE: 2000-11-28			
; PRIOR APPLICATION NUMBER: 60/189,816			
; PRIOR FILING DATE: 2000-03-16			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 3083			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (122)..(2235)			
US-10-616-788-1			
Alignment Scores:			

Pred. No. :	0	3083	Length:
Score: .	394.00	738	
Percent Similarity:	100.0%	Conservative: 0	
Best Local Similarity:	100.0%	Mismatches: 0	
Query Match:	100.0%	Indels: 0	
DB:	7	Gaps: 0	

US-10-616-788-2 (1-738) x US-10-616-788-1 (1-3083)

QY	1	MetAlaPOTrPLeuGlnLeuCySerValPhePheThrValAsnAlaCysLeuSngLy	20
DB	22	ATGGCCCGGTGGCTGCACCTGCTGCCCTCTTACCGGTCAAGCCCTGCACCGGC	81
QY	21	SerGlnLeuAlaValAlaAlaGlyGlySerGlyValaGlaATrGlyValAspThrCysGly	40
DB	82	TGCGACGTGGCTGTGGCGGTGGCGGGTCCGGCCGGCGGTGGGGGGGTGCACACTGGGC	141
QY	41	TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyAsnIleThrPheLyTyR	60
DB	142	TGGAGGGAGTGGGGCCAGCCAGCAAGAAACAGTGGGTCTGACACTCACCTTCAATAT	201
QY	61	AspAsnCyStrThrThyTleuAsnProValGlyLyShIleValIleAlaAspAlaGlnAsn	80
DB	202	GACAAATTGACCACTTACTTGATCAGTGGGGAAGCATGTATTGCTGACGCCCAAGAT	261
QY	81	IleThrIleSerGlnThyAlaCysShIAspGlnValAlaValThrIleLeuTrpSerPro	100
DB	262	ATCACCAATACGCAATATGCTTGCATGACAGTGCACAGTGCACCATCTTGGTCCCA	321
QY	101	GlyAlaLeuGlyIleGlyPheLeuLySgLyPheArgValIleLeuGlnGlyLeuLySser	120
DB	322	GGGGCCCTCCGGATCGAATCTCTGAAGAGATTCGGGTAAATCTGGAGAGCTGAAGTGG	381
QY	121	GlyGlyAlaArgGlnCysGlnGlnLeuIleLeuLyAspProLySgGlnLeuAsnSerSerPhe	140
DB	382	GAGGGAACAACAGTGCACAACTGATTTCTTAAAGAGATCCACACAGCTCAACAGTACCTTC	441
QY	141	LyAsArgThrGlyMetGlnSerGlnProPheLeuAsnMetLySgPheGlyIleThrAspTyR	160
DB	442	AAAGAACCTGGATGGAAATCTCAACCTTCTCGAATATGAATTTGAAACGATTTATTC	501
QY	161	ValLySValValProPheProSerIleLySAsnGlnSerAsnTyRHisProPhePhe	180
DB	502	GTAAGGTGTGCCCTTTCTTCCTTCAATTAAGCAAGCAATTACACCCCTTCTCTTT	561
QY	181	ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLySProPheTrp	200
DB	562	AGAACCCAGCCGTGACCTGTGTGTACACGCCGGAACAATCTGATTAACCCCTTCTGG	621
QY	201	LySPProAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis	220
DB	622	AAAGCTCGGAACCTTAACATCAGCCAGCATGGCTCGACATGCAAGTGTCTTCGACAC	681
QY	221	AlaProHisAsnPheGlyPheArgPhePheTyRLeuHisTyRlyLeuLySHisGlnGly	240
DB	682	GCACCGCAACACTTCGGCTTCGGTTCCTTCTTCACTTCACTTAACAAGCTCAAGCAGAAGGA	741
QY	241	ProPheLySArgLySThrCysLySglnGlnIleThrGlnIleThrHisSerCysLeuLeu	260
DB	742	CCCTTCAAGCGAAMAACTGTAAAGAGAGGAACTACAGAGACGACGCTGCCCTCTT	801
QY	261	GlnAsnValSerProGlyAspTyRTrpIleGlyLeuValAspAspThrAsnThrArg	280
DB	802	CAAAATGTTTCTCCAGGGGATTAATTAATGAGCTGTGTGAATGACACTTAACACAAAGA	861
QY	281	LySValMetHisTyRAlaLeuLySProValHisSerProTrpAlaGlyProIleArgAla	300
DB	862	AAAGTATGATTAATGCTTAAAGCAAGTCACTCCCTGGGGCGGGCCCATCAAGGCC	921
QY	301	MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet	320
DB	922	ATGGGCATCAAGTGCACGTGGTATGTCATATGGCATTTGGCAGCGCTTCACTGTGATG	981

QY 141 LysArgThrGlyMetGluSerGlnProPheLeuAenMetLysPheGluThrAspTyrPhe 160
 Db 442 AAAAGAACTGGAATGGAATCTCAACCTTCTGTAATGAAATTGAAACGAGTTATTTC 501
 QY 161 ValLysValValProPheProSerIleLysAenGluSerAenTyrHisProPhePhe 180
 Db 502 GTAAAGGTGGCTCCCTTCTCCATTAATAAACAAGCAATACCACTCCCTTCTCTCT 561
 QY 181 ArgThrArgLysCysAenPheLeuLeuGlnProAenLeuAenCysLysProPheThr 200
 Db 562 AGAAGCCGAGCTGTGACCTGTGTACAGCCGAGCAATCTAGCTGTGAAACCTCTCGG 621
 QY 201 LysProArgAenLeuAenIleSerGlnHisGlySerAenMetGlnValSerPheAenHis 220
 Db 622 AAGCTCGGAACCTGGAACATCAGCCAGATGGCTCGGACATGACGGTCTCTTGACAC 681
 QY 221 AlaProHisAenPheGlyPheArgPhePheTyrLeuHisTyrTyrLysLeuLysGly 240
 Db 682 GCACCGCAACACTTCGGCTTCGTTCTTCTATCTTCACTACAGCTCAAGCAAGAGAG 741
 QY 241 ProPheLysArgLysThrCysLysGlnGluLysThrGluLysThrThrSerCysLeuLeu 260
 Db 742 CTTTCAAGGAGAAAGACCTGTAGCAGAGCAAACTACAGAGACCAAGCTGCTCTCT 801
 QY 261 GlnAenValSerProGlyAspTyrIleIleGluLeuValAspAspThrAenThrArg 280
 Db 802 CAAATGTCTTCCAGGGGATTAATTAATTAATGACCTGGTGATGACATCAACAACAAGA 861
 QY 281 LysValMetHisTyrValLeuLysProValHisSerProTyrIleGlyProIleArgAla 300
 Db 862 AAATGTATGCAATATGCTTAAACCCAGTGCATCCCGTGGCGGCGCATCAGAGACC 921
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 Db 922 ATGGCCATCACAAGGCCATGGTAGCTATATCGGCACTTCCGAGCGCTTCACTGTAAG 981
 QY 321 CysArgLysLysGlnGlnGluAenIleTyrSerHisLeuAenGluLysSerGlySer 340
 Db 982 TGCCGCAAGAGCAACAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1041
 QY 341 SerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgProLysValPheLeu 360
 Db 1042 TCCACATACACTGCAGCACTCCCAAGAGAGAGCTCCGCGCGGCGAGAGTCTTCTC 1101
 QY 361 CysTyrSerSerLysAenPheGlyLysAenHisMetAenValValGlnCysPheAlaTyrPhe 380
 Db 1102 TGCTATTCCAGTAAGATGSCCAAGATCAATGAATGCTCCAGTGTTCCTACTCTC 1161
 QY 381 LeuGlnAenPheCysGlyCysGluValAlaLeuAenPheLeuTyrGluAenPheSerLeuCys 400
 Db 1162 CTCGAGACTTCTGTGGCTGTGAGGTGGCTGTGACCTGTGGAGAGACTTCAAGCTCTGT 1221
 QY 401 ArgGlnGlyGlnArgGluTyrValIleGlnLysIleHisGlySerGlnPheIleIleVal 420
 Db 1222 AGAAGAGGCGAGAGATGGGTATCCAGAGATCCAGAGTCCAGTTCATCATTTGTG 1281
 QY 421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAenTyrLysHisLysGlyGly 440
 Db 1282 GTTGTTCCTCAAGGTATGAATCTTGTGTGACAGAGAACTCAACAACAAGAGAGGT 1341
 QY 441 GlyArgGlySerGlyLysGlyLysLeuPheLeuValAlaValSerAlaIleAlaGlyLys 460
 Db 1342 GGGCGAGGCTCGGGAGAGAGAGCTCTTCTGTGGTGGGTGTGACCATTTGCCGAAAG 1401
 QY 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 Db 1402 CTCGCGCAGGCGCAAGAGTTGCTCGCGCGCTCAGCAAGTTATGCGCTACTCTT 1461
 QY 481 AspTyrSerCysGlyLysValProGlyLysLeuAenPheLeuSerThrLysTyrArgLeu 500
 Db 1462 GATTATTCCTGCGAGGAGAGAGTCCCGGTATCTTAGCCGATACCAAGTACAGACTC 1521
 QY 501 MetAenLeuProGlnLeuCysSerHisLeuHisSerArgAenHisGlyLeuGlnGlu 520

Db 1522 ATGACAACTCTCTCAGCTCTGTCCACCTGCACTCCGAGACCAAGCGCTCCAGAG 1581
 QY 521 ProGlyGlnHisThrArgGlnGlySerArgArgAenTyrPheArgSerLysSerGlyArg 540
 Db 1582 CCGGGGAGCAGCAGGCGAGCGGCGAGAGAACTCACTTCCGAGCAAGTACAGCGCGG 1641
 QY 541 SerLeuTyrValAlaIleCysAenMetHisGlnPheIleAspGluGluProAspTyrPhe 560
 Db 1642 TCCCTATAGCTCCCATTTGCCAATGACCACTTTATTAACAAGAGCCGACTGGTTC 1701
 QY 561 GlnLysGlnPheValProPheHisProProProLeuArgTyrArgGluProValLeuGlu 580
 Db 1702 GAAAGAGATTGCTTCCCTTCCATCTCTCCACTGCGCTACCGGAGCGCACTTGAG 1761
 QY 581 LysPheAenSerGlyLeuValLeuAenAenValMetCysLysArgProGlyLysSerAen 600
 Db 1762 AAATTTGATTCCGGGCTTGTGTTTAAATGATGATGTATGCAAAACAGGCGCTGAGAGTAC 1821
 QY 601 PheCysLeuLysValGluAlaProValLeuGlyAlaThrGlyProAlaAenSerGlnHis 620
 Db 1822 TTTGCTTAAGGTAGAGCGGCTGTCTTGGGCAACCGGACCAAGCTCCAGCAC 1881
 QY 621 GluSerGlnHisGlyGlyLeuAenPheGlyGluAlaArgProAlaLeuAenPheGlySer 640
 Db 1882 GAGAGTCAGATGGGGGCTGAGCAAGAGCGGAGCGCGGCTGCGCTTGAACGGTAGC 1941
 QY 641 AlaAlaLeuGlnProLeuLeuHisThrValLysValGlySerProSerAenMetProArg 660
 Db 1942 GCGCGCTGCAACCCCTGCGCACAGGTGAAGCGGCGAGCCCTTCGACATGCGCGG 2001
 QY 661 AspSerGlyIleTyrAenSerSerValProSerSerGlyLeuSerLeuProAenMetGlu 680
 Db 2002 GACTCAGGATCTATGACTGTCTGTGCCCTCATTCGAGCTGTCTTGCACATGAGAA 2061
 QY 681 GlyLeuSerThrAenPheGlnThrGluThrSerSerLeuThrGluSerLysSerSerSer 700
 Db 2062 GACTCGACGAGCAGACAGACAGAAAGCTTCTTCCGAGGAGAGCGTCTCTCTTCA 2121
 QY 701 GlyLeuGlyGlnGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
 Db 2122 GGGCTGGTGAAGAGAACTCTGCTGCTTCTTCCAAAGCTCTCTTCTGAGTCAATGC 2181
 QY 721 LysAlaAenPheGlyCysArgSerTyrThrAenGlyLeuHisAlaValAlaPro 738
 Db 2182 AAAGCAATCTTGTGTGCGGACGACTACATGAATCAACCGCGGTGCCCT 2235

RESULT 5
 US-09-912-157-7
 : Sequence 7, Application US/09912157
 : Patent No. US20020165348A1
 : GENERAL INFORMATION:
 : APPLICANT: Presnell, Scott R.
 : APPLICANT: Kuestner, Rolf E.
 : APPLICANT: Gao, Zeren
 : TITLE OF INVENTION: Human Cytokine Receptor
 : FILE REFERENCE: 00-49
 : CURRENT APPLICATION NUMBER: US/09/912,157
 : CURRENT FILING DATE: 2001-07-23
 : NUMBER OF SEQ ID NOS: 13
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 7
 : LENGTH: 2341
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (86)...(2302)
 US-09-912-157-7
 Alignment Scores:
 Pred. No.: 0 Length: 2341
 Score: 3918.00 Matches: 734

Percent Similarity: 99.6%
 Best Local Similarity: 99.5%
 Query Match: 99.2%
 DB: 3
 Gaps: 0

US-10-616-788-2 (1-738) x US-09-912-157-7 (1-2341)

Qy 1 MetAlaProTribLeuGlnLeuCySerValPhePheThrValAlaAlaCysLeuAlaGly 20
 Db 86 ATGGCCCCGGTGGTGGAGCTGCTGCTCTTCTTTACGCTCAAGCTGCTGCTCAAGGC 145
 Qy 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyValAlaAlaAlaAlaAlaAlaAla 40
 Db 146 TCGCAGCTGCTGGTGGCGCTGGCGGGGTCGGCGCGCGCGCGCGCGCGCGCGCGCG 205
 Qy 41 ThrArgGlyValGlyProAlaSerThrArgAlaSerGlyLeuValIleThrPheValTyr 60
 Db 206 TGGAGGGAGTGGGGCCAGCGACAGAAACAGTGGGCTGTACAAATCATCACTTCAAAATAT 265
 Qy 61 AspAlaSerThrThrThrValLeuAlaProValGlyValIleValIleAlaAlaAlaAla 80
 Db 266 GACATTTGTACCACTTCTTGAATTCAGTGGGAAAGCATGTGATGCTGACGCCAGAT 325
 Qy 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValIleThrIleLeuTyrSerPro 100
 Db 326 ATCAACATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCAATCTTGGTCCCA 385
 Qy 101 GlyAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGlnGluLeuLysSer 120
 Db 386 GGGGCGCTCGGCATCGAATCTTCAAAAGATTTGGGTAAATACGAGAGAGCTGAATCG 445
 Qy 121 GluGlyValArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAlaSerSerPhe 140
 Db 446 GAGGAAAGACAGTGCACAACTGATTTAAAGATTCGAAAGCAGTCAACAGTACGCTTC 505
 Qy 141 LysArgThrGlyMetGlnSerGlnProPheLeuAlaMetLysPheGluThrAspTyrPhe 160
 Db 506 AAAAGAACTGGAAATGGAATCTCAACCTTCTGAAATGAAATTTGAAACGATTAATTC 565
 Qy 161 ValLysValValProPheProSerIleLysAlaGlnLysSerValIlePhePhePhe 180
 Db 566 GTAAAGGTGTCCCTTTCTTCCATTTAAACAAAGCAATATCCACCTTCTTCTTCTT 625
 Qy 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAlaMetLysCysLysProPheTyr 200
 Db 626 AGAACCCGAGCTGTGACCTGTGTGTACAGCCGGAACATCTGATTTAAACCTTCTG 685
 Qy 201 LysProArgAlaLeuAlaIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 Db 686 AAGCCTCGAATCTGAACATCAGCGACATGCTCGACATGCAAGTGTCTTCAACAT 745
 Qy 221 AlaProHisAspPheGlyPheArgPhePheTyrLeuHisGlyTyrLysLeuLysHisGlyGly 240
 Db 746 GCACCGCACAATTCGGCTTCCGTTCTTCTTCACTTCACTAACAAGCTCAAGCAAGAGA 805
 Qy 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGluThrThrSerCysLeuLeu 260
 Db 806 CCTTTCAAGGAAAGACCTTGAAGCAGAGCAACATCAAGAGACGACCACTGCTCTT 865
 Qy 261 GluAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrAsnThrThrArg 280
 Db 866 CAABAATTTCTTCCAGGGGATTTATATTAATTAAGCTGTGATGACATTAACAACAAGA 925
 Qy 281 LysValMetHisGlyTyrAlaLeuLysProValHisSerProTyrAlaGlyProIleArgAla 300
 Db 926 AAGGTATGATATATGCTTAAAGCCAGTCACTCCCGTGGCGCGCCATCAAGAGCC 985
 Qy 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 Db 986 GTGGCCATCAAGGACAGTGTGATGATATGCGCATTTCCGAGCGCTTCACTGATG 1045
 Qy 321 CysArgLysValGlnGlnGlnAlaIleTyrSerHisLeuAspGlnGlnSerGlnSer 340

Db 1046 TGCAGCAAGAACCAAGAAATATATATTCATTTAGATGAGAGAGCTGAGTCT 1105
 Qy 341 SerThrTyrThrAlaAlaLeuProArgLysGlnLeuArgProAlaProLysValPheLeu 360
 Db 1106 TCCACATACACTGACAGACTCCCAAGAGAGAGGCTCCGCGCGCGCGCGCGCGCG 1165
 Qy 361 CysTyrSerSerLysAspGlyGlnAlaHisIleMetAsnValValGlnCysPheAlaTyrPhe 380
 Db 1166 TGCATTTCCAGTAAAGATGGCCAGAAATCAATGAATTCGCTCAAGTGTTCCTACTTC 1225
 Qy 381 LeuGlnAspPheCysGlyCysGlnValAlaLeuAspLeuTyrGlnAspPheSerLeuCys 400
 Db 1226 CTCAGGACTTCTGTGCTGAGAGTGGCTTGGAACCTGTGGAGAACTTCAGCTCTGT 1285
 Qy 401 ArgGlnGlyGlnArgGluTyrValIleGlnLysIleHisGlnSerGlnPheIleVal 420
 Db 1286 AGAAGAGGAGAGAGATGGGTATCCAGAAAGTCCACAGATCCCACTTCATCATATG 1345
 Qy 421 ValCysSerLysGlyMetLysTyrPheValAspLysValAsnTyrLysHisLysGlyGly 440
 Db 1346 GTTTGTTCCAAAGGTATGAAGTACTTTGTGACAAAGAAATCTCAACAACAAGAGGT 1405
 Qy 441 GlyArgGlySerGlyLysGlyGlnLeuPheLeuValAlaAlaSerAlaIleAlaGlnLys 460
 Db 1406 GCGCAGAGCTCGGGAAAGAGAGCTCTTCTGGTGGCGGTGACGATTCGCGAAAG 1465
 Qy 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 Db 1466 CTCGCGCAGGACCAAGCAGAGTTCGTCGCGCGCTCAGCAAGTTATTCGCGCTACTT 1525
 Qy 481 AspTyrSerCysGlnGlnAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500
 Db 1526 GATTAATTCCTGCAAGGAGAGAGTCCCGGTATCTTAACCTGATCAAGTAAAGATC 1585
 Qy 501 MetAspAlaLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGln 520
 Db 1586 ATGACAAATCTTCTCAAGCTCTGTTCCTTCCACTTGCACCTCCGAGACAGCGCTCCAGAG 1645
 Qy 521 ProGlyGlnHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540
 Db 1646 CCGGGGAGACACGCGACAGGCGCAGAGAAAGAACTTCCGAGCAAGTCAAGCGCG 1705
 Qy 541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGlnGluProAspTyrPhe 560
 Db 1706 TCCCTATACGCTCCCATTTGCAACATGACCAAGTATTAACAGAGAGCCCACTGATTC 1765
 Qy 561 GluLysGlnPheValProPheHisProProProLeuAlaGlyTyrArgLysProValLeuGln 580
 Db 1766 GAABAAGAGTTCCTTCCCTTCCATCTCTCCCACTGCGCTACCGGAGCGAGCTTGGAG 1825
 Qy 581 LysPheAspSerGlyLeuValLeuAlaAspValMetCysLysAspProGlyLysSerAsp 600
 Db 1826 AAATTTGATTCGGGCTTGTTTAAATGATGTATGTCAGAAACAGAGGCTGAGAGTGA 1885
 Qy 601 PheCysLeuLysValGlnAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620
 Db 1886 TTCTGCTTAAAGGTATGAGGGGCTGTCTTGGGGCAACCGGACACCGCACTCCCAAGAC 1945
 Qy 621 GluSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
 Db 1946 GAGAGTCAGATGGGGCTTGGACCAAGACGGGAGAGCCCGGCTGCTTGAACGTGAC 2005
 Qy 641 AlaAlaLeuGlnProLeuLeuHisThrValLysValGlySerProSerAspMetProArg 660
 Db 2006 GCGGCTGCAACCTCTGTCGACACGAGTAAAGCGGCGAGCCCTCGGACATGCGCGG 2065
 Qy 661 AspSerGlyIleTyrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln 680
 Db 2066 GACTCAGGCAATCATATCTGTGTGCTTCAATCCAGAGTGTCTTGGCCATGATGAA 2125
 Qy 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerSerSerSer 700
 Db 2126 GACCTTCACAGCAACAGCAAGAAAGCTTCCCTTACGAGAGAGCTGTCTCTTCA 2185

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Qy 701 G1VLeuG1yG1uG1uPProAlaLeuProSerIySleuLeuSerSergIySerCys 720
Db 2186 GGCCTGGGTGAGAGAGAACTCCCTCCCTTCCCAAGCTCCTCTTCTGCGGATCAGC 2245
Qy 721 LyeAlaApleuG1yCySargSerTyThrAapG1uLeuH1sAlaValAlaPro 738
Db 2246 AAGCAATCTTGCTGCTGCGGAGCTAGTGAATCACTCCAGCGGATCGCCCT 2299

RESULT 6
US-10-717-282-7
; Sequence 7, Application US/10717282
; Publication No. US2004007052A1
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86) ... (2302)
US-10-717-282-7

Alignment Scores:
Pred. No.: 0 Length: 2341
Score: 3918.00 Matches: 734
Percent Similarity: 99.6% Conservative: 1
Best Local Similarity: 99.5% Mismatches: 3
Query Match: 99.2% Indels: 0
DB: Gaps: 0

US-10-616-788-2 (1-738) x US-10-717-282-7 (1-2341)
Qy 1 MetAlaProTrpLeuG1nLeuCySerValPhePheThrValAlaAlaCysLeuAangIy 20
Db 86 ATGGCCCCGGCGGAGCTCTGCTCGCTCTTTTCGGTCACAGCGCTGCTTAACGGC 145
Qy 21 SerG1nLeuAlaValAlaAlaG1yG1SerG1yArG1aTrpG1yValAapThrCyG1y 40
Db 146 TCGGAGCTGGCTGGCGCGCTGGCGGCTCGGCGCGCGCGCGCGCGAGACCTGTGCG 205
Qy 41 TrpArG1yValG1yProAlaSerArG1aAnSerG1yLeuTyraAnIleThrPheLeuTy 60
Db 206 TGGAGGGAGAGGGGCGAGCGACAGAAACAGTGGCGTGTACACATCACTTCAAAATAT 265
Qy 61 AspaAnCySerThrThyTrpLeuAnProValG1yIyS1sValIleAlaAapAlaG1aAn 80
Db 266 GACAAATGTACCACTTACTTGAATCCAGTGGGAGAGCATGTGATGCTGAGAGCCCAAT 325
Qy 81 IleThrIleSerG1nTyraAlaCyS1sAapG1nValAlaValThrIleLeuTrpSerPro 100
Db 326 ATCCACATCAAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCACTTCTTGTGCTCCA 385
Qy 101 G1yAlaLeuG1yIleG1uPheLeuLeuG1yPheArG1yValIleLeuG1uLeuIySer 120
Db 386 GGGGCGCTCGGATCGAATTCCTGAAGAAGATTTGGGTAATATCGAGAGACTGAAGTCG 445
Qy 121 G1uG1yArG1nCySargG1nLeuIleLeuIyAapProIyS1nLeuAnSerSerPhe 140
Db 446 GAGGGAAGACAGTCCCAACATGATTTCTAAAGATCCGAGAGAGCTCCACAGTACGCTTC 505
Qy 141 LysArG1nThrG1yMetG1uSerG1nProPheLeuAnMetLysPheG1uThrAapTyPhe 160

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Db 506 AAAAGAACTGGATGGAATCTCAACCTTCTCTGAATATGAATTTGAAACGAGTATTTC 565
Qy 161 ValLysValAlaProPheProSerIleIyAangIySerArAnTyTrs1sProPhePhe 180
Db 566 GTAAGGTGTCTCTTTCTTCTCATTTAAAGAAAGCAATTAACCACTTCTTCTTTT 625
Qy 181 ArG1nThrArG1aCySapPheLeuLeuG1nProAapAAnLeuAlaCyS1ySProPheTy 200
Db 626 AGAACCGAGCTGTGACCTGTGTTGTACAGCCGAGACATCTTACCTGTAAACCTTCTG 685
Qy 201 LyeProArG1nLeuAnIleSerG1nIleG1ySerAapMetG1nValSerPheAapH1s 220
Db 686 AAGCTCGAACTGAAACATCAAGCAGCATGCTCGGACATGACAGGTGCTCTTCAGCAT 745
Qy 221 AlaProH1sAnPheG1yPheArG1nProPhePheTyLeuH1sTyTyLeuIyS1yG1y 240
Db 746 GACCCGACAACTTCGCTTCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 805
Qy 241 ProPheLysArG1nThrCyS1yS1nG1uG1nThrThrG1uThrThrSerCyS1eLeu 260
Db 806 CTTTCAAGGAGAAAGACTGTAAAGCAGAGCAAACTACAGAGACAGACAGCTCTCTT 865
Qy 261 G1nAAnValSerProG1yAapTyTrIleIleG1uLeuValAapAapThrAenThrArG 280
Db 866 CAAATGTTTCTCAGGGGATATATATATGAGCTGGTGAATGACATAACACACAGAGA 925
Qy 281 LysValMetH1sArG1nAlaLeuIySProValH1sSerProTrpAlaG1yProIleArG1a 300
Db 926 AAAGTATGATTAATGCTTAAGCCAGTCACTCCCGGGCGGCGCCATCAAGAGCC 985
Qy 301 MetAlaIleThrValProLeuValAlaIleSerAlaPheAlaThrPheThrValMet 320
Db 986 GTGGCATCACTGACCTGACCTGATGCTATGCTGCGGAGCTCTTCACTGATG 1045
Qy 321 CysArG1yLysG1nG1nLeuAnIleTySerH1sLeuAapG1uG1uSerSergIySer 340
Db 1046 TGGCGAGAGAGCAACAAAGAAATATATATATCACTTGAATGAAGAGCTCGAGTCT 1105
Qy 341 SerThrTyThrAlaAlaLeuProArG1uArG1uArG1uProArG1uValPheLeu 360
Db 1106 TCCACATACACTGACACATCCCAAGAGAGAGCTCCGGCGGCGGAGAGTCTTCTC 1165
Qy 361 CysTySerSerIySapG1yG1nAnH1sMetAAnValAlaG1nCyPheAlaTyPhe 380
Db 1166 TGCTATTCCAGTAAAGTGGCCAGAAATCACATGAATGTGCTCCAGTCTTCCGCTACTTC 1225
Qy 381 LeuG1nAapPheCySargIyCyS1uValAlaLeuAapLeuTrpG1uAapPheSerLeuCy 400
Db 1226 CTCAGGACTTCTGTGGCTGTGAGTGGCTCTGACCTGTGGAGAGCTTCAGCTCTGT 1285
Qy 401 ArG1uG1yG1nArG1uTrpValIleG1nIyS1sIleH1sG1uSerG1nPheIleIleVal 420
Db 1286 AGAGAGGGCAGAGAGATGGATCCAGAAATCCACAGATCCAGATTCATTTGTG 1345
Qy 421 ValCySerIySargIyMetLysTyTrPheValAapLysIySapH1sTyTrs1sIyS1yG1y 440
Db 1346 GTTTGTTCCAAAGTATGAATGATCTTTGTGACAAAGAACTACAAACCAAGAGAT 1405
Qy 441 G1yArG1ySerG1yIySargIyLeuPheLeuValAlaValSerAlaIleAlaG1uLys 460
Db 1406 GGGCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGTGGCGGTGTCAGCATTTGCCAAAG 1465
Qy 461 LeuArG1nAlaIySargIySerSerAlaAlaLeuSerIySapH1sIleAlaValTyPhe 480
Db 1466 CTCGGCAGGCGCAAGAGAGATTTGTCGGCGGCTCAGCAAGTATTCGGCGCTACTTT 1525
Qy 481 AapTySerCySargIyAapValProG1yIleLeuAapLeuSerThyTyTyTyArG1e 500
Db 1526 GATTTATTCCTGAGAGAGAGTCCCGGATATCTTGAACCTGAGTACCAAGTACAGCTC 1585
Qy 501 MetAapAnLeuProIyLeuCySerH1sLeuH1sSerArG1aAph1sG1yLeuG1nG1u 520

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Db 1586 ATGACACATCTTCCAGCTGTTCCACTTGACCTCCGAGACCAAGGCTCCAGAG 1645
 Qy 521 ProglYglnhsthrAargGlnGlySerAargAargAntyrPheAargSerLysSerGlyAarg 540
 Db 1646 CCGGGGAGCAGCAGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1705
 Qy 541 SerLeuYrValAlaIleCysAsnMetHicglnPheIleAargGlnGluProAspTrophe 560
 Db 1706 TCCCTTAATGCTGCGCATTTGCAATGCAACGATTATTGACAGAGAGCCGACTGGTTTC 1765
 Qy 561 GluLysglnPheValProPheHicProProLeuAargTyrAargGluProValLeuGlu 580
 Db 1766 GAAAGAGAGTTCGTTCCCTTCATCTCTCCACGCGCTACCGGAGCCAGTCTGGAG 1825
 Qy 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGluSerAsp 600
 Db 1826 AATATTGATTCGGGCTTGTGTTTAAATGATGTCATGTCAAACAGGGCTGAGAGTGAC 1885
 Qy 601 PheCysLeuLysValGluAlaProValLeuGlnValAlaThrGlyProAlaAspSerGlnHic 620
 Db 1886 TTTCTGCTTAAGGTAGAGGCGGCTGTCTTGGGCAACCGGACCGGACTCCAGAC 1945
 Qy 621 GluSerGlnHicGlyGlyLeuAspGlnAspGlyGluAlaAargProAlaLeuAspGlySer 640
 Db 1946 GAGAGTCAGCATGGGGGCTTGACCAAGACGGGAGGCGCGCTGCGCTTGAGCGTATGC 2005
 Qy 641 AlAlaLeuGlnProLeuLeuHicThrValLysAlaGlySerProSerAspMetProAarg 660
 Db 2006 GCCCCCTGCMAACCCCTGCTGCACACGGTGAAACCGGCAACCCCTCGACATCGCGG 2065
 Qy 661 AspSerGlyIleYrAspSerSerValProSerSerGlyLeuSerLeuProLeuMetGlu 680
 Db 2066 GACTCAGGACATATGACTCTGTGTGCTGCTCATCCAGCTGTCTGCTGCACTAATGAA 2125
 Qy 681 GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSer 700
 Db 2126 GAACTCTGACGAGCAGACGAGAAACGCTTCCCTGACGAGAGAGCTCTCTCTTCA 2185
 Qy 701 GlyLeuGlnGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
 Db 2186 GCGCTGGGTGAGGAGAACTCTGCTCTCTTCAAGCTCTCTCTTCTGAGGTATGC 2245
 Qy 721 LysAlaAspLeuGlyCysAargSerYrThrAspGluLeuHicAlaValAlaPro 738
 Db 2246 AAGGACATCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2299

RESULT 7

US-10-842-006-1
 ; Sequence 1, Application US/10842006
 ; Publication No. US20040235104A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Ruey-Bing
 ; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
 ; FILE REFERENCE: MP103-071P1M
 ; CURRENT APPLICATION NUMBER: US/10/842,006
 ; CURRENT FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: 60/469522
 ; PRIOR FILING DATE: 2003-05-08
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatsSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 4477
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (90)...(2309)
 ; US-10-842-006-1

Alignment Scores:

Pred. No.: 0 Length: 4477
 Score: 3908.00 Matches: 732

Percent Similarity: 99.5% Conservative: 2
 Best Local Similarity: 99.2% Mismatches: 4
 Query Match: 99.0% Indels: 0
 DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x US-10-842-006-1 (1-4477)

Qy 1 MetAlaProTropLeuGlnLeuCysSerValPhePheThrValAsnAlaCysLeuAsnGly 20
 Db 90 ATGGCCCCGGGCGAGCTCTGCTCGCTCTTTACGGGCAACGGCTGCTCAACGGC 149
 Qy 21 SerGlnLeuAlaValAlaIleGlySerGlyAargAlaTropGlyValAspThrCysGly 40
 Db 150 TCGAGCTGCTGTGGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 209
 Qy 41 TrpAargGlyValGlyProAlaSerAargAsnSerGlyLeuTyrAsnIleThrPheLysTyr 60
 Db 210 TGAAGGGAGTGGGGCCAGCAGCAAGAGTGGGCTGTACACATCACTTCAATAT 269
 Qy 61 AsnAsnCythrThrTyrTrpLeuAsnProValGlyLysHicValIleAlaAspAlaGlnAsn 80
 Db 270 GACAAATGTACCACTTACTTGAATCCAGTGGGAGAGATGTGATGCTGACGCCAGAT 329
 Qy 81 IleThrIleSerGlnTyrAlaCysHicAspGlnValAlaValThrIleLeuTyrSerPro 100
 Db 330 ATCACCATCAGCCAGTATGCTTGCATGACCAAGTGGACGACCATTTCTTGGTCCCA 389
 Qy 101 GlyAlaLeuGlnGlyIleGluPheLeuLysGlyPheAargValIleLeuGlnGluLeuLysSer 120
 Db 390 GGGGCTCTCGGCATCGAATCTCTGAAAGATTTGGGTAATATCGAGAGAGCTGAATCG 449
 Qy 121 GluGlyAargGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
 Db 450 GAGGAGAGACAGTGCACAACTGATTTCTAAAGATCCGAGACGCTCAACAGTACGCTTC 509
 Qy 141 LysAargThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe 160
 Db 510 AAGAACTGGATGAAATCTCAACCTTCTGTAATATGAAATTTGAAACGATTAATTC 569
 Qy 161 ValLysValValProPheProSerIleLysAsnGluSerAsnTyrHicProPhePhe 180
 Db 570 GTAAAGTTGTCCTTTTCTTCATTTAAAGCAATTTACCACTTTCTTCTT 629
 Qy 181 ArgThrAargAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTyr 200
 Db 630 AGAACCCGAGCTGTGACCTGTGTATCAGCCGACATCATGCTGTGTAACCTTCTCG 689
 Qy 201 LysProAargAsnLeuAsnIleSerGlnHicGlySerAspMetGlnValSerPheAspHic 220
 Db 690 AAGCTTCGAACTGAACTGACATCAGCAGCATGCTCGACATGAGGTGCTTTCGACAC 749
 Qy 221 AlaProHicAsnPheGlyPheAargPhePheTyrLeuHicTyrLysLeuLysHicGlnGly 240
 Db 750 GCACCGCACAACCTTCCGCTTCCGTTTCTTATCTTCACTTCAACAGCTCAAGCAAGAGGA 809
 Qy 241 ProPheLysAargLysThrCysLysGlnGlnGlnThrGluThrThrSerCysLeuLeu 260
 Db 810 CTTTCAAGCGAAAGACCTGTGAGCAGACCAACTACAGAGATGACAGCTGCTCTCT 869
 Qy 261 GluAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspTyrAsnThrThrArg 280
 Db 870 CAATATGTTCTCCAGGGAGATATATATATGAGTGTGTGATGACCTTAACACAAAGA 929
 Qy 281 LysValMetHicTyrAlaLeuLysProValHicSerProTyrAlaGlyProIleAargAla 300
 Db 930 AAGTATGATATATATGCTTAAGCCAGTGCATCTCCCGTGGGCGGCCCATCAGAGCC 989
 Qy 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 Db 990 GTGGCATCAGAGGCGACATGTAGTATCGCATTCGCAATTCGCGACTTCACTGATG 1049
 Qy 321 CysAargLysGlnGlnGlnLeuIleTyrSerHicLeuAspGlnGluGluSerSerGluSer 340


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Qy 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
Db 630 AGAACCGAGACCTGTGACCTGTTCTTACAGCCGAGCAATCTAGCTTTAAACCTTCTGG 689
Qy 201 LysProArgAsnLeuAsnLysSerGlnHisGlySerAspMetGlnLysPheAspHis 220
Db 690 AACCTCGGAACCTGAACTACAGCAGCATGCTCGGACATGACGAGTGTCTTGCACAC 749
Qy 221 AlaProHisAsnProGlyPheAspGlyPhePheTyrLeuHisGlyLysGlnGly 240
Db 750 GACCCGACCACTTCGGCTTCCTGTTCTTCTATCTTCACTACAGCTTCAGCAGAAAGA 809
Qy 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGlnThrThrSerCysLeuLeu 260
Db 810 CTTTCAAGGAAAGACCTGTGAGCAGAGCAACTACAGAGATGACCAAGCTGCTCTT 869
Qy 261 GlnAsnValSerProGlyLysPyrLysLysLysLeuValAspAspThrAsnThrThrArg 280
Db 870 CAAATGTTTCTCCAGGGAGTTATATATAGCTGATGATGACATACACACAAAGA 929
Qy 281 LysValMetHisGlyAlaLeuLysProValHisSerProTrpAlaGlyProLysArgAla 300
Db 930 AAGGTATGATATATGCTTAAAGCCAGTGCATCCCGTGGCCGCGCATCAGAGCC 989
Qy 301 MetAlaLeuThrValProLeuValValLysSerAlaPheAlaThrLeuPheThrValMet 320
Db 990 GTGGCCATCAACAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATG 1049
Qy 321 CysArgLysLysGlnGlnGlnLysLysLysSerHisLysAspGlnGlnGlnSerGlnSer 340
Db 1050 TGGCGAAGAGCAACAGAAATATATATTCATTCATTAAGAGAGAGCTCGAGTCT 1109
Qy 341 SerThrThrAlaAlaLeuProArgGlnArgLysProArgProLysValPheLeu 360
Db 1110 TCACATATACCTGACAGCTCCCAAGAGAGAGCTCCGCGCGCGAGAGTCTTCTC 1169
Qy 361 CysThrSerSerLysAspGlnGlnAsnHisMetSerAsnValGlnCysPheAlaTyrPhe 380
Db 1170 TGCATATCCAGTAAGATGAGCAGAAATCAATGATATGCTCCAGTGTCTTCTTCTC 1229
Qy 381 LeuGlnAspPheCysGlyCysGlnValAlaLeuAspLeuTrpGlnAspPheSerLeuCys 400
Db 1230 CTCACAGACCTTGTGCTGCTGAGGTGCTGCTGAGCCTGAGGAGAGCTTCAAGCTCTGT 1289
Qy 401 ArgGlnGlnArgGlnArgGlnValLysLysLysLysLysLysLysLysLysLysLysLys 420
Db 1290 AGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1349
Qy 421 ValCysSerLysGlnMetLysTyrPheValAspLysLysLysLysLysLysLysLysLys 440
Db 1350 GTTGTGTTCCAAAGATGAAATGATCTTGTGTGCAAGAAAGAACTACAAACCAAGAGAGT 1409
Qy 441 GlyArgGlySerGlyLysGlyLysGlyLysPheLeuValAlaValSerAlaLeuAlaGlyLys 460
Db 1410 GGCCTGAGGCTCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1469
Qy 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheLeuAlaValTyrPhe 480
Db 1470 CTCGCGCAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1529
Qy 481 AspTyrSerCysGlnGlyAspValProGlyLysLeuAspLeuSerThrLysTyrArgLeu 500
Db 1530 GATTATTTCCGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1589
Qy 501 MetAspAsnLeuProGlnLeuCysSerHisLysHisSerLysArgAspHisGlyLeuGlnGlu 520
Db 1590 ATGAGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1649
Qy 521 ProGlyGlnHisGlyThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540
Db 1650 CCGGGGAGAGCAACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1709
Qy 541 SerLeuTyrValAlaLeuCysAsnMetHisGlnPheLeuAspGlnLysProAspTrpPhe 560

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Db 1710 TCCTTAAGCTCCGCAATTCGAAACATGCAACAGTTATTTACAGAGAGAGAGAGAGAG 1769
Qy 561 GlnLysGlnPheValProPheHisProProProLeuArgTyrArgLysProValLeuGlu 580
Db 1770 GAAAGAGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1829
Qy 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyPyrProLysSerAsp 600
Db 1830 AATTTGATTCGGAGCTTGTGTTTAAATGATGATGATGATGATGATGATGATGATGATG 1889
Qy 601 PheCysLeuLysValGlnAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620
Db 1890 TTCTGCTTAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1949
Qy 621 GluSerGlnHisGlyLysLeuAspGlnAspGlyLysLysLysLysLysLysLysLysLys 640
Db 1950 GAGAGTCAGCATGGAGGAGCTGAGACCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 2009
Qy 641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
Db 2010 GCGGCGCTGCAACCCCTGCTGACACGGTAAAGCCGAGCCCTTCGACATGCGCGG 2069
Qy 661 AspSerGlyLysThrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGlu 680
Db 2070 GACTCAGGATCTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2129
Qy 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSerSer 700
Db 2130 GAGCTCGACGAGACAGACAGAAAGTCTTCTTCTGACGAGAGAGAGAGAGAGAGAGAG 2189
Qy 701 GlyLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 720
Db 2190 GGCCTGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2249
Qy 721 LysAlaAspLeuGlyCysArgSerTyrThrAspGlnLeuHisAlaValAlaPro 738
Db 2250 AAGGCAATCTTGTGTTGCTGCGAGCTACATGATGAACTCCAGCGGCTGCGCCCT 2303

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RESULT 9

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US-09-912-157-1
; Sequence 1, Application US/0912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)
; US-09-912-157-1

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Alignment Scores:

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Pred. No.: 0 Length: 2383
Score: 3901.00 Matches: 734
Percent Similarity: 97.7% Conservative: 1
Best Local Similarity: 97.6% Mismatches: 3
Query Match: 98.8% Indels: 14
DB: 3 Gaps: 1

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US-10-616-788-2 (1-738) x US-09-912-157-1 (1-2383)

Qy 1 MetAlaProTrpLeuGlnLeuCysSerValPhePheThrValAlaAlaCysLeuAsnGly 20

Db	86	ATGGCCCCGTGAGCTGACGCTGCTCCGCTCTTTACGGTCAAGCCCTGCCCAAGGC	145
OY	21	SerGlnLeuAlaValAlaIaIaGlySerGlyArgAlaTrpGlyValAspThrCysGly	40
Db	146	TGCGACGCTGCGTGTGGCCCGCTGGCGGGTCCGGCCCGCGGGGCGCGCAACACTGTGGC	205
OY	41	TrpArg-----GlyValGlyPro	46
Db	206	TGAGAGATGAAGAGCGGCTGCCAGCCCCGCGCTTTGCTGTCTAATAGAGGAGTGGGGCCA	265
OY	47	AlaSerArgAsnSerGlyLeuTrpAsnIleThrPheLeuTyrAspAsnGlyThrTrp	66
Db	266	GCCAGCAAAACAGTGGGCTGTACAACATCACCTTCAATATAGACATTTGACATTCAC	325
OY	67	LeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAsnIleThrIleSerGlnTyr	86
Db	326	TTGAATCCAGTGGGAGACATGTGATTTGCTGACGCCCAAGATATACCATTCAGCCAGTAT	385
OY	87	AlaCysHisAspGlnValAlaValThrIleLeuTrpSerProGlyValAlaGlyIleGlu	106
Db	386	GCTTCCATGACCAAGTGGCAGTCAACATTTCTTGGTCCCAAGGGGCGCTGGCATCGAA	445
OY	107	PheLeuLeuGlyPheArgValIleLeuGluGluLeuLeuLysSerGluGlyArgGlnCysGln	126
Db	446	TTCCGAAAGGATTTCCGGGTAATACTCGAGGAGCGTAATCGAGAGGAAGACAGTGC	505
OY	127	GlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPheLysArgThrGlyMetGlu	146
Db	506	CACCTGATTTCTTAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATCGAA	565
OY	147	SerGlnProPheLeuAsnMetLysPheGluTrpAspTyrPheValIysValValProPhe	166
Db	566	TCTCAACCTTCTCTGAATATGAAATTGAAACGGAATTATTTGTAAGAGGTGTGCTCTTT	625
OY	167	ProSerIleLeuValAsnGluSerAsnTyrHisProPhePheArgThrArgAlaCysAsp	186
Db	626	CCTTCCATTAATAAAGAAAGCAATTAACCCCTTCTTTTGAAGCCGAGCGTGTGAC	685
OY	187	LeuLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrpLysProArgAsnLeuAsn	206
Db	686	CTGTGTTTACACCCCGGACATCTAGCTTTAAACCTTTGGAAGCTCGGAACCTGAAC	745
OY	207	IleSerGlnHisGlySerAspMetGlnValSerPheAspHisAlaProHisAsnPheGly	226
Db	746	ATCAGCCAGCATGGCTCGGACATGACGAGTGTCTTTCGACATGCAACCGACAACCTCGGC	805
OY	227	PheArgPhePheTyrLeuHisTyrTyrLeuLeuLysHisGluGlyProPheLysArgLysThr	246
Db	806	TTCCCTTTCTTCTATCTTCATCTTCAACAGCTCAAGAGCAAGAGGACCTTTCAAGCCAAAGAAC	865
OY	247	CysLeuSerGlnGluThrThrGlnTrpThrTrpSerCysLeuLeuGlnAsnValSerProGly	266
Db	866	TGTAAAGCCAGACAACTACAGAGACAGACAGCTGCTCTCTTCAAAATGTTTCTCGAGG	925
OY	267	AspTyrIleIleGluLeuValAspAspThrAsnThrThrArgLysValMetHisTyrAla	286
Db	926	GATTATATATATTGAGCTGTGGATGACATAACAAACAAGAAAGATGATGATATATGCC	985
OY	287	LeuLysProValHisSerProTrpAlaGlyProIleArgAlaMetAlaIleThrValPro	306
Db	986	TTAAAGCCAGTCCACTCCCGTGGGCGCGGAGCCATCAGAGCCGTGCACTACAGTGC	1044
OY	307	LeuValIleValIleSerAlaPheAlaThrLeuPheThrValMetCysArgLysLysGlnGln	326
Db	1046	CTGGTAGTATATCGGCATTCGGAGCGCTTCTACGTATGTGGCCGAAGAAAGCAACA	1104
OY	327	GlnAsnIleTyrSerHisLeuAspGluGlnSerSerGlnSerSerThrTyrThrAlaAla	346
Db	1106	GAAATATATATATTCACATTTAATGAAGAGAGCTCGAGTCTTCCACATACCTGACGCA	1164
OY	347	LeuProArgGluArgLeuArgProArgProLysValPheLeuCysTyrSerSerLysAsp	366

Dd	1166	CTCCCAAGAGAGAGGCTCCGGCCGGCGCGCAAGGCTTCTCTGTGATTCAGAAAGAT	1225
Oy	367	GIYGLIAsnhiIwneArAnValaGInCyvPhealAryrPheLengInAerPheCyseGIy	386
Dd	1226	GCCCAAGAAATCACTGAATGTCCTCCAGAGTTCCTCCGCTCTTCCTCCAGAACTTCGTGAGC	1285
Oy	387	CyAGIuValAlaLeuAerLeuTProLInAerPheSerLeuCyvAerGluGIyLInAerGlu	406
Dd	1286	TGTGAAGTGGCTCTGGACCTGTGGAGAAAGCTTCAGCCTCTGTAGAGAAAGGGCAAGAGAA	1345
Oy	407	TrpValIIGlnInLyILehiAGIuSerGInPheIleIleValaCyvSeSerGIyMec	426
Dd	1346	TGGGTCAATCCAGAAAGTTCACAGAGTCCAGATTCACTATGGTGTTCCTCCAAAGATG	1405
Oy	427	LyvTrPheValAerLyAlaLyvAerLyvAerLyvGIyGIyLACGIySeGIyLyv	446
Dd	1406	AAAGTACTTGTGGACAAGAAAGTACAACAACAAGAGAGGTGGCGCGAGCTCCGGGAGAA	1465
Oy	447	GIYGLIuLeuPheLeuValAlaValSerAlaIleAlaGluLyvLeuAerGlnAlaLyGln	466
Dd	1466	GGAAGGCTCTCTGTGTGGCGGTGTCAAGCAATGGCCGAAAGCTCCGCAAGCCCAAGCAG	1525
Oy	467	SeSeSerSerAlaAlaLeuSerLyvPheIleAlaValaTyrrPheAerTyrrSeCyGIuGIy	486
Dd	1526	AGTTTCCTCCGGCGCGCTTCAGCAAGTTTATGCCCGCTATCTTGATTAATTCCTGGAGGGA	1585
Oy	487	AerValAProGIyLLeuAerLeuSerThryLyvTyrrAerLeuMetAerLeuProGln	506
Dd	1586	GAGGTCCCGGTATCTTAAGCTCGATGACCAAGTACAGACTCAATGACAAATCTTCCTCAG	1645
Oy	507	LeuCyvSerThryvLeuhiASeArGrAerPhrhiAGIyLeuGInGInuProGInGInhiAThrArg	526
Dd	1646	CTGTGTCCCACTTGGACATCCGAGACCAAGCGGCTTCAGAGAGCGGGGACACACAGGA	1705
Oy	527	GIInGISeArGrAerGrAntTyrrPheArGrSerLyvSeGIyAerSeSerLeuTyvAlaIle	546
Dd	1706	CAGGGCAGCAGAAAGAACTACTTCGAGAGAACTAGAGCCGGTCCCTATAGCTGGCCATT	1765
Oy	547	CyAsnMetchiAGInPheIleAerGluGInuProAerTrpPheGluLyvGlnPheValPro	566
Dd	1766	TGGACATGACCAAGTTTATTGACGAGAGCCCGACTGGTTGAAAACAGATTGCTTCCC	1825
Oy	567	PhehiAerProProLeuAerGTYrArgGInuProValLeuGInLyvPheAerSeGIyLeu	586
Dd	1826	TTCATCTCTCTCCACTGGCGTCAACGGGAGCCAGACTTGGAGAAATTTGAATTCGGGCTTG	1885
Oy	587	ValLeuAerAerValMetCyvLyvAerProGIyPProGInuAerAerPheCyvLeuLyvValGlu	606
Dd	1886	GTTTAAATATATCTCAATGTGCAAACCAAGGGCTTGAGAGTACTTTCGCTTAAAGTAGAG	1945
Oy	607	AlaProValLeuGIyValaThrGIyProAlaAerSeGIyInhiAGIuSeGIyInhiAGIy	626
Dd	1946	GCGGCTGTCTTGGGGCAACCGGACCAAGCCGACTCCAGACAGAGATCAGACATGGGGGC	2005
Oy	627	LeuAerGlnAerGIyGluAlaArGrProAlaLeuAerGIySerAlaAlaLeuGlnProLeu	646
Dd	2006	CTGACACCAAGACGGGAGGCGCGGCTGTGCTTCGTAAGGATGGCGGCTCCACACCTTG	2065
Oy	647	LeuhiAerThryAlaLyvAlaGIySerProSeArAerMetCProArAerSeGIyLyIeTyvAer	666
Dd	2066	CTGCACACGGGTGAAGCGCGAGCCCTTCGACATGCCCGGGGACTTCAGGACTCATAGAC	2125
Oy	667	SeSeSerValAProSeSerGIyLeuSeSerLeuProLeuMetGIyGIyLeuSeTrhAerGln	686
Dd	2126	TGCGTGTGCTCAATCCAGAGCTGTCTTGCCATGATGAAAGGACTCTCCAGCGGACAG	2185
Oy	687	ThrGIuThrSeSerLeuThryGluSerValAerSeSeSeSeGIyLeuGIyGluGlu	706
Dd	2186	ACAGAAACGTCTTCCTGTGACGGAGAGCGTGTCTCTCTTCACGGGCTGGGTGAGGAGAA	2245
Oy	707	ProProAlaLeuAerProSeLyvLeuLeuAerSeGIySerCyvLyvAlaAerLeuGIyCyv	726
Dd	2246	CTCTCGGCGCTTCCTTCCAGGCTCTCTTCTGTGGGTATGGAAGCAAGATCTTGATTC	2305

Qy 727 ArgSerThrAspGluLeuHisAlaValAlaPro 738
 Db 2306 CGAGCTACACTGATGAACTCCAGCGGTCGCCCTT 2341
 RESULT 10
 US-10-717-282-1
 ; Sequence 1, Application US/10717282
 ; Publication No. US20040077052A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Premeil, Scott R.
 ; APPLICANT: Kuestner, Rolf E.
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Human Cytokine Receptor
 ; FILE REFERENCE: 00-49
 ; CURRENT APPLICATION NUMBER: US/10/717,282
 ; CURRENT FILING DATE: 2003-11-19
 ; PRIOR APPLICATION NUMBER: US/09/912,157
 ; PRIOR FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PasteSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 2383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (86) ... (2344)
 US-10-717-282-1
 Alignment Scores:
 Pred. No.: 0 Length: 2383
 Score: 3901.00 Matches: 734
 Percent Similarity: 97.7% Conservative: 1
 Best Local Similarity: 97.6% Mismatches: 3
 Query Match: 98.8% Indels: 14
 DB: 7 Gaps: 1
 US-10-616-788-2 (1-738) x US-10-717-282-1 (1-2383)
 Qy 1 MetAlaProTrrPLeuGlnLeuCySerValPhePheThrValAlaMetAlaCyLeuAlaGly 20
 Db 86 ATGCCCCCGTGGCTGCACTGCTGCTGCTTCTTTACGTCAACGCTGCTCAAGGC 145
 Qy 21 SerGlnLeuAlaValAlaAlaGlySerGlyAlaArgAlaTrpGlyValAspThrCyGly 40
 Db 146 TCGCAGCTGCTGTGGCGCTGCGGCGTCCGCGCGCGCGCGCGCAACCTGTGGC 205
 Qy 41 TrpArg-----GlyValGlyPro 46
 Db 206 TGGAGAGTGAAGCGCGCTGCCGACCCCGCTTGTGCTTAATGAGGGAGTGGGCGCA 265
 Qy 47 AlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLeuTyrAspAsnCyThrThrTyr 66
 Db 266 GCCAGCAGAAACATGGGCTGTACACATCCTTCAATATGACAAATGTACACCTAC 325
 Qy 67 LeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsnIleThrIleSerGlnTyr 86
 Db 326 TTGAATCAGTGGGAGAGCATGTATGCTGACCCCGAATATCATCATCAGCCAGAT 385
 Qy 87 AlaCyHisAspGlnValAlaValThrIleLeuTrpSerProGlyAlaLeuGlyTyrGln 106
 Db 386 GCTTGCATGACCAAGTGGCAGTCAACATTTTGGTCCCAAGGGCGCTCGGCAATGCA 445
 Qy 107 PheLeuYsglyPheArgValIleLeuGlnGluLeuYsgSerGlnGlyArgGlnCyGln 126
 Db 446 TTCTGAAAGATTTCCGGTAACTCTGAGAGAGCTGAGAGCGGAAGCAATGCGCA 505
 Qy 127 GlnLeuIleLeuYsaPProGlyGlnLeuAsnSerSerPheLysArgThrGlyMetGln 146
 Db 506 CAATGATTTCTAAAGATCCGAAACAGCTCAACAGTAGCTTCAAAAGAACTGAGATGGA 565
 Qy 147 SerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheValLysValValProPhe 166

Db 566 TCTCAACCTTCCGAATATGAATTTGAACGATATTATTCGTAAGGTTGTCCTTT 625
 Qy 167 ProSerIleLysAsnGluSerAsnTyrHisProPhePheLeuThrAlaCyAsp 186
 Db 626 CTTTCATTTAAAGCAAGCAATTACACCTTTCTTCTTAAAGCCGCGCTGTAC 685
 Qy 187 LeuLeuGlnProAspAsnLeuAlaCyLysProPheTrpLysProArgAsnLeuAsn 206
 Db 686 CTGTGTACAGCCGGAACATCTAGCTGTAAACCTTCTGAAAGCTCGGACCTGAC 745
 Qy 207 IleSerGlnHisGlySerAspMetGlnValSerPheAspHisAlaProHisAsnPheGly 226
 Db 746 ATCAGCAGAGATGCTGGACATCAGATGCTCTTCAACATGACCGCAACATTCGGC 805
 Qy 227 PheArgPhePheTyrLeuHisTyrLysLeuLysHisGlnGlyProPheLysArgThr 246
 Db 806 TTCCGTTCTTCTTCTTCTTCACTCAACAGCTCAAGCAGCAAGGACCTTCAAGCGAAGACC 865
 Qy 247 CyLeuGlnGlnThrThrGlnThrThrSerCyLeuLeuGlnAsnValSerProGly 266
 Db 866 TGTAAAGAGAGCAACTACAGAGACACAGCTGCTCTTCAAAATGTTCTCCAGGG 925
 Qy 267 AspTyrIleIleGlnLeuValAspAspThrAsnThrArgLysValMetHisTyrAla 286
 Db 926 GATTATATTAATGAGCTGGTGGATGACATTAACACAAAGAAAGATGATTAATGCC 985
 Qy 287 LeuLysProValHisSerProTrrPAlaGlyProIleArgAlaMetAlaIleThrValPro 306
 Db 986 TTAAAGCAGTGCATCCCGTGGCGCGGCGCCATCAGAGCCGTCATCACTCAGTGC 1045
 Qy 307 LeuValValIleSerAlaPheAlaThrLeuPheThrValMetCyAspGlyLysGln 326
 Db 1046 CTGTGTACATATCGGATTCGACCTCTTCACTGTGATGTCGCGAAGAACACAA 1105
 Qy 327 GlnAsnIleTyrSerHisLeuAspGlnGluSerSerGluSerSerThrTyrThrAla 346
 Db 1106 GAAATATATATTCATCACTTAAAGAGAGAGCTCTGAGCTTCCATCACTACGACGA 1165
 Qy 347 LeuProArgGlnArgLeuArgProArgProLysValPheLeuCyTyrSerSerLysAsp 366
 Db 1166 CTCCCAAGAGAGAGCTCCGGCGCGCGCGCAAGGCTTTCTCTGTATTCAGATTAAGAT 1225
 Qy 367 GlyGlnAsnHisMetAsnValAlaGlnCyPheAlaTyrPheLeuGlnAspPheCyGly 386
 Db 1226 GGCAGATATCAAGATGTGTCCAGTGTTCCTCACTTCCACGAGACTTGTGGC 1285
 Qy 387 CyGlnValAlaLeuAspLeuTrpGluAspPheSerLeuCyAspArgGlnGlyGlnArgGln 406
 Db 1286 TGTAGGTGGCTGTGGACCTGTGGAAAGACTTCAAGCTCTGTAGAAAGGCGAAGAA 1345
 Qy 407 TrpValIleGlnLysIleHisGluSerGlnPheIleValValCySerLysGlyMet 426
 Db 1346 TGGGTATCCAGAAATCCAGAGTCCAGTTCATATTCGTTGTTCCAAAGATATG 1405
 Qy 427 LysTyrPheValAspLysLysAsnTyrLysHisLysGlyGlyAlaArgLysSerGlyLys 446
 Db 1406 AAGTACTTGTGGCAAGAAAGACTCAAAACAAAGAGGTGGCCAGGCTCGGGAAA 1465
 Qy 447 GlyLysLeuPheLeuValAlaValSerAlaIleAlaGlnLysLeuArgGlnAlaLysGln 466
 Db 1466 GAGAGCTTCTTCTGTGGCGGTGTCCAGCATTCGCAAAAGCTCCCGCAGGCCAAGCAG 1525
 Qy 467 SerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSerCyGlnGly 486
 Db 1526 AGTTGTCGCGCGGCTCAGCAAGATTATCGCGCTTATGTTATTCCTGAGAGGA 1585
 Qy 487 AspValProGlyLysLeuAspLeuSerThrLysTyrArgLeuMetAspAsnLeuProGln 506
 Db 1586 GAGCTCCCGGTATCTTAAGACTGATACCAAGTACAGACTTCATGCAATCTTCTCAG 1645
 Qy 507 LeuCySerHisLeuHisSerArgAspHisGlyLeuGlnGlnLysProGlyGlnHisThrArg 526

QY 327 GluAsnIleTyrSerHisLeuAspGluGluSerGluSerSerThrThrAlaAla 346
 Db 1106 GAAATATATATATTCACATTATGATGAAAGAGCTCTGAGTCTTCACATACACGACGA 1165
 QY 347 LeuProAlaGluArgLeuArgProArgProIleValPheLeuCytyrSerSerIleAsp 366
 Db 1166 CTCCTCAAGAGAGAGCTCCGCGCGCGGAAAGTCTTCTCTGCTATTCCAGTAAAGAT 1225
 QY 367 GlyIleAsnHisMetAsnValValGlnCysPheAlaIlePheLeuGluAspPheCysGly 386
 Db 1226 GGCAGATACATGATGATGCTGACAGTTCGCTACCTTCCTCCAGACCTTCCTGCGC 1285
 QY 387 CysGluValAlaAlaAspLeuTTrpGluAspPheSerLeuCytyrGluGluValArgGlu 406
 Db 1286 TGTAGAGTGGCTCTGAGACTCTGAGAACTTCAGCTCTGTAAAGAGGCGCAGAGAA 1345
 QY 407 TrpValIleGlnIleValHisGluSerGlnPheIleIleValValCysSerIleGlyMet 426
 Db 1346 TGGGTATCCAGAAAGATCCAGAGTCCAGTTCATCATTTGTTTTCCTCCAAAGTATG 1405
 QY 427 LysTyrPheValAlaAspIleValAsnTyrIleHisIleGlyGlyArgGlySerGlyLys 446
 Db 1406 AAGTACTTGTGGAACAAGAACTACAAACAAAGAGGTTGGCCGAGGCTCGGAGAA 1465
 QY 447 GlyIleLeuPheLeuValAlaValSerAlaIleAlaGlyIleLeuArgGlnAlaLysGln 466
 Db 1466 GGAAGAGCTCTTCGTTGGCGGTGTCAAGCTTCGCAAAAGCTCCGCGCAGGCAAGAG 1525
 QY 467 SerSerSerAlaAlaLeuSerIlePheIleAlaValTyrPheAspTyrSerCysGluGly 486
 Db 1526 AGTTGCTCCGCGGCTCAGCAAGTATTCGCGCTTCTATCTTATTTCTTCGAGGGA 1585
 QY 487 AspValProGlyIleLeuAspLeuSerThrLysTyrArgLeuMetAspAsnLeuProGln 506
 Db 1586 GAGCTCCCGGTATCTTATGACTGATGATCAAGATCAAGATCAAGATCAAGATCAAG 1645
 QY 507 LeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGluProGlyGlnHisThrArg 526
 Db 1646 CTCGTGTTCCCACTGCACTCCCGAGACCAAGCCCTCCAGAGCGGCGGACACACGCGA 1705
 QY 527 GlnGlySerArgAsnTyrPheArgSerIleSerGlyArgSerIleTyrValAlaIle 546
 Db 1706 CAGGCGAGCAAGAACTACTCTCCGAGCAAGTCAAGCCGCTCCCTATAGCTGCCACT 1765
 QY 547 CysAsnMetHisGlnPheIleAspGluGluProAspTTrpPheGluLysGlnPheValPro 566
 Db 1766 TGCACATGCAACCAATTATGACGAGAGGCCCACTGCTCGAAAGCACTTCGTTCC 1825
 QY 567 PheHisProProProLeuArgTyrArgGluProValLeuGlnLysPheAspSerGlyLeu 586
 Db 1826 TTCATCTCTCTCACTGCGCTACCGGAGCCAGTCTTGAGAAATTTGAGGCTG 1885
 QY 587 ValLeuAsnAspValMetCysLysProGlyProGluSerAspPheCysLeuLysValGlu 606
 Db 1886 GTTTTAATATGATGATGTAACCAAGGCTTGAAGTACTTCTGCTTAAAGTGAAG 1945
 QY 607 AlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHisGluSerGlnHisGlyGly 626
 Db 1946 GCGGCTGTTCTTGGGGGCAACCGACACCACTCCAGCAGAGATCAGACATGGGGGC 2005
 QY 627 LeuAspGlnAspGlyGlyIleArgProAlaLeuAspGlySerAlaAlaLeuGlnProLeu 646
 Db 2006 CTGACCAAGACGCGGAGCGCGGCTGCTTGAAGTACGCGGCTCCCAACCCCTG 2065
 QY 647 LeuHisThrValIleValIleGlySerProSerAspMetProArgAspSerGlyIleTyrAsp 666
 Db 2066 CTGACACGAGTGAAGCGGAGCGCGCTCCGACATGCGCGGACTCAGGATCTATGAC 2125
 QY 667 SerSerValProSerSerGluLeuSerLeuProLeuMetGluGlyLeuSerThrAspGln 686
 Db 2126 TCGTCTGCGCTCATCCGAGCTGTCTGCACTGATGAGAAAGACTTCCACGAGCAG 2185

QY 687 ThrGluThrSerSerLeuThrGluSerValSerSerSerSerGlyLeuGlyGluGlu 706
 Db 2186 ACAGAAACGCTCTTCTCGAGAGAGAGCTGTCTCTCTTCAAGGCTCGGGAGAGAGAA 2245
 QY 707 ProProAlaLeuProSerIleValLeuSerSerGlySerCysValAlaAspLeuGlyCys 726
 Db 2246 CTTCTCCCTCTCTCTTCCAGAGCTCTCTCTTCTGCGGATCAGCAAGAGATCTTGCTGC 2305
 QY 727 ArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
 Db 2306 CGCAGCTTACACTGATGAACTCCACGCGCGCCCT 2341
 RESULT 12
 US-10-717-282-4
 ; Sequence 4, Application US/10717282
 ; Publication No. US20040077052A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Kuestner, Rolf E.
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Human Cytokine Receptor
 ; FILE REFERENCE: 00-49
 ; CURRENT APPLICATION NUMBER: US/10/717,282
 ; CURRENT FILING DATE: 2003-11-19
 ; PRIOR APPLICATION NUMBER: US/09/912,157
 ; PRIOR FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 2383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (86) ... (2344)
 US-10-717-282-4
 Alignment Scores:
 Pred. No.: 0 Length: 2383
 Score: 3891.00 Matches: 732
 Percent Similarity: 97.5% Conservative: 1
 Best Local Similarity: 97.3% Mismatches: 5
 Query Match: 98.6% Indels: 14
 DB: 7 Gaps: 1
 US-10-616-788-2 (1-738) x US-10-717-282-4 (1-2383)
 QY 1 MetAlaProTrpLeuGlnLeuCysSerValPhePheThrValAsnAlaCysLeuAsnGly 20
 Db 86 ATGGCCCCGTTGGCTGAGCTGTCTCTCTCTTTCAGGTCACAGCCTGCTTACGCGC 145
 QY 21 SerGlnLeuAlaValAlaAlaGlyIleSerGlyArgAlaIleTrpGlyValAspThrCysGly 40
 Db 146 TCGAGCTGGCTGTGGCGCTGTGGCGGCTCGGCGCGCGCGCGCGCGCGCGCGCACTGTGCG 205
 QY 41 TrpArg-----GlyValGlyPro 46
 Db 206 TGGAGATGAAAGCGGCTGCCGACCCGCGCTTGTGTCTATGAGGAGTGGGGCCA 265
 QY 47 AlAserArgAsnSerGlyLeuTyrPheIleThrPheLysTyrAspAsnCysThrThrTyr 66
 Db 266 GCGCAGCAAAACAGTGGCTGTACACATCACTTCAAAATATGACATTTGTATCACCACTAC 325
 QY 67 LeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsnIleThrIleSerGlnTyr 86
 Db 326 TTGAATCAATGGGGAAGCATGTGATTTCTGACGCCCAAGATATCACATCAAGCACTAT 385
 QY 87 AlaCysHisAspGlnValAlaValThrIleLeuTyrSerProGlyAlaLeuGlyIleGlu 106
 Db 386 GCTTGCATACCAAGGAGGAGTCAACATCTTTGATCCCAAGGGGCGCTCGCATCGAA 445
 QY 107 PheLeuLysGlyPheArgValIleLeuGlnGluLeuLysSerGluGlyArgGlnCysGln 126

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1662)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (82)..(1)
 OTHER INFORMATION:
 US-10-343-348-15

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0	3857.00	4392	732	1	5	4	0
Percent Similarity:	98.8%						
Best Local Similarity:	98.7%						
Query Match:	97.7%						

US-10-616-788-2 (1-738) x US-10-343-348-15 (1-4392)

QY 1 MetAlaProTrieuGlnLeuCySerValPhePheThrValAlaAlaCyAlaLeuAnGly 20
 DB 1 ATGGCCCCGCGGCGAGCTCTGCTCCGCTCTTACGGTCACAGCCTGCTCAAGGCG 60
 QY 21 SerGlnLeuAlaValAlaAlaGlySerGlyValArgAlaTrpGlyValAspThrCyGly 40
 DB 61 TCGAGCTGCGTGGCGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyraAlaIleThrPheLeuTyr 60
 DB 121 TGGAGGGGAGTGGGCG 180
 QY 61 AspAsnCySerThrTrpTyrLeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsn 80
 DB 181 GACATATGTACCACTACTTGAATCCAGTGGGAAGCATGTGCTGACGCCAGAT 240
 QY 81 IleThrIleSerGlnTyrAlaCyHisAspGlnValAlaValIleThrIleLeuTrpSerPro 100
 DB 241 ATCCACATCAGCCAGTATGCTTGCATGACCAAGTGCAGCATCTTTGGTCCCA 300
 QY 101 GlyAlaLeuGlyIleGlnPheLeuLysGlyPheArgValIleLeuGlnGlnLeuLysSer 120
 DB 301 GGGGCGCTCGGCGATCGAATTCCTGAAGGATTTGGGTAATCTGGAGAGCTGAAGTCG 360
 QY 121 GlnGlyArgGlnCySerGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
 DB 361 GAGGGAAGACAGTGCACCAACTGATCTMAAGATCCGAAGCAGCTCAACAGTAAGCTTC 420
 QY 141 LysArgThrGlyMetGlySerGlnProPheLeuAsnMetLysPheGlnLysThrAspTyrPhe 160
 DB 421 AAAAGAACTGAATGGAATCTCAACTTCTGAAATGAAATTTGAAACGAGTATATTC 480
 QY 161 ValLysValValProPheProSerIleLysAsnGlnSerAsnTyrHisProPhePhePhe 180
 DB 481 GTAAAGGTGTCCCTTTTCTTCATTAAGAAAGCAATTAACACCCTTTCTTCTT 540
 QY 181 ArgThrArgAlaCyAspLeuLeuLeuGlnProAspAsnLeuAlaCyLysProPheTrp 200
 DB 541 AGAAGCCGAGCTGTGACCTGTTGTTACAGCCGAGCAATGAGTTGTAACCTTCTG 600
 QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 DB 601 AAGGCTCGAAGCTGAACATGACGACAGCTGCTCGACATGACGAGTGTCTCTGACCAT 660
 QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuLysHisGlyGly 240
 DB 661 GCACCGCAACTTCGCTTCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 720
 QY 241 ProPheLysArgLysThrCyLysGlnGlnGlnThrGlnLysThrSerCyLeuLeu 260
 DB 721 CTTTCAAGGAAAGACCTGTAGCAGAGCAAACTACAGAGACGACAGCTGCTCTCTT 780

QY 261 GlnAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrTrpThrArg 280
 DB 781 CAATATTTTCTCCAGGGGATTTATATATATGAGCTGTGTGATGACATTAACACACAGA 840
 QY 281 LysValMetHisTyrAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAla 300
 DB 841 AAGATGATCATTAATGCTTAAAGCCAGTGCATCCCGGTGGGCGGCGCATCAGAGCC 900
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 DB 901 GTGGCCATTCACAGTGCACGTGTAGTATATCGCATTCGCGACCTCTTCACTGTATG 960
 QY 321 CyAspArgLysGlnGlnGlnGlnIleTyrSerHisLeuAspGlnGlnSerGlnSer 340
 DB 961 TGGCGAAGAGCAACAGAAATATATATTCATTAATGAGAGAGCTCTGAGTCT 1020
 QY 341 SerThrTyrThrAlaAlaLeuProArgGlyArgLeuArgProArgProLysValPheLeu 360
 DB 1021 TCCACATACACTGACAGACTCCCAAGAGAGGCTCCGCGCGCGCGCGAGTCTTCTC 1080
 QY 361 CyAspTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCyPheAlaTyrPhe 380
 DB 1081 TGCTATTCAGTAAGATGCGCAGAAATCAGATGATGTCTCCAGTGTTCGCTACTTC 1140
 QY 381 LeuGlnAspPheCySerGlyCySerGlyValAlaLeuAspLeuTrpGlnAspPheSerLeuCy 400
 DB 1141 CTCGAGACTTCGTGCTGTAGGTGGCTTGTGACCTGTGGAGAGACTTCAGCTCTGT 1200
 QY 401 ArgGlnGlyGlnArgGlnTrpValIleGlnLysAlaHisGlnSerGlnPheIleVal 420
 DB 1201 AGAAGAGGCGAGAGAGATGGGTATCCAGAGATCCAGAGTCCAGCTTCATCATTTGTG 1260
 QY 421 ValCySerSerLysGlyMetLysTyrPheValAspLysValAsnTyrLysHisGlyGly 440
 DB 1261 GTTGTTCAGAAAGTATGAAATCTTTGTGCAAGAGAACTAACAACCAAGAGAGGT 1320
 QY 441 GlyArgLysSerGlyLysGlyLysPheLeuValAlaValSerAlaIleAlaGlnLys 460
 DB 1321 GGGCGAGGCTCGGAGAAAGAGCTTCTGTGGCGGTGTGAGCATTTGCGAAG 1380
 QY 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 DB 1381 CTCGCGAGGCCAAGAGAGATTCGTCCGCGGCTCAGCAAGTTTATCGCGCTTACTTT 1440
 QY 481 AspTyrSerCySerGlnLysAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500
 DB 1441 GATTAATCTCGCAGGAGAGAGTCCCGGTATCTGAGACTGAGTACCAAGTACAGACTC 1500
 QY 501 MetAspAsnLeuProGlnLeuCySerHisLeuHisSerArgAspHisGlyLeuGlnG 520
 DB 1501 ATGACAAATCTTCTCAAGCTGTGTTCCACTGTGCACTCCAGACACAGGCTTCAGG 1560
 QY 520 LysProGlyGlnHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerG 539
 DB 1561 AGCCGGGAGCATGACAGCGCACAGGCGAGAGAGAACTACTCTCCGAGCAAGTACAG 1620
 QY 539 YargSerLeuTyrValAlaIleCyAsnMetHisGlnPheIleAspGlnLysProAspTyr 559
 DB 1621 CCGGTCCCTATAGCTGCGCATTTGCAACATGACAGCTGATTAATGACAGAGCCGACTG 1680
 QY 559 PheGlnLysGlnPheValProPheHisProProProLeuAspTyrArgGlnLysProVal 579
 DB 1681 GTTCGAAGACAGATGCTTCCCTTCCATCTCTCCAGTGGCTGACGGGAGGCAAGTCTT 1740
 QY 579 uGlnLysPheAspSerGlyLeuValLeuAsnAspValMetCyLysProGlyProGln 599
 DB 1741 GAGAAATTTGATTCGGGCTGTGTTTAATGATGATGATGATGAAACAGGCGCTGAGAG 1800
 QY 599 AspPheCyLeuLysValAlaLysProValLeuGlyAlaThrGlyProAlaAspSerG 619
 DB 1801 TGACTTCTGCTAAAGATGAGCGGCTGTCTTGGGGCAACCGGACACAGCTCCCA 1860
 QY 619 HisGlnSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspG 639


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Db      1027 TGGCGAGAGAGCAAGAAATATATATATTCATTAGATGAGAGAGCTCGAGCTT 1086
Qy      341 SerThrTyThrAlaAlaLeuProArgGluArgLeuArgProArgProValPheLeu 360
Db      1087 TCCACATACCTGACAGACTCCCAAGAGAGAGCTCCGCGCGCGCGAGAGCTTTCTC 1146
Qy      361 CybTySerSerIysAspGluGlnAsnHisMetAsnValValGlnCybPheAlaTyPhe 380
Db      1147 TGCATTTCAGTAAAGATGGCAGAAATCAATGATGCTGCTCACTGCTTCTTC 1206
Qy      381 LeuGlnAspPheCybGlyCybGluValAlaLeuAspLeuTrpGluAspPheSerLeuCyb 400
Db      1207 CTCAGAGACTTCTGTGCTGTGAGAGTGGCTCTGAGACTGTGAGAGACTTCAGCTCTCT 1266
Qy      401 ArgGluGlnArgGluTrpValIleGlnIysIleHisGlnSerGlnPheIleVal 420
Db      1267 AGAGAGGAGAGAGAGATGGGTATCATCAGAAAGATCCAGAGTCCAGTTTATCATTTGTG 1326
Qy      421 ValCybSerIysGlyMetIleTybPheValAspIlyAsnTybTybHisIleGlyGly 440
Db      1327 GTTGTTCAGAGATGATAGTACTTGTGTGAGCAAGAGAACTAACAAACMAAGAGAGT 1386
Qy      441 GlyArgGlySerGlyIysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluIys 460
Db      1387 GCGCGAGGCTCGGGAGAGAGAGCTTCTGTGCGGTGCGGTGATGCCATTGCCGAAAG 1446
Qy      461 LeuArgGlnAlaIysGlnSerSerSerAlaAlaLeuSerIysPheIleAlaValTybPhe 480
Db      1447 CTCGCGAGGCGCAAGAGAGTGTGCTCGCGCGCTCAGCAAGTTTATCGCGTCTACTT 1506
Qy      481 AspTySerCybGluGlyAspValProGlyIleLeuAspLeuSerThrTybTybArgLeu 500
Db      1507 GATTATTCCTCGCGAGAGAGCTCCCGGTATCTTAACCTGAGTACCAAGTACAGACTC 1566
Qy      501 MetAspAsnLeuProGlnLeuCybSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
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Qy      601 PheCybLeuIysValGluAlaProValIleGlyValaThrGlyProAlaAspSerGlnHis 620
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Qy      621 GluSerGlnHisGlyGlyLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640
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RESULT 15

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US-10-749-144-9
; Sequence 9, Application US/10749144
; Publication NO. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; PRIORITY FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
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Matches: 722
Conservative: 3
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US-10-616-788-2 (1-738) x US-10-749-144-9 (1-2786)

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Search completed: March 1, 2006, 08:12:27
Job time : 1349 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 07:09:05 ; Search time 2424 Seconds
(without alignments) 667.481 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
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Searched: 7218512 seqs, 109618070 residues

Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Database : Published Applications NA New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3706	93.9	2894 9 US-11-072-512-1429	Sequence 1429, Ap
2	325	8.2	612 6 US-09-925-065A-50990	Sequence 50990, A
3	325	8.2	612 6 US-09-925-065A-50991	Sequence 50991, A
4	325	8.2	2387 6 US-09-925-065A-672368	Sequence 672368,

5	254	6.4	539 6 US-09-925-065A-829666	Sequence 829666,
6	225	5.7	1385 8 US-10-750-185-36133	Sequence 36133, A
7	225	5.7	1385 8 US-10-750-623-36133	Sequence 36133, A
8	151.5	3.8	1365 8 US-10-750-185-50374	Sequence 50374, A
9	151.5	3.8	1365 8 US-10-750-623-50374	Sequence 50374, A
10	135.5	3.4	1701 5 US-09-978-360A-33	Sequence 33, Appl
11	135	3.4	1515 7 US-10-063-703-157	Sequence 157, App
12	135	3.4	1515 12 US-11-102-220-157	Sequence 157, App
13	118	3.0	1001 9 US-11-204-111-244	Sequence 244, App
14	116.5	3.0	16382 12 US-11-108-172-1112	Sequence 1112, Ap
15	116.5	3.0	16382 12 US-11-000-688-239	Sequence 239, App
16	112.5	2.8	3280 8 US-10-821-234-167	Sequence 167, App
17	112	2.8	1001 9 US-11-204-111-245	Sequence 245, App
18	109	2.8	3805 8 US-10-510-524-2	Sequence 2, Appl
19	109	2.8	3805 8 US-10-955-054A-144	Sequence 144, App
20	109	2.8	3805 9 US-11-245-147-170	Sequence 170, App
21	106.5	2.7	1400 12 US-11-136-527-6247	Sequence 6247, Ap
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23	105	2.7	4768 8 US-10-719-111-1	Sequence 1, Appl
24	104.5	2.6	2714 8 US-10-918-857-1	Sequence 1, Appl
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28	104	2.6	3805 9 US-11-245-147-214	Sequence 214, App
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30	104	2.6	88421 12 US-11-205-109-1	Sequence 1, Appl
31	103.5	2.6	2948 7 US-10-918-857-9	Sequence 9, Appl
32	103.5	2.6	3038 7 US-10-922-166-19	Sequence 19, Appl
33	103.5	2.6	3038 8 US-10-918-857-5	Sequence 5, Appl
34	103.5	2.6	6820 7 US-10-922-166-14	Sequence 14, Appl
35	103.5	2.6	116856 12 US-11-143-980-1	Sequence 1, Appl
36	102	2.6	4558 9 US-11-177-894-4	Sequence 4, Appl
37	101	2.6	4400 12 US-11-136-527-1982	Sequence 1982, Ap
38	101	2.6	4767 12 US-11-145-035-23	Sequence 23, Appl
39	101	2.6	5265 12 US-11-122-329-81	Sequence 81, Appl
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41	100.5	2.5	2070 9 US-11-040-218-30	Sequence 30, Appl
42	100.5	2.5	2070 9 US-11-040-218-32	Sequence 32, Appl
43	100.5	2.5	3073 12 US-11-113-424-11	Sequence 11, Appl
44	100.5	2.5	4195 9 US-11-075-047A-5	Sequence 5, Appl
45	100.5	2.5	4195 12 US-11-076-427A-11	Sequence 11, Appl

ALIGNMENTS

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Sequence 1429, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SERI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKUJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978

PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1429
LENGTH: 2894
TYPE: DNA
ORGANISM: Homo sapiens
US-11-072-512-1429

Alignment Scores:
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Score: 3706.00 Matches: 694
Percent Similarity: 99.7% Conservative: 2
Best Local Similarity: 99.4% Mismatches: 2
Query Match: 93.9% Indels: 0
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US-10-616-788-2 (1-738) x US-11-072-512-1429 (1-2894)

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DB 1170 TGCTATTCAGTAAAGATGGCCAGAAATCAATGATGTGCTCAAGTGTTCGCTACTTC 1229
QY 381 LEUGLAPRPHCYSGLYCYSGILVALALEUAAPRLEUTRGLUAPRPHESERLEUCY 400
DB 1230 CTCACGACTTCTGTGGCTGTGAGTGGCTGTGACCTGTGGAGAACCTTCACTCTGT 1289
QY 401 ARGGLUGLYGAPRGLUTRVALILEGLINLVSHISGLUSERGLNPHLEILEVAL 420
DB 1290 AGAGAAAGGAGAGAAATGGATCATCCAGAAATCCAGAGTCCAGTTCATATTG 1349
QY 421 VALCYSESERLYSGLYMEGLYTRPHEVALAPRPLYASANTYRISHISLYSGLY 440
DB 1350 GTTTGTTCCAAAGTATGAAATCTTTGTGGAACAAGAACATCAACAACAAGAGGT 1409
QY 441 GLYARGLYSERGLYSGLYGILEUPHELEUVALALEVALSERALALEGLULY 460
DB 1410 GCGCGAGCTCGGGGAAAGAGAGCTTCTGTGGTGGCTGTCAACCTTCGGAAG 1469
QY 461 LEUAARGLALAYEGLINSETHSERVALALEUSERLYPHELEVALATYRPH 480
DB 1470 CTCGCCAGGCCAAGAGATGCTCGCGGCGCTCAGCAAGTTATCGCGTACTT 1529
QY 481 APPTYSERCYSGILUGLYAPRVALPROGLYILEUAAPRSETHRYTYRATYLEU 500
DB 1530 GATTATTCCTGCGAGGAGAACGTCCTCCGATCTGAGCTGATCCAAAGTACAGATC 1589
QY 501 METAPRANLEUPROGLINLEUCYSETHILEUHIISERARGAPHIISGLYLEUGL 520
DB 1590 ATGACAAATCTTCTCAGCTCTGTCCCACTCCAGCCAGAACCAAGCCCTCCAGAG 1649
QY 521 PROGLYGLNHIISHRTRXGGLNGLYSEARGARGASNTYRPHARGSERLYSERGLYARG 540
DB 1650 CCGGGGAGCAGCAGCAGAGGCGAGAGGAAGTACTTCCGAGCAAGTACAGCGCG 1709
QY 541 SERLEUTRYVALALECYAANMECHISGLNPHILEAPGLUGLUPROAPRTYRPH 560
DB 1710 TCCCTATACGTCCCATTTGCAACATGACCAATTTATGACAGAGCCCACTGGTT 1769
QY 561 GLULYEGLINPHEVALPROPHETIAPROPROLEUAARGTYRARGLUPROVALLEUG 580
DB 1770 GAAAGGAGTTCCTTCCTTCCATCTCTCCACTCGCTACCGGAGCGAGCTTGGAG 1829
QY 581 LYEPHEAPRSETHYLEUVALLEUAANAPRVALMECYLYAPRPROGLYUSERAS 600
DB 1830 AAATTTGATTCGGGCTTGTGTTTAAATGATGATGTGCAAAACAGAGGCTTGAGAGT 1889
QY 601 PHECYLEUVALAGLUALAPROVALILEUGLYALATHRGLYPROLAPRSETHIS 620
DB 1890 TTCTGCTTAAAGTAAAGGCGGCTGTCTTGGGCAACCGGACCAAGCTCCAGCAC 1949
QY 621 GLUSERGLNHIISGLYGLYLEUAAPRGLYGLUALAARGPROLALAEUAAPGLYSE 640
DB 1950 GAGAGTCAGATGGGGCTGTGACCAAGAGGAGGCGCGCTGCTGACGATGAC 2009
QY 641 ALALALEUGLINPROLEUENHISHTHRVALGLYALGLYSEPROSERAPRMECTPROARG 660
DB 2010 GCGGCCCTTGCAACCTCTGTGCAACGAGTAAAGCGGAGCGCTTCGACATGCGCGG 2069
QY 661 APPSERGLYLETYRAPHSESERVALPROSESERGLUENUSERLEUPROLEUMETGL 680

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Db 2070 GACCAAGCATATGATGCTGTGTGCTCCATCCAGCTGTCTTCCCATATGAA 2129
Qy 681 G1yleuSerThraapGlnthrglnthSerSerleuthrglnSerSerSer 700
Db 2130 GAACTCTCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2189
Qy 701 G1yleuG1ylg1ug1ug1ug1ug1ug1ug1ug1ug1ug1ug1ug1ug1ug 720
Db 2190 GGCCTGGGTGAGGAGAACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2249
Qy 721 LysH1aAspleuG1yCySargSerTyThraapG1uLeuH1aVala1aPro 738
Db 2250 AAGCAATCTTGTGTCGCCGACGACGACGACGACGACGACGACGACGAC 2303

RESULT 2
US-09-925-065A-50990
; Sequence 50990, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50990
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-50990

Alignment Scores:
Pred. No.: 1.62e-20 Length: 612
Score: 325.00 Matches: 68
Percent Similarity: 55.7% Conservative: 5
Best Local Similarity: 51.9% Mismatches: 54
Query Match: 8.2% Indels: 54
Gaps: 2
DB: 6

US-10-616-788-2 (1-738) x US-09-925-065A-50990 (1-612)
Qy 153 MetLysPheGlnthraapTyrrPheValVala1aProPheProSerIleLysAnglu 172
Db 9 CTAATACTAAACATGATCTTATCTCTTAATA----- 44
Qy 173 SerAsnTyrtHisProPhePheArgThraG1aCySAspleuLeuLeuGlnProasp 192
Db 45 -----GCTGTGACCTGTGTTACAGCCGAC 71
Qy 193 AsnLeuA1aCySylsProphe----- 199
Db 72 AACTAGCTGTAAACCTG-TAAGTAATAGTGTCTTATCTATCAAGTCAAGATATC 130
Qy 199 ----- 199
Db 131 GCCACTATGATGCTGTAGGAGCTCTGCTGCTCATCTGGGCTCTTACTTTTCCA 190
Qy 200 ---TrrLysProArgAsnLeuAen1leSerglnH1eG1ySerAspMetGlnValSerPhe 218
Db 191 GTCGGAAGCTCTCGAAGCTGGAACATCAAGCAGATGCTCGACATGCAAGGTCTTTC 250

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Qy 219 AspH1a1aProH1aAsnPhleg1yPheArgPhePheTyrluH1eTyrrlyLysLysH1s 238
Db 251 GACCAYGACCGACCAACTTCGCTTCGCTTCCTTCTTATCTTCACTAAGCTCAAGCAC 310
Qy 239 GluG1yProPheLysArgLysThrCySylsGln 249
Db 311 GAAGACCTTTCAGGCAAGAAAGCTGTACAG 343

RESULT 3
US-09-925-065A-50991
; Sequence 50991, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50991
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-50991

Alignment Scores:
Pred. No.: 1.62e-20 Length: 612
Score: 325.00 Matches: 68
Percent Similarity: 55.7% Conservative: 5
Best Local Similarity: 51.9% Mismatches: 54
Query Match: 8.2% Indels: 54
Gaps: 2
DB: 6

US-10-616-788-2 (1-738) x US-09-925-065A-50991 (1-612)
Qy 153 MetLysPheGlnthraapTyrrPheValVala1aProPheProSerIleLysAnglu 172
Db 9 CTAATACTAAACATGATCTTATCTCTTAATA----- 44
Qy 173 SerAsnTyrtHisProPhePheArgThraG1aCySAspleuLeuLeuGlnProasp 192
Db 45 -----GCTGTGACCTGTGTTACAGCCGAC 71
Qy 193 AsnLeuA1aCySylsProphe----- 199
Db 72 AACTAGCTGTAAACCTG-TAAGTAATAGTGTCTTATCTATCAAGTCAAGATATC 130
Qy 199 ----- 199
Db 131 GCCACTATGATGCTGTAGGAGCTCTGCTGCTCATCTGGGCTCTTACTTTTCCA 190
Qy 200 ---TrrLysProArgAsnLeuAen1leSerglnH1eG1ySerAspMetGlnValSerPhe 218
Db 191 GTCGGAAGCTCTCGAAGCTGGAACATCAAGCAGATGCTCGACATGCAAGGTCTTTC 250
Qy 219 AspH1a1aProH1aAsnPhleg1yPheArgPhePheTyrluH1eTyrrlyLysLysH1s 238
Db 251 GACCAYGACCGACCAACTTCGCTTCGCTTCCTTCTTATCTTCACTAAGCTCAAGCAC 310
Qy 239 GluG1yProPheLysArgLysThrCySylsGln 249

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Db      311  GAGGACCTTTCAGCGAAGACCTGTAGCAG  343
RESULT 4
US-09-925-065A-672368
; Sequence 672368, Application US/09925065A
; Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 672368
LENGTH: 2387
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-672368

Alignment Scores:
Pred. No.: 9,21e-20 Length: 2387
Score: 325.00 Matches: 68
Percent Similarity: 55.74 Conservative: 5
Best Local Similarity: 51.94 Mismatches: 5
Query Match: 8.2% Indels: 54
DB: Gaps: 2

US-10-616-788-2 (1-738) x US-09-925-065A-672368 (1-2387)
QY      153  MelysPhegIuThAspTyRPhelAllysValLProPheProSerIleLysAsnGlu  172
      :::::  :::::  :::::  :::::
Db      1784  CTAAACCTPAAACACATGATCTTATCTCTTAATA-----  1819
QY      173  SerAenTyRHIsProPhePhePheArgThxArgAlaCyAsPLeuLeuGlnProksp  192
      :::::  :::::  :::::  :::::
Db      1820  -----GCTGTGACCTGTGTTTACAGCGCGAG  1846
QY      193  AsnLeuAlaCybLysProPhe-----  199
      |||||  |||||  |||||
Db      1847  AATCTAGCTTGTAACCTCG- TAACTAATAGTCTTATCTATCAAGTTCAAAGTATC  1905
QY      199  -----  199
Db      1906  GCCACTATGATGTTAGGGGTAGCGCTGTGGTGTCTCACTGGGTCTTACTTCTTCCA  1965
QY      200  ---TTPLyProCArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPhe  218
Db      1966  GTCTGGAGGCTTCGGAAACCTGACATCAAGCAGCATGCTGGACATCAAGGTGCTTC  20353
QY      219  AspHisAlaProHisAsnPheGlyPheArgPhePheTyLeuHisTyLeuLeuLysHis  238
Db      2026  GACCATGACCGCACACACTTGCGGTCTTCGTTCTTCTTCACTACCAAGTCAAGCAC  20855
QY      239  GluGlyProPheLysArgLysThrCybLysGln  249
Db      2086  GAAGGACCTTTCACAGCGAAGACCTGTAGCAG  2118
RESULT 5
US-09-925-065A-829666
; Sequence 829666, Application US/09925065A

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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 829666
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-829666

Alignment Scores:
Pred. No.: 6.4e-14 Length: 599
Score: 254.00 Matches: 56
Percent Similarity: 51.3% Conservative: 5
Best Local Similarity: 47.1% Mismatches: 5
Query Match: 6.4% Indels: 54
DB: Gaps: 2

US-10-616-788-2 (1-738) x US-09-925-065A-829666 (1-599)
QY 153 MethylPhegIuThAspTyrPheAlaValProPheProSerIleLysAenGlu 172
DB 299 CTAACACTAAACAACTGATATCTTATCTCTTAATA----- 334
QY 173 SerAnTyGnIserProPhePhePheAgtThArgAlaCyAsPLeuLeuGlnProAer 192
DB 335 -----GCCTGGACTGTGTGTTACAGCGGAGC 361
QY 193 AsnLeuAlaCyVlyserProPhe----- 199
DB 362 AATCAGCTGTAAACCTG- TAAAGTAATAGTCTTATCTATCAAGTCAAGTATC 420
QY 199 ----- 199
DB 421 GCCACTATGATGGTGTAGGGTAGGCTCTGTGTCTCACTGGGCTCACTCTTCCA 480
QY 200 ---TTPlySProAgtAsnLeuAsnIleSerGlnIsgLySerAspMetGlnValSerPhe 218
DB 481 GTCTGGAAGCTTCGGAACTCTGAACATCAAGCCAGCATGCTCGGACATGCAAGGTCTTCT 540
QY 219 AspHisAlaProHisAsnPheGlyPheAgtPhePheTyGLeuHisTyxLyLeuLys 237
DB 541 GACCATGACCGGACCAACTTCGGCTTCGTTCTTATCTTCACTCAAGGTCAG 597

RESULT 6
US-10-750-185-36133
; Sequence 36133, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PAMTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

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FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36133
LENGTH: 1385
TYPE: DNA
ORGANISM: Bovine 19866881362247
US-10-750-185-36133

Alignment Scores:
Pred. No.: 9.34e-11 Length: 1385
Score: 225.00 Matches: 41
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 95.3% Mismatches: 0
Query Match: 5.7% Indels: 0
DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x US-10-750-185-36133 (1-1385)

Cy 62 AsnCyThrThrTyLeuAsnProValGlyYshHisValIleAlaAspAlaGlnAsnIle 81
Db 824 GACTGCACCACTTACTTGAATCCAGTGGGAGACATGATGCTGACGCCAGAACATC 883
Cy 82 ThrIleSerGlnTyAlaCyshHisAspGlnValAlaValThrIleLeuTrpSerProGly 101
Db 884 ACCATCAGTCAGTATGCTGCGACAGCACCAAGTGGCTGCACCATCTTGTGTCCTCCGGG 943
Cy 102 Alaleugly 104
Db 944 GCCCTCGGT 952

RESULT 7
US-10-750-623-36133
Sequence 36133, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36133
LENGTH: 1385
TYPE: DNA
ORGANISM: Bovine 19866881362247
US-10-750-623-36133

Alignment Scores:
Pred. No.: 9.34e-11 Length: 1385
Score: 225.00 Matches: 41
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 95.3% Mismatches: 0
Query Match: 5.7% Indels: 0
DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x US-10-750-623-36133 (1-1385)

Cy 62 AsnCyThrThrTyLeuAsnProValGlyYshHisValIleAlaAspAlaGlnAsnIle 81
Db 824 GACTGCACCACTTACTTGAATCCAGTGGGAGACATGATGCTGACGCCAGAACATC 883
Cy 82 ThrIleSerGlnTyAlaCyshHisAspGlnValAlaValThrIleLeuTrpSerProGly 101
Db 884 ACCATCAGTCAGTATGCTGCGACAGCACCAAGTGGCTGCACCATCTTGTGTCCTCCGGG 943
Cy 102 Alaleugly 104
Db 944 GCCCTCGGT 952
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Db 824 GACTGCACCACTTACTTGAATCCAGTGGGAGACATGATGCTGACGCCAGAACATC 883
Cy 82 ThrIleSerGlnTyAlaCyshHisAspGlnValAlaValThrIleLeuTrpSerProGly 101
Db 884 ACCATCAGTCAGTATGCTGCGACAGCACCAAGTGGCTGCACCATCTTGTGTCCTCCGGG 943
Cy 102 Alaleugly 104
Db 944 GCCCTCGGT 952

RESULT 8
US-10-750-185-50374
Sequence 50374, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50374
LENGTH: 1365
TYPE: DNA
ORGANISM: Bovine 19866881634056
US-10-750-185-50374

Alignment Scores:
Pred. No.: 0.000636 Length: 1365
Score: 151.50 Matches: 62
Percent Similarity: 39.1% Conservative: 42
Best Local Similarity: 23.3% Mismatches: 119
Query Match: 3.8% Indels: 43
DB: 8 Gaps: 9

US-10-616-788-2 (1-738) x US-10-750-185-50374 (1-1365)

Cy 296 GlyProIleArgAlaMetAlaIleThrValProLeuValVal----- 309
Db 314 GGGATATTTCCTCTGCGAGTAGTAACACTTGAATGCTACAGCCAGCGTCCCTGACA 373
Cy 310 -----IleSerAlaPheAlaThrLeuPheThrValMetCyArgLyValGlnGln 326
Db 374 AGGGGTCATTATCTGCCATGAGTTTGCAGTCGGCGTGAAGCTTACTGCTGTCGAGA 433
Cy 327 GluAsnIleTySerHisIleAspGlnGluSerSerGlnSerThrTyThrAlaAla 346
Db 434 GATGACATTAATGCTTCTCTCCGCCACAGAAAGATCAAGAACTTCTTCAATACC 493
Cy 347 LeuProArgLysLeuArgProArgProArgProValPheLeuCyTySerSerLysAsp 366
Db 494 -----ACGTAATGCTCTCCATTAAGGTTTGTGTGTTACCTTCTGAAATA 541
Cy 367 GlyGlnAsnHisMetAsnValValGlnCyPheAlaTyPheLeuGlnAspPheCyGly 386
Db 542 TGCTTCATCAGC-----ACAGTTTGTACTTACGATGAGTTTCTTCAAAACCGTCGAGA 595
Cy 387 CysGluValAlaLeuAspLeuTyGluAspPheSerLeuCyArgGluGlnArgGlu 406
Db 596 AGTGAACTTATCTTGAAGATGCGCAGAAAAGAAATACCGAGATGGGTCCCGTCAG 655
Cy 407 TrpValIleGlnLysIleHisGluSerGlnPheIleIleValValCySerLysGlyMet 426
Db 656 TGGCTTACCACTCAGAAAGACAGCGGATGAAGTATTTCTTCTTTCATGATGATAC 715
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Qy 427 LyeTyrPheValAspLysLysAsnTyrLysHISLysGlyLysArgLysSerGlyLys 446
Db 716 ACC-----ACGTGCATGTTACTGTGACGAGAAAGAGGGCCCTGTGAGAGCTCC 769
Qy 447 GLyGluPhePheValAlaValSerAlaIleAlaGluLysValArgLysAlaLysGln 466
Db 770 CGAGACTGTTCCACTCGCTTTAACTCTTTCGAGTATCTGAG----- 817
Qy 467 SerSerSerAlaAlaLysSerLysPheIleAlaValTyrPheAspTyrSerCyseGluGly 486
Db 818 ---AGCCAGGCTCATCTGCAAAATACGTGTGCTTACTTACAG-----GAGGGT 865
Qy 487 AspValProGly-----IleLeuAspLysSerThrLysTyrArgLysMetAspAsn 503
Db 866 GACATCCGACAGACCTACAGGGCACTACGCTGTGCCCCACGTACCGCTTCACAGAGAC 925
Qy 504 LeuProGlnLeuCyseSerHISLysHISerArgAspHISGlyLeuGlnIleProGlyGln 523
Db 926 GCTACAGGTTTCTGTGAGAG-----CTCCCTCCGTCGCAAGCAG 964
Qy 524 HIEThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyr 543
Db 965 CATGTGTGCGTGGGAGAGAG-----TCACGCACTGTCTCAC 1000
Qy 544 ValAlaIleCyseAsnMet 549
Db 1001 TACAGCTGTGCTCTCTG 1018

RESULT 9

US-10-750-623-50374
; Sequence 50374, Application US/10750623
; Publication No. US2005028753A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50374
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Bovine 19866881634056
US-10-750-623-50374

Alignment Scores:

Pred. No.: 0.00636 Length: 1365
Score: 151.50 Matches: 62
Percent Similarity: 39.1% Conservative: 42
Best Local Similarity: 23.3% Mismatches: 119
Query Match: 3.8% Indels: 43
DB: 8 Gaps: 9

US-10-616-788-2 (1-738) x US-10-750-623-50374 (1-1365)

Qy 296 GLyProLeuArgAlaMetAlaIleThrValProLeuValVal----- 309
Db 314 CGGATATTTCTCTGCGAGTAGTAACAACCTGTGATGCTCAGCAGCGTCCCTAGCA 373
Qy 310 -----IleSerAlaPheAlaThrLeuPheThrValMetCyseArgLysLysGln 326
Db 374 AGGGGTCATTATCTGCGCATGTTTCGACTGCGCTGAAGCCTGTACTTGTCTGTGAGA 433

Qy 327 GluAsnIleTyrSerHISLysAspGlnGluSerSerGlnSerSerThrTyrThrAlaAla 346
Db 434 GATGACATATAGTTCTCTCCCTCCACAGAAAGATCAAGAAAGCTTCTTCAAGTACC 493
Qy 347 LeuProArgGlnArgLeuArgProArgProLysValPheLeuCyseTyrSerSerLysAsp 366
Db 494 -----ACGCTACGCTCCCTCATTAAGGTTCTGTGTTTAACTTCTGAAATA 541
Qy 367 GLyGlnAsnHISMetAsnValAlaGlnCysePheAlaTyrPheLeuGlnAspPheCyseGly 386
Db 542 TGGTTCATAC-----ACAGTTGTACTTACTGAGATTCTTCAAAACCGCTGACA 595
Qy 387 CyseGluValAlaLeuAspLeuTyrGluAspPheSerLeuCyseArgGlnGlnArgGln 406
Db 596 AGTGAATTAATCTTGAAGATGCGAGAAATAAATAAGCCAGATGGGTCCCGTGCAG 655
Qy 407 TyrValIleGlnLysIleHISLysGlnPheIleIleValAlaCyseSerLysGlyMet 426
Db 656 TGGCTTACCACTCAGAAAGCAAGCGAGATTAAGTCAATTTCTTCTTCCAAATGGTAAAC 715
Qy 427 LyeTyrPheValAspLysLysAsnTyrLysHISLysGlyGlyArgLysSerGlyLys 446
Db 716 ACC-----ACGTGCATGTTACTGTGACGAGAAAGAGGGCCCTGTGAGAGCTCC 769
Qy 447 GLyGluPhePheValAlaValSerAlaIleAlaGluLysValArgLysAlaLysGln 466
Db 770 CGAGACTGTTCCACTCGCTTTTAACTCTTTCGAGTATCTGAG----- 817
Qy 467 SerSerSerAlaAlaLysSerLysPheIleAlaValTyrPheAspTyrSerCyseGluGly 486
Db 818 ---AGCCAGGCTCATCTGCAAAATACGTGTGCTTACTTACAG-----GAGGGT 865
Qy 487 AspValProGly-----IleLeuAspLysSerThrLysTyrArgLysMetAspAsn 503
Db 866 GACATCCGACAGACCTACAGGGCACTACGCTGTGCCCCACGTACCGCTTCACAGAGAC 925
Qy 504 LeuProGlnLeuCyseSerHISLysHISerArgAspHISGlyLeuGlnIleProGlyGln 523
Db 926 GCTACAGGTTTCTGTGAGAG-----CTCCCTCCGTCGCAAGCAG 964
Qy 524 HIEThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyr 543
Db 965 CATGTGTGCGTGGGAGAGAG-----TCACGCACTGTCTCAC 1000
Qy 544 ValAlaIleCyseAsnMet 549
Db 1001 TACAGCTGTGCTCTCTG 1018

RESULT 10

US-09-978-360A-33
; Sequence 33, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleref, Lydie
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56. US4. CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273

PRIOR FILING DATE: -09-04
 PRIOR APPLICATION NUMBER: US 09/191,997
 PRIOR FILING DATE: 1998-11-13
 PRIOR APPLICATION NUMBER: US 09/215,435
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: PCT/IB98/02122
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: US 09/247,155
 PRIOR FILING DATE: 1999-02-09
 Remaining Prior Application data removed - See file wrapper or PAM.
 NUMBER OF SEQ ID NOS: 810
 SOFTWARE: Patent.pm
 SEQ ID NO 33
 LENGTH: 1701
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 245..1399
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 245..796
 OTHER INFORMATION: Von Heljne matrix
 OTHER INFORMATION: score 5.10
 FEATURE:
 NAME/KEY: polyA_signal
 LOCATION: 1669..1674
 FEATURE:
 NAME/KEY: polyA_site
 LOCATION: 1687..1701
 US-09-978-360A-33

Alignment Scores:
 Pred. No.: 0.026 Length: 1701
 Score: 135.50 Matches: 89
 Percent Similarity: 33.2% Conservative: 56
 Best Local Similarity: 20.4% Mismatches: 172
 Query Match: 3.4% Indels: 121
 Gaps: 16

US-10-616-788-2 (1-728) x US-09-978-360A-33 (1-1701)

QY 204 AsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 223
 DB 320 AATGCAATATGATGAAAGATGGCCCTTCATCTGTGAATTCACCC--TCACAGGC 376
 QY 224 AsnPheGlyPheArgPhePheTyLeuHisTyLeuValGluGlyProPheLeu 243
 DB 377 -----TGCCTAAGCACAATGAATATATAA 403
 QY 244 ArgLys-----ThiCysLysGlnGlu 250
 DB 404 AAAAAGGTGTCAAGCGCGAAGCGTGGGATCGGAACATCATGCTGTGAAGAATA 463
 QY 251 GlnThrThrGluThrSerCysLeuLeuGlnAsnValSerProGlyAspTyrIle-11 270
 DB 464 GAG-----GAGACAGTGAAGTGA-CTTCACAAACCACTCCCTGGGAAACAGATACAT 516
 QY 270 eGluLeuValAspAspThrAsnThrAsnThrArgLysValMetHisTyLeuValLeuLysProVa 290
 DB 517 GGCCTTATCAACACAGCACTATC-----ATCGGGTTTCTCAAGT 558
 QY 290 IHisSerProTyrPheGlyProIleArgAlaMetAlaIleThrValProLeuValIle 310
 DB 559 GTTGAAGCACACACAGAAAGAAAGAGCGAGCTTCAAGTGTGATTCAGAGACTGGGA 618
 QY 310 eSerAlaPheAlaThrLeu----- 316
 DB 619 TAGGAAGGTGTCAAGGTGAGCTGACTCATATTTCTCACTTGTGGCAGCACTGCAT 678
 QY 317 -----PheThrValMetCysArgLysValGlnGlnAsnIleTySerHis 332

DB 679 CCGACATAAAGAAAGAGTGGCTGCTGC-----CCAAACAGAGCGCTCTTCCC 729
 QY 332 sLeuAspGlnGluSerSerGlnSerThrTyThrAlaAlaLeu----- 347
 DB 730 TCTGGATTAACAACAAAGAGCGGAGGCTGCTGCTCTCTGCTGTCTGCT 789
 QY 348 -----ProArgLysValArgLeu 353
 DB 790 GGTGGCCACATGGGTGCTGTGGCAGGATCTATATGATGAGGACAGAAAGATCA 849
 QY 353 g-----ProArgProLysValPheLeuCysTyrSe 363
 DB 850 GAAGACTCTCTTTTACACACACACTACTGCCCCCATTAAGGTTGTGGTTACCC 909
 QY 363 rSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPheLeuGlnAs 383
 DB 910 ATCTGAATATGTTTCCATCAC-----ACAAATTTGTACTCTCAATATTTCTTCAAA 963
 QY 383 pPheCysGlyCysGlnValAlaLeuAspLeuTPGluAspPheSerLeuCysArgLysGlu 403
 DB 964 CATTGCAAGAGTGAAGTCACTCTGAAAAGTGGCAGAAAAGAAATAGCAGATGG 1023
 QY 403 yGlnArgGluTyrPheValIleGlnLysIleHisGlnSerGlnPheIleValValCysSe 423
 DB 1024 TCCAGTGCAGTGGCTTGCACCTCAAAAGAGCAGACAGAAAGTGGCTCTTCTTTC 1083
 QY 423 rLysGlyMetLysTyThrPheValAspLysValAsnTyrLysHisLysGlyLysArgL 443
 DB 1084 CAATGACGTCAACAGTGTGTGCGATGTACTGTGCAAGAGGAGGAGTCCCACTGA 1143
 QY 443 ySerGlyLysGlyGlnLeuPheLeuValAlaValSerAlaIleAlaGlnLysLeuArgL 463
 DB 1144 GAACCTTCAA--GACCTCTTCCCTGCTTTTAACTTTTCTGCAAGTATCAAG-- 1198
 QY 463 nAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSe 483
 DB 1199 -----AGCCAGATTGATCTGCAAAATAGCTGTGTCTTACTTTAGAGAT 1245
 QY 483 rCysGlnGlyAspValProGlyTyrLeuAspLeuSerThrLysTyrArgLeuMetAspAs 503
 DB 1246 TGATACAAAGAGCATTAACAATGCTCAAGTGTCTGCCCCCAAGTACCACTATGAAGA 1305
 QY 503 nLeuProGlnLeuCysSerHisIleHisSerArgAspHisGlyLeuGlnIleuProGlyL 523
 DB 1306 TGCCACTGCTTTGTGCAAACTT-----CT 1332
 QY 523 nHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerLysArgSerLeuTy 543
 DB 1333 CCAATGCAAGCAG-----CAGGTGTCAAGAGAAAGATACAAAGCTGCCA 1380
 QY 543 rValAlaIleCysAsnMet-----HisGlnPheIleAspGlnIleuProAspTyrPh 560
 DB 1381 CGATGGCTGTGCTCTGTGAGCCCAACCAT----- 1411
 QY 560 eGluLysGlnPheValProPheHisProProPheLeuArgTyrArgLys 576
 DB 1412 -GAGAAGCAAGAGACCTTAAGGCTTCTATCCACCAATTAAGGGA 1459
 RESULT 11
 US-10-063-703-157
 Sequence 157, Application US/10063703
 Publication No. US2006008901A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filtvaroff, Ellen
 APPLICANT: Gerltisen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,703
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-703-157

Alignment Scores:
Pred. No.: 0.0249 Length: 1515
Score: 135.00 Matches: 77
Percent Similarity: 34.4% Conservative: 50
Best Local Similarity: 20.9% Mismatches: 150
Query Match: 3.4% Indels: 93
DB: Gaps: 12

US-10-616-788-2 (1-738) x US-10-063-703-157 (1-1515)
QY 204 AsnleuAnlIeserglnhIsglySerApmetGlnValSerPheApmHlaIarPchIs 223
DB 433 AATGCAAAATATGAATGAAGATGGCCCTTCATGTCTGTAATTTCACCC--TCACCAAGGC 489
QY 224 AsnRheGlyPheArghPheRheTyLeuHieTyTyLeuYbHISGLUGlyProRheLyS 243
DB 490 -----TGCCTAGACCAATATGAATATATAA 516
QY 244 ArgLyS-----ThCyLySGlnGlu 250
DB 517 AAAAAGGTGTCAAGGCCGGAAGCCTGGGATCCGAACATCACTGCTGTGAAGAAGAT 576
QY 251 GlnThrThrglvThrThSerCyLeuLeuGlnAnValSerProGlyApmTyTle-11 270
DB 577 GAG-----GAGACAGTAGAAGTAGAA-CTTCACAAACCACTCCCTGGGAAACAGATACAT 629
QY 270 eGluLeuValAspArghRheRheThrThrThArgLyValMetHieTyTyAlaLeuYsProVa 290
DB 630 GGGCTTTATCAACACAGCACTATC-----ATCGGGTTTCTCAGGT 671
QY 290 IhISerProTrpIaGlyProIleArgAlaMetAlaIleHieTyTyAlaLeuVal11 310
DB 672 GTTGAACCCACACCAAGAAAGAAACAAAGCAGCTTCAGTGTGATTCAGTGAAGTGGGA 731
QY 310 eSerAlaPheAlaThreU-----316
DB 732 TAGTGAAGTGTCTAGCTGAGCTGACTCATATTTTCTACTTGTGACAGCATGCAT 791
QY 317 -----PheThrValMetCyArghLyLyGlnGlnAnIleTySerH 332
DB 792 CCGACATAAAGAAACAGTTGTGCTGC-----CCACAAACAGGCGCTTCC 842
QY 332 vLeuAspGluIuserSerGlnSerThrTyThralaIaleu-----347
DB 843 TCTGGATACAAACAAAGCAAGCGGAGGCTGCTCCTCTCGTGTCTGCT 902
QY 348 -----ProArgGluArgLeuAr 353
DB 903 GGTGGCCACATGGGTGCTGTGTCGAGGAGTCTATCTAATGTGAGGACCAAGAGATCAA 962
QY 353 g-----ProArgProLyValIleLeuCyTyTse 363
DB 963 GAAGACTCTCTTTTCAACCACTACTGCCCCCATTAAGGTTCTTGAGTTTACC 1022
QY 363 rSerLyAspGlyGlnAnHieMetAnValIaGlyPheAlaTyRPhleuGlnIs 383
DB 1023 ATCTGAATAATGTTCATGCAC-----ACAATTTTACTTCACTGAATTTCTTCAAA 1076
QY 383 pPheCyegLyCyegLyValAlaLeuApmLeuTyTgIuApmPheSerLeuCyArghGlu 403
DB 1077 CCAATTGCAAGAAAGTGAAGTCACTTGAAGAGTGCAGAAAAAGAAATATGACAGATGGG 1136

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QY 403 yGlnArghIuTrpValIleGlnLySIlleHISGLUGlySerGlnPheIleIleValValCyse 423
DB 1137 TCAAGCAGTGGCTTCCCACTGAAAAGAGCAGACAGAAAGTGTCTTCTTTC 1196
QY 423 rLySGlyMetLyTyRPhValApmLyValenTyTyLeuHieLySGlyGlyArg 443
DB 1197 CAATGACGTCAACAGTGTGCGATGATCTGTGCAAGAGGAGGCGAGTCCAGTGA 1256
QY 443 ySerGlyLySGlyGlnLeuPheLeuValAlaValSerAlaIleAlaGlnLyValArg 463
DB 1257 GAACCTTCAA--GACCTTCTCCCTTGCCTTAACTTTTCTGACAGTATTAAGA-- 1311
QY 463 nAlaLyGlnSerSerAlaIaleuSerLyPheIleAlaValTyRPhArTyse 483
DB 1312 -----AGCCAGATTGATCTGCAACAAATACGTGTGTACTTGAAGAGAT 1358
QY 483 rCySGlyAspValProGlyTleuApmLeuSerThrTyTyArgLeuMetArpAe 503
DB 1359 TGATACAAAAGAGATTAACAATGCTCTCAGTGTGCCCCCAAGTACCACTCATGAAGA 1418
QY 503 nLeuProGlnLeuCySerHleu 511
DB 1419 TGCCACTGCTTCTGTGCAGAACTT 1443

RESULT 12
US-11-102-240-157
; Sequence 157, Application US/11102240
; Publication No. US2005026047A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESSI
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-102-240-157

Alignment Scores:
Pred. No.: 0.0249 Length: 1515
Score: 135.00 Matches: 77
Percent Similarity: 34.4% Conservative: 50
Best Local Similarity: 20.9% Mismatches: 150
Query Match: 3.4% Indels: 93
DB: Gaps: 12

US-10-616-788-2 (1-738) x US-11-102-240-157 (1-1515)
QY 204 AsnleuAnlIeserglnhIsglySerApmetGlnValSerPheApmHlaIarPchIs 223
DB 433 AATGCAAAATATGAATGAAGATGGCCCTTCATGTCTGTAATTTCACCC--TCACCAAGGC 489
QY 224 AsnRheGlyPheArghPheRheTyLeuHieTyTyLeuYbHISGLUGlyProRheLyS 243
DB 490 -----TGCCTAGACCAATATGAATATATAA 516

```

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Qy 244 Arglys-----ThCysLysGlnlu 250
Db 517 AAAAGTGTCTCAAGGCGGAAGCTGTGGAGTCCGAACATCATCTGTTGTAAGAGAT 576
Qy 251 GlnThrThrgluthrThSerCysLeuLenglnnValSerProglYAspTyrIle-I 270
Db 577 GAG-----GAGACAGTGAAGTGA--CTTCAACAACCACTCCCTGGGAAACAGATACAT 629
Qy 270 eglLeuValAspThrThrThrThrThrArgLysValMetHisTyrAlaLeuLysProva 290
Db 630 GGTCTTATCCACAACAGCACTATC-----ATCGGTTTTCTCAGGT 671
Qy 290 LHisSerProtrpAlaglyProileArgAlaMetAlaIleThrValProleuValIal 310
Db 672 GTTGGACCAACACCAAGAAACAAACCGGAGCTTCACTGATTCAGTACGAGGGA 731
Qy 310 eSerAlaPheAlaThrLeu----- 316
Db 732 TAGTGAAGTGTCTACGGTCACTGACTCATATTTTCTTACTTGTGGCAGCATGTCAT 791
Qy 317 -----PheThrValMetCysArgLysLysGlnGlnGlnGlnIleTyrSerHis 332
Db 792 CCGACATTAAGGAAACAGTTGTGCTCTGC-----CCACAAACAGGCGTCCCTTCCC 842
Qy 332 sLeuAspGlnGluSerSerGlnSerSerThrTyrThrAlaAlaLeu----- 347
Db 843 TCTGGATTAACAACAAAGCAAGCGGAGCTGCTGCTCTCTCTGCTGCTGCT 902
Qy 348 -----ProArgGluArgLeu 353
Db 903 GGTGGCCACATGGGTGCTGTGGAGGAGATCTATATGTCAGAGGACGAAAGATCA 962
Qy 353 g-----ProArgProLysValPheLeuCysTyrSe 363
Db 963 GAAGACTCTCTTCTTCTACACCACTACTGCCCCCATTAAGGCTTCTGCTGTTTCCC 1022
Qy 363 rSerLysAspGlyGlnnHisMetAlaValGlnCysPheAlaTyrPheLeuGln 383
Db 1023 ATCTGAATAATGTTTCCATCC-----ACAAATTGTTACTTCACTGAATTTCTCAAAA 1076
Qy 383 PheCysGlyCysGlnValAlaLeuAspLeuTrpGluAspPheSerLeuCyBatGln 403
Db 1077 CCATTCGAGAAGTGAAGTCACTCTTGAAGAGTGCAGAAAAGAAATAGCAGAGATGG 1136
Qy 403 yGlnAspGlnTyrValIleGlnLysIleHisGlnSerGlnPheIleIleValValCysSe 423
Db 1137 TCCAGTGCAGTGGCTTCCCACTCAAAAGAGGACAGACAAAGTGGTCTTCTTCTTTC 1196
Qy 423 LysGlyMetLysTyrPheValAspLysValSerTyrLysHisLysGlyGlyArg 443
Db 1197 CAATGACGTCAACAGTGTGCGCATCTGTGGCAAGGCGAGGAGTCCCACTGA 1256
Qy 443 ySerGlyLysGlyGlnLeuPheLeuValAlaValSerAlaIleAlaGluLysLeuArg 463
Db 1257 GAACCTCAAA--GACTCTTCCCTTACCTTTAACCCTTTTCGACAGTATCTAAGA-- 1311
Qy 463 nAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSe 483
Db 1312 -----AGCCAGATTCACTGCACAAATAGCTGTGCTTACTTATAGAGAT 1358
Qy 483 rCyGlnGluLysAspValProglYIleLeuAspLeuSerThrLysTyrArgLeuMetAsp 503
Db 1359 TGATACAAAGACATTAACAATGCTCTCAGTGTCTGCCCAAGTACCACTCATGAAGA 1418
Qy 503 nLeuProGlnLeuCysSerHisLeu 511
Db 1419 TGCCACTGCTTCTCTGCAGAACTT 1443

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RESULT 13
 US-11-204-311-244
 ; Sequence 244, Application US/11204311
 ; Publication No. US20060040304A1
 ; GENERAL INFORMATION:

```

APPLICANT: Blumenfeld, Maria
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueterec, Lydie
APPLICANT: Cohen, Amick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62.US4.DIV
CURRENT APPLICATION NUMBER: US/11/204,311
PRIORITY FILING DATE: 2005-08-15
PRIORITY APPLICATION NUMBER: US/10/294,934
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US 09/671,317
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US 09/536,178
PRIORITY FILING DATE: 2000-03-23
PRIORITY APPLICATION NUMBER: PCT/IB00/00403
PRIORITY FILING DATE: 2000-03-24
PRIORITY APPLICATION NUMBER: US 60/126,269
PRIORITY FILING DATE: 1999-03-25
PRIORITY APPLICATION NUMBER: US 60/131,961
PRIORITY FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SOFTWARE: Patent.pm
SEQ ID NO 244
LENGTH: 1001
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-192-334 : polymorphic base G or A
FEATURE:
NAME/KEY: misc_binding
LOCATION: 481..500
OTHER INFORMATION: 12-192-334.misl, potential
FEATURE:
NAME/KEY: misc_binding
LOCATION: 502..521
OTHER INFORMATION: 12-192-334.misl, potential complement
FEATURE:
NAME/KEY: primer_bind
LOCATION: 815..834
OTHER INFORMATION: upstream amplification primer, complement
FEATURE:
NAME/KEY: primer_bind
LOCATION: 346..365
OTHER INFORMATION: downstream amplification primer
FEATURE:
NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-192-334 potential probe
US-11-204-311-244
Alignment Scores:
Pred. No.: 0.562 Length: 1001
Score: 118.00 Matches: 74
Percent Similarity: 37.8% Conservative: 37
Best Local Similarity: 25.2% Mismatches: 117
Query Match: 3.0% Indels: 66
DB: 9 Gaps: 15
US-10-616-788-2 (1-738) x US-11-204-311-244 (1-1001)
Qy 477 AlValTyrPheAspTyrSerCysGlnGlyAspValProglYIle----- 491
Db 33 GCATCTCCAGCTCTTACAGCTCCACGGAGGCTTCCGGGGCTAAAGCGAGAGGGG 92
Qy 492 -----LeuAspLeuSerThrLysTyrArgLeuMetAspAsnLeu 504
Db 93 CCAAGCTCATCCCACTGCCAGCTGACCTCACTTCTCAAAAGACAGTGAAGAGAGG 152
Qy 505 ProGlnLeuCySerHisLeuHisSerArgAspHisGlyLeuGlnGlu-----ProglY 522
Db 153 CTTGAGGCTGTCTTTCAGGTCAACCACTGTGAAAGGACAGCAATATATGACCAAGG 212

```

```

QY 523 GlnHletharGlnGlySerArgArgAntyrPheArgSerGlyArgSerLeu 542
Db 213 CAGACACTACCC-----CTCAGGATGACTCTCCACATCCAGGAGCTTAGGCC-- 263
QY 543 TyValAlaIleCysAenMetHleGlnPheIleApsIleuProApsTrpPheGlu 562
Db 264 -----AGTACACACAACTTT-----CCCTGCTGCCACGAGG 296
QY 563 GlnPheValProPheHis---ProProProLeu----- 572
Db 297 CGAGGGAGGCTTTGATGCTGCTCCCTTAAAGCTGGGTAACCGGCTCACTTTGAA 356
QY 573 -----ArgTyArgGluProValLeuGluPheApsSerGlyLeuValAen 589
Db 357 GACCTGACCGGGAGAGAGAGCGGCTTCCAGCGCTCAACAGTGCAGCTTGAG 416
QY 590 AspValMet-----CysLysProGlyProGluSerApsPheCysLeuLysValGlu 606
Db 417 GACAAAGGCTATCTCGACTCGACGACCTTCAAGGCTTCCAC-----ACTTTGCTCC 467
QY 607 AlaProValLeuGlyAlaTrpGly---ProAlaApsSerGlnHisGluSerGlnHisGly 625
Db 468 TCACCTTGCAACAGGGGCTTCTGCTGCTGCTGCTTCTTAAAGCACCCAGT----- 518
QY 626 GLyLeuApsGlnApsGlyGluAlaArgProAlaLeuApsGlySerAlaAlaLeuGlnPro 645
Db 519 ---ATGATGACACAGCAGAGACACACACAGTCCCAAGACCTGCTGGGCTTACGAGCC 575
QY 646 LeuLeuHisThrValIleValAlaGlySerProSerApsMetProArgApsSerGlyIleTy 665
Db 576 TTAGCATCTGCT-----GCAGGGGTCTCCCTTACACTCCCATGCTGGGAGAGAACAC 629
QY 666 ApsSerSerValProSerSerGluSerLeuLeuProLeuMetGluGlyLeuSerThrAs 685
Db 630 AGACACACAGGAGCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 689
QY 685 pGlnThrGluThrSerSerLeuThrGluSerVal-----SerSerSerSerGlyL 702
Db 690 CAGAGCTCAGCCCAAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 749
QY 702 euGlyGluGluGluProProAlaLeuProSerLeuLeuSerSerGlySerCysLysA 722
Db 750 GCGGGCATGAGAG-----AACAAAGCATGAGCATCTTCTGCTCTGCTC----- 790
QY 722 laApsLeuGlyCysArgSerTyThrApsGluLeuHis 734
Db 791 -----AGCTGCCGACGAGCCCTCCCGCTCCAC 820

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RESULT 14
US-11-108-172-1112
; Sequence 1112, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Lodee, Michael J.
; APPLICANT: Seeriet, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15

```

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; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1112
; LENGTH: 16382
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-108-172-1112

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Alignment Scores:
Pred. No.: 27.4 Length: 16382
Score: 116.50 Matches: 156
Percent Similarity: 31.4% Conservative: 99
Best Local Similarity: 19.2% Mismatches: 253
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DB: 12 Gaps: 39

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QY 55 -----AsnIleThrPheLysTyraApsCysThrThrTyLeuApsProVal----- 70
Db 576 GTCTTAAAGTGTGCTCTTACAGCCCTTCAATGTCGAGCCAGCTACAGCTCAGTGTCTC 635
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QY 89 -----His-----ApsGlnValAlaValThrIleLeuTrpSer 99
Db 696 CAGAAACATACGACTGCAACCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 752
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Db 753 -----GGCAACCATATATATATATATATATATATATATATATATATATATAT 782
QY 120 SerGluGlyArg-----GlnCysGlnGlnLeuLeu 130
Db 783 TCCCAATCTGCGATATATTGGCTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 842
QY 131 LysApsProLysGlnLeuApsSerPheLysArgThrGly-----MetGlu 146
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; NUMBER OF SEQ ID NOS: 1596
 ; SOFTWARE: Patent version 3.2
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 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial sequences: primer
 ; NAME/KEY: misc feature
 ; LOCATION: (1..16382)
 ; OTHER INFORMATION: fc fragment of 199 binding protein (FCGBP)
 ; OTHER INFORMATION: gene.
 US-11-000-688-239

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Percent Similarity:	116.50					
Best Local Similarity:	31.4%					
Query Match:	19.2%					
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US-10-616-788-2 (1-738) x US-11-000-688-239 (1-16382)

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 QY 39 CyGgLYTrpArgLYValGlyProAlaSerArgAsnSerGlyLeuTYr----- 54
 DB 531 -----AAGGGGTACGTGACATTCATCAATGCAAGTTCTATCCAGAGCGGAT 575
 QY 55 -----AsnIleThrPheLYrTYrAspAsnCyethrThrTYrLeuAsnProVal----- 70
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 QY 71 ---GlyHisIleValIleAlaAspAlaGlnAsnIleThrIleSerGlnTYrAlaCyv--- 88
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 QY 89 -----His-----AspGlnValAlaValThrIleLeuTrpSer 99
 DB 696 CAGAAACATACGACCTGCAACATGTGTGAGAGCTGCTACCAAGCTGCTGCTG--- 752
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 QY 131 LyAspProLYrGlnLeuAsnSerPheLYrArgThrLYr-----MetGlu 146
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 QY 226 GlyPheArgPhePheTYrLeuHisTYrLYrLeuLYrHisGluGlyProPheLYrValLYs 245
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 QY 246 ThrCyLeuGlnGluGlnThrThrGluThrTrpSerCyLeuLeuGlnAsnValSerPro 265
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Qy      644 ---GlnProLeuHtSerValThrValLysValLysProSerAepMetProArgAepSer 662
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 06:49:29 ; Search time 344 Seconds
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3813.490 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3690	93.5	2319	3	US-09-747-259-17	Sequence 17, App
3	3248	82.3	3948	3	US-09-749-451-125	Sequence 125, App
4	321.5	8.1	3120	3	US-09-949-002-117	Sequence 117, App
5	321.5	8.1	3120	3	US-09-949-002-126	Sequence 126, App
6	321.5	8.1	3223	2	US-08-620-694A-9	Sequence 9, Appl1
7	321.5	8.1	3223	2	US-08-620-694A-9	Sequence 9, Appl1
8	321.5	8.1	3223	3	US-09-022-255-9	Sequence 9, Appl1
9	321.5	8.1	3223	3	US-09-022-255-9	Sequence 9, Appl1
					US-08-978-773-3	Sequence 3, Appl1

10	321.5	8.1	3223	3	US-09-022-253-9	Sequence 9, Appl1
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13	321.5	8.1	3223	3	US-09-022-257-9	Sequence 9, Appl1
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16	300	7.6	3288	3	US-09-022-255-1	Sequence 1, Appl1
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23	300	7.6	3288	3	US-09-549-679-1	Sequence 1, Appl1
24	294.5	7.5	28976	3	US-09-949-002-689	Sequence 689, App
25	294.5	7.5	28976	3	US-09-949-002-698	Sequence 698, App
26	145	3.7	23024	3	US-09-949-016-12807	Sequence 12807, A
27	145	3.7	23024	3	US-09-949-016-17529	Sequence 17529, A
28	136	3.4	1810	3	US-09-949-016-5787	Sequence 5787, App
29	136	3.4	2171	3	US-09-976-594-762	Sequence 762, App
30	135.5	3.4	1701	3	US-09-599-360B-56	Sequence 56, Appl
31	135	3.4	1515	3	US-09-747-259-11	Sequence 11, Appl
32	126	3.2	601	3	US-09-949-002-3686	Sequence 3686, App
33	126	3.2	601	3	US-09-949-002-4016	Sequence 4016, App
34	126	3.2	5105	3	US-09-919-039-293	Sequence 293, App
35	122	3.1	1574	3	US-09-023-655-829	Sequence 829, App
36	121	3.1	23995	3	US-09-949-016-17363	Sequence 17363, A
37	120	3.0	1918	3	US-09-268-311-17	Sequence 17, Appl
38	120	3.0	2165	3	US-09-796-844-17	Sequence 17, Appl
39	119.5	3.0	2165	3	US-09-188-930-226	Sequence 226, App
40	119.5	3.0	2165	3	US-09-312-283C-226	Sequence 226, App
41	119.5	3.0	4262	3	US-09-949-016-2134	Sequence 2134, App
42	119	3.0	4609	3	US-09-322-478-21	Sequence 21, Appl
43	119	3.0	4609	3	US-09-586-106D-21	Sequence 21, Appl
44	119	3.0	4609	3	US-10-799-870-21	Sequence 21, Appl
45	118	3.0	1001	3	US-09-671-317-244	Sequence 244, App

ALIGNMENTS

RESULT 1
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; Sequence 1429, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1429
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1429

Alignment Scores:
Pred. No.: 0
Score: 3706.00
Percent Similarity: 99.7%
Best Local Similarity: 99.4%
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DB: 3
Length: 2894
Matches: 694
Conservative: 2
Indels: 0
Gaps: 0

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Db	270	GACAATTGTACCACTTAATTGAATTCAGATGGGGAGCATGTGATGTGCAGAGCCCAAGAT	329
QY	81	IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrSerPro	100
Db	330	ATCACCATCAAGCCAGTATGCTTGGCATGACCAAGTGGAGTCCACCATCTTGTGGCCCCA	389
QY	101	GlyAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGluGluLeuLysSer	120
Db	390	GGGGCCCTCGGCATCGAATTCCTCGAAGAGATTCGGGTAAATACAGAGACTGAAGTCG	449
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Db	450	GAGGAAACAGTGTCCACCAACTGATCTTAAGAGATCCAAAGCACTCAACAGTACGCTTC	509
QY	141	LysArgThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe	160
Db	510	AAAAGAACTGGAAATGAATCTCAACTCTTCCGAATTAAGAAATTGAAACGGAATTAATTC	569
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QY	181	ArgThrArgAlaCysAspLeuLeuGlnProAsnLeuAlaCysLysProPheTyr	200
Db	630	AGAACCGAGGCTGTGACCTGTGTGTTACAGCGCGAACAATCTTAGCTGTAAACCTTCTCG	689
QY	201	LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis	220
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OY	461	LeuArgIyAlaIyGlnSerSerSerAlaAlaLeuSerIySphIleAlaValTyRPh	480
Db	1470	CTCCGCCAGGCGCAAGAGAGTTCGTCCGGCGCTCAGCAAGTTTATGCCGTACTATT	1529
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OY	501	MetAspAsnLeuProGlnLeuCySerSerIyLeuHsIySerArgAspHsGlyLeuGlnIu	520
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OY	581	LysPheAspSergIyLeuValLeuAsnAspValMetCyAspProGlyProGlnSerAsp	600
Db	1830	AAATTGATTCGGGCTTGTTTAAATGATGATCATGTGCAACCAAGGCGCTGAGAGTAC	1889
OY	601	PheCyAspLeuValGlnIuAspValLeuGlyAlaThrGlyProAlaAspSergIyHsIy	620
Db	1890	TTCTGCTTAAGGTAGAGCGCGCTGTTCTTGGGCAACCGGACCAAGCCGACTCCACAC	1949
OY	621	GlySerGlnHsIyGlyGlyLeuAspGlnAspGlyGlyAlaArgProAlaLeuAspGlySer	640
Db	1950	GAGAGTCAAGATGGGGGCTGGACCAAGACGGAGAGGCCGGCTTGCCCTTGACGTAGC	2009
OY	641	AlaAlaLeuGlnProLeuLeuHsIyThrValLysAlaGlySerProSerAspMetProArg	660
Db	2010	GCCGCCCTGCAACCCCTGCTGTCACACGGTGAACCGGGAGCCCTCGACATCCCGCG	2069
OY	661	AspSergIyIleTyRAspSerSerValProSerSergIyLeuSerLeuProLeuMetGln	680
Db	2070	GACTCAAGGCATCTATGACTCGTCTGTGCCCCCTCAATCCAGAGCTGTCTTGCCACTATGAA	2129
OY	681	GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSer	700
Db	2130	GGACTCTCGAGGACCAAGACGAAGAAAGCTTCTCTGACGGAGACGGTCTCTCTTCA	2189
OY	701	GlyLeuGlyGlnGlnIuProProAlaLeuProSerIySphLeuLeuSerSergIySerCyS	720
Db	2190	GGCTTGGGTAGAGAGAACTCCCTCGCCCTTCTTCCAAGCTCCTCTTGGGTATGATCG	2249
OY	721	LysAlaAspLeuGlyCyAspSerTyThrAspGlnLeuHsIyAlaValAlaPro	738
Db	2250	AAACCAATCTTGTTGCCGACCTACACGATGATCACTCCACGCGGTGCGCCCT	2303
RESULT 2			
US-09-747-259-17			
; Sequence 17, Application US/09747259			
; Patent No. 6569645			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Chen, Jian			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Li, Hanzhong
 APPLICANT: Hillan, Kenneth
 APPLICANT: Tumas, Daniel
 APPLICANT: Vanlookeren, Menno
 APPLICANT: Vandlen, Richard
 APPLICANT: Watanabe, Colin
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William
 APPLICANT: Yanaura, Daniel
 TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 FILE REFERENCE: P13161R1C1P1(US)
 CURRENT APPLICATION NUMBER: US/09/747,259
 CURRENT FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: US 09/311,832
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: US 60/172,096
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: PCT/US99/31274
 PRIOR FILING DATE: 1999-12-30
 PRIOR APPLICATION NUMBER: US 60/175,481
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: PCT/US00/04341
 PRIOR FILING DATE: 2000-02-18
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US 60/191,007
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: PCT/US00/07532
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: PCT/US00/15264
 PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: US 60/213,087
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: US 09/644,848
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/242,837
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: PCT/US00/30873
 PRIOR FILING DATE: 2000-11-10
 PRIOR APPLICATION NUMBER: US 60/253,646
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: 2000-12-01
 NUMBER OF SEQ ID NOS: 39
 SEQ ID NO 17
 LENGTH: 2319
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-09-747-259-17
 Alignment Scores:
 Pred. NO.: 0
 Score: 3690.00
 Percent Similarity: 96.08
 Best Local Similarity: 95.88
 Query Match: 93.58
 DB: 3
 Gaps: 3
 US-10-616-788-2 (1-738) x US-09-747-259-17 (1-2319)
 Oy 24 AlaValAlaAlaGlyGlySergIyArg-----AlaTrpGlyValaAsp-----Thr 38
 Db 52 GCGGTTGAGAGGGGAGGAGATGCCAGCGCTTCGCTCAGGAGTGTCTCGTGGTTGTC 111
 Oy 39 CysGlyTTPaArgGlyValGlyProAlaSerArgaenSergIyLeuTyranenleThrPhe 58
 Db 112 AGTGAAGAGCAGGGAGTGGGCTCAGCCAGCAGCAAAACAGTGGGCTGTACAAATCACCTTC 171

QY	59	YYSYIYASPAASNYSTHThThThThLeuasnProValGlyIYshIleValIleAlaAspAla	78
Db	172	AAATATGCAATGTGACCACTTACTTGAATTCAGTGGGAAAGCATGTATGTCTACGCC	231
QY	79	GIAnsnIleThThIleSerGlnThThAlaCysHisAspGlnValAlaValThThIleuThP	98
Db	222	CAGAAATATCACCAATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCAACATTTCTTGG	291
QY	99	SerProGlyValAlaLeuGlyIleGlnPheLeuIYsgIYPhaArgValIleLeuGlnGluLeu	118
Db	292	TCCCAAGGAGGCGCTCCGGATCGAAATCTCTGAAGAGATTTCCGGTAAATCTGGAGGAGCTG	351
QY	119	LYSserGlnGlyArgGlnCysGlnGlnLeuIleLeuIYsAspProIYsgIleuIYsnSer	138
Db	352	AAAGTCGAGGGAAGACAGCTGCCCAACATGATTTCTAAAGATTCGAGACACTCAACAGT	411
QY	139	SerPheIYsArgThrgIYmetGluSerGlnProPheIYsAsnMetLYsPheGluThrAsp	158
Db	412	AGCTTCAAAAGACCTGMAATGAAATCTCAACCTTCTCGAATATGAAATTTGAAAACGAGT	471
QY	159	ThrPheValLYsValIleProPheProSerIleLYsAsnGlyuserAsnThThIleProPhe	178
Db	472	TATTTGTAAGATTTGCTCCCTTTCTTCTCAATTAAGAGCAATTTACCACTTTC	531
QY	179	PhePheArgThrArgAlaCysAspIleuLeuGlnProAspAsnLeuAlaCysIYsAspPro	198
Db	532	TTCTTTAGAAACCGAGCGCTGACCTGTGTGTTACAGCCGACCAATCTAGTTGTAAACC	591
QY	199	PheThrIYsProAlaGlnLeuAsnIleSerGln-----	209
Db	592	TTCTGGAAGCTCGGAACCTGMAATCAGCCAGAGTGGCTCGACATGCAAGTCTCTTC	651
QY	210	-----HisGlySerAspMetGlnValSerPheAspHisAlaProHisAsnPhe	225
Db	652	GACCAAGACCGCATGGCTGGGACATGACAGGTGTCTTTGCACAGACGACCGCAACAATTC	711
QY	226	GlyPheArgPhePheIYrLeuHisIYrLYsIleuLYshIsgIYgIYProPheLYsArgLYs	245
Db	712	GGCTTCGGTTCCTTCATCTTCACTAACAGCTCAAGACGAAAGACCTTTCAAGGAAAG	771
QY	246	ThrCysLYsGlnGlnGlnThThGlnThThThSerCysLeuLeuGlnAsnValSerPro	265
Db	772	ACCTGTAAGCAGGACCACTCAAGAGATGACAGCTGCCTTCCAAAGATTTCTTCA	831
QY	266	GlyAspThrIleIleGlnLeuValAspAspThraAsnThThArgLYsValMetHisIYr	285
Db	832	GGGATATATATATATGAGTGTGTGATGACCTTAACCAACAAAGAAAGTATGATGATAT	891
QY	286	AlaLeuLYsProValHisSerProThralaGlyProIleArgAlaMetAlaIleThThVal	305
Db	892	GCCTTAAAGCCAGGCACTCCCGCGGGCCGAGCCATCAAGAGCCGTGGCATCAACATG	951
QY	306	ProLeuValValIleSerAlaPheAlaThrLeuPheThrValMetCysArgLYsLYsGln	325
Db	952	CCACTGTAGTCATATGGCATTTGCCACGCTCTTCACTGTAGTGTCCGCAAGACAA	1011
QY	326	GlnGlnAsnIleIYrSerHisIleuAspGlnGlyuserGlnSerSerThThThAla	345
Db	1012	CAAGAAAATATATATTCACATTTTGATGAAAGAGAGCTCTGAGTCTTCCACATACCTGCA	1071
QY	346	AlaLeuProArgGlnArgLeuAspArgProArgProLYsValPheLeuCysIYrYSerSerLYs	365
Db	1072	GCACTCCCAAGAGAGAGCTCCGGCCGGCCGAGAGGCTTTCTCTGTATTTCCAGTAA	1131
QY	366	AspGlyGlnAsnHisMetAsnValValGlnCysPheAlaIYrPheLeuGlnAspPheCys	385
Db	1132	GATGGCCAGATACATCAATATGTGTCTCAGAGTGTTCCTACTTCTCCACAGACTTGTGT	1191
QY	386	GlyCysArgIleValAlaLeuAspLeuThrgIYsAspPheSerLeuCysArgGlnGlyGlnArg	405
Db	1192	GGCTGTAGAGGTGCTCTGACCTGTGGGAAAGCTTCAAGCTCTGTATAAGAAAGGCAAGAA	1251

QY 406 GUTRPVALLIEGLNLYSLHLSGUSERGlnpheilelleValCySerLyGly 425
 DB 1252 GAATGGGTCTCCAGAAAGATCCAGAGTCCCAAGTTATCATTTGGTTTGTTCAGAAAGT 1311
 QY 426 MetLySerPheValAspLySLYAsnTYrLYAsnLYSLYGLYATAGGlySerGly 445
 DB 1312 ATGAGACTTCTTGGCAAGAAAGAACTAACAAACAAAGAGGTGGCCAGGCTCGGGG 1371
 QY 446 LySGlyGLNLeuPheLeuValAlaValSerAlileAlaGLYLYLeuValAspGlyAlaLYS 465
 DB 1372 AAAGAGAGCTCTCTCGTGGGTGCGGTGCAGCCATTCGCAAAAGCTCCCGCAGGCCAAG 1431
 QY 466 GlnSerSerSerAlaAlaLeuSerLyPheAlileAlaValTYrPheAspTYrSerCyGlu 485
 DB 1432 CAGAGTTCTGTCGGCGGCTCAGCAAGTTATTCGCCCTCATTTGATTATTCCTGGAG 1491
 QY 486 GLYAspValProGlyLYLeuAspLeuSerThLYrTYrGLNLeuLeuAspLeuPro 505
 DB 1492 GGAAGAGTCCCGGTATCTAGACCTGATACCAAGTACAGACTCATGACCAATCTTCCT 1551
 QY 506 GlnLeuCySerSerAlileuHLSerLYAsnTYrAspHLSGLYLeuGlnGluProGlyLYNHLSThr 525
 DB 1552 CACCTCTGTTCCACCTCGACCTCCGAGACCAAGCTCCAGAGCGGGGAGCAGCAGC 1611
 QY 526 ArgGLNLYSerArgArgAsnTYrPheArgSerLySerGlyArgSerLeuTYrValAla 545
 DB 1612 CGACAGGGCGAGCAAGAACTACTTCCGAGCAAGTCAAGCCGGTCCCTCATAGTCCGC 1671
 QY 546 ILeCyAsnMetHLSGlnPheAlileAspGlnGluProAspTYrPheGlnLYSLNpheVal 565
 DB 1672 ATTGGCAACATGACACCGATTATTGACGAGAGCCGACGATGTTGAAAAGAGTTCGTT 1731
 QY 566 ProPheHLSProProProLeuArgTYrArgGluProAlaLeuGlnLYSLYSLYSLYSLY 585
 DB 1732 CCTTCCATCTCTCCATCGCTGCTACCGGAGCCATCTTGAGAAATTTGATTCGGGC 1791
 QY 586 LeuValLeuAsnAspValMetCyLYSLYProGlyProGlyLeuSerAspPheCyLeuLYVal 605
 DB 1792 TTGGTTTAAATATGATGTCATGTGCAACCGGCTGAGTACGACTTCTGCTTAAAGTGA 1851
 QY 606 GlnAlaProValLeuGlyAlaAlaThrGlyProAlaAspSerGlnHLSGLYSLY 625
 DB 1852 GAGCGGCTGTTCTTGGGGCAACCGGACCAAGCCGACTCCAGCAGCAGAGTCAAGCATGGG 1911
 QY 626 GLYLeuAspGlnAspGlyLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 645
 DB 1912 GGGCTTGACCAAGACGGGAGGCGCGGCTGCTTGAAGGTAGCGCGCGCTGCAACCC 1971
 QY 646 LeuLeuHLSerThValLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 665
 DB 1972 CTGCTGACACCGGTGAAGGCGCGGCGCTCGGACATGCGCGGAGCTCAGGCATCTAT 2031
 QY 666 AspSerSerValProSerSerGlnLeuSerLeuProLeuMetGlnGlyLeuSerThAsp 685
 DB 2032 GACTCGCTGCGCTCATCCGAGCTGCTCTGCACTGATGAGAGACTCTCGACGAGC 2091
 QY 686 GlnThrGlnThrSerSerLeuThrGlnSerValSerSerSerSerGlyLYSLYLYSLY 705
 DB 2092 CAGACGAAACGCTTCTCGACGAGAGCGGTGCTCTTCAAGGCGCGGAGGAG 2151
 QY 706 GlnProProAlaLeuProSerLyLeuLeuSerSerGlySerCyLYSLYSLYSLY 725
 DB 2152 GAACCTCTGCGCTCTTCCAGCTCTCTCTTCTGGTCAATGCAAGAGATCTTGGT 2211
 QY 726 CyAspSerTYrThrAspGlnLeuHLSAlaValAlaPro 738
 DB 2212 TGCAGAGTACACTGATGAATCCAGCGGTGCGCCCT 2250

; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yungting
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Reena
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
 ; FILE REFERENCE: 803
 ; CURRENT APPLICATION NUMBER: US/09/799,451
 ; CURRENT FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 948
 ; SOFTWARE: pc_FL_genes Version 2.0
 ; SEQ ID NO 125
 ; LENGTH: 3948
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (60) .. (1844)
 US-09-799-451-125
 Alignment Scores:
 Pred. No.: 0
 Score: 3248.00
 Percent Similarity: 99.7%
 Best Local Similarity: 99.5%
 Query Match: 82.3%
 DB: 3
 Gaps: 0
 Length: 3948
 Matches: 609
 Conservative: 1
 Mismatches: 2
 Indels: 0
 Gaps: 0

US-10-616-788-2 (1-738) x US-09-799-451-125 (1-3948)
 QY 127 GlnLeuIleLeuLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 146
 DB 6 CAACATAATCTTAAAGATCCGAAGAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGA 65
 QY 147 SerGlnProPheLeuAsnMetLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 166
 DB 66 TCTCAACCTTCTCTGAATATGAATTTGAAGGATTTATTTGTAAGGTGTGCTCTTTT 125
 QY 167 ProSerIleLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 186
 DB 126 CTTTCATTAATAAAGCAAGCAATTAACACCTTTCTCTTTTGAACCCGAGCTGTGAC 185
 QY 187 LeuLeuLeuGlnProAspAsnLeuAlaCyLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 206
 DB 186 CTGTTGTACAGCGGACCAATCTAGCTTGAACCTTTCTGGAAGCTCGAAACCTGAAC 245
 QY 207 ILeSerGlnHLSGLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 226
 DB 246 ATGAGCAGAGATGGCTCGGACATGCAAGAGGTGCTTGGACACGACGACGACCACTTCG 305
 QY 227 PheArgPhePheTYrLeuHLSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 246
 DB 306 TTCCGTTCTCTCATCTTCACTCAAGCTCAAGCAAGAAAGACCTTTCAAGCGAAAGACC 365
 QY 247 CyLeuGlnGlnGlnThrThrGlnThrThrSerCyLeuLeuGlnAsnValSerProGly 266
 DB 366 TGTAAAGAGAGAACTACAGAGATGACGAGTGCCTCTCTCAAAATGTTTCTCAAGGG 425
 QY 267 AspTYrIleIleGlnLeuValAspAspThrAsnThrThrArgLYSLYSLYSLYSLYSLY 286

RESULT 3
 US-09-799-451-125
 ; Sequence 125, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:

Db	426	GATTATATATATTGAGCTGGTGGATGACATTACACAAAGAAAATGATGATTATGGC	485
OY	287	LeuIysPProValIHISerProTrrPalglYProIleaYAlaMetAlaIleThrValPro	306
Db	486	TTAAAGCCAGCATCCTCCCGGTGGGCGGGGCCCATGACAGCGGTGGCCATTCACAGTGCCA	545
OY	307	LeuValValIIESerAlaPheAlaThrLeuPheThrValMetCysArgIlyslYsgInGln	326
Db	546	CTGGTAGTCATATCGGCATTCCGAGCGCTTTCACGTATGTGGCCGCAAGAAAGCAACAA	605
OY	327	GIuaenIleYSerSerIleuNapIugIuSerSerGIuSerSerThrYrThrAlaIa	346
Db	606	GAAATATATATATTCACATTTAAGTGAAGAGAGCTGTGAAGTCTTCCCATATACACTGCAGCA	665
OY	347	LeuProArgIuaYArgLeuArgProArgProIyValPheLeuCyArYrIserSerIyAsp	366
Db	666	CTCCCAAGAGAGAGGCTCCGGCGGGCGGAAGGTCTTTCGTGCTATTCAGTAAAGAT	725
OY	367	GIYGIuaenHISemecAsnValAlaGInCyPheAlaYrPheLeuGlnNapPheCysGIY	386
Db	726	GGCCAGAAATCAGATGATGTGCTCCAGTGTTCGCTACCTTCCCTCCAGACATTCGTGGC	785
OY	387	CysGIuValAlaLeuNapLeuTrpGIuNapPheSerLeuCyArgGIuGIuGlnArgIu	406
Db	786	TGTGAGGTGGCTCTGGACCTGTGGGAAGCTTCAGCTCTGTAGAAAGGGCGAAGAA	845
OY	407	TrpValIIEGlnIlyslIeHISgluSerGlnPheIleIleValAlaCysSerIyslYmet	426
Db	846	TGGGTGCATCCAGAAATCCACGAGTCCCATGTTCAATGTGTGGTTGTTCCAAAGGTATG	905
OY	427	LyslYrPheValAlaPrlYslYAsnYrYrIyWHISlyGslYGIYArGIYserGIYlyIyV	446
Db	906	AAGTACTTGTGTGGACAGAGAACTTACAAACCAAGAGAGGTGGCCGAGGCTCGGGGAAA	965
OY	447	GIYGIuNapPheLeuValAlaValSerAlaIleAlaGlnIlyLeuArgIlnAlaYsgIn	466
Db	966	GAGAGGCTTCTTCGTGGTGGGTGTCAAGCATTTGCCAAAGCTCCGACAGGCAAGCAG	1022
OY	467	SerSerSerAlaAlaLeuSerIyPheIleAlaValYrPheNapYrSerCyGIuGIY	486
Db	1026	AGTTGCTCGCGGCGCTCAGCAAGTTATTCGCGCTACTTGTGATTATTCGCGAGGGA	108
OY	487	AspValAlProGIYIleLeuNapLeuSerThrIlyYrYrArgLeuMetAspNapLeuProGln	506
Db	1086	GACGTCCCCGGATATCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAG	1144
OY	507	LeuCySerSerHISleuHISerArgAspHISglYleuGlnGlnIuProGIYGIuHISThrArg	526
Db	1146	CTCTGTTCCTCCACTCACACTCCGAGACCAAGCGCTCCAGAGAGCGGGGACGACAGCCAA	120
OY	527	GIuGIYserArgArgAsnYrPheArgSerIySerGIYArgSerLeuYrValAlaIle	546
Db	1206	CAGGGCAGCAAGAGAACTACTTCCGAGCAAGTCAAGGCCGGTCCCTTATACGTGGCCATT	126
OY	547	CysAsnMetHISglnPheIleAspGIuGIuProAspYrPheGIuIlysgInPheValPro	566
Db	1266	TGCACATATGCACAGTTATTTACGAGGAGCCGAGCTGGTTGSAAGCAAGCATTCGTTCCC	132
OY	567	PheHISProProProLeuArgYrYrArgIuProValLeuGIuIlyPheAspSerGIYleu	586
Db	1326	TYCCATCTCTCCCTCACTGGCTTACCGGAGCAAGTCTTGAGAAATTTATTCGCGGCTTG	138
OY	587	ValLeuAsnAspValMetCysIyAsPProGIYProGIYserAspPheCysIeIuYslValGIu	606
Db	1386	GTTTAAATAGATCATGTGCAAAACAGGGCCCTGAGATGATCTTCTGCTTAAAGGTAGAG	144
OY	607	AlaPProValLeuGIYAlaThrGIYProAlaAspSerGIuHISgluSerGIuHISglYGIY	626
Db	1446	GCGGCTGTTCTTGGGGCAACCGGACCAAGCCGACTCCCAACAAGAGTCAAGCATGGGGGC	150
OY	627	LeuAspGIuNapGIYGIuAlaArgProAlaLeuAspGIYSerAlaIleuGlnIuProLeu	646

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Db      1506 TTGAGCCAAAGCGGGAGAGCGCCGGCTGACCGGTAGCGCGCCGCTTGAACCCCTG 1555
QY      647 LeuHsrValIlyValAGlySerProSerApmMetProArgAapSerGlyIleTyAsp 666
Db      1566 CTGCAACACGGGTGAAGCCGGACGCCCTTCGGACATGCGCGGACCTAGGATATTAGAC 1625
QY      667 SerSerValProSerSerGlnLeuSerLeuProLeuMetGlnGlyLeuSerThrAspGln 686
Db      1626 TGGTGTGGCCCTCATCCGACCTCTCTCTGCACTGATGGAAAGACCTCTGCACGGACAG 1685
QY      687 ThrGlnThrSerSerLeuThrGlnSerValSerSerSerSerGlyLeuGlyGlnGln 706
Db      1686 ACAGAAACGTCTTCCCTCGACGGAGAGGTGTCTCTCTTCAGGCTCGGGTGAAGAGAA 1745
QY      707 ProProAlaLeuProSerLybLeuLeuSerSerGlySerCybValAlaAapLeuGlyCys 726
Db      1746 CCTCTCGCCCTCTCTCCAGACTCTCTCTCTGCGGTCAAGCAAGACAGATCTTGTTGC 1805
QY      727 ArgSerTyThrAapGlnLeuHsrAlaValAlaPro 738
Db      1806 CGCAGCTACACTGATGAATCTCCACGCGGTGCCCCCT 1841

RESULT 4
US-09-949-002-117
; Sequence 117, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 3120
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-117

Alignment Scores:
Pred. No.: 1,38e-24 Length: 3120
Score: 321.50 Matches: 183
Percent Similarity: 35.9% Mismatches: 106
Best Local Similarity: 22.7% Indels: 161
Query Match: 8.1% Gaps: 34
DB: 3

US-10-616-788-2 (1-738) x US-09-949-002-117 (1-3120)
QY      31 GlyArgAlaTrpGlyValAapThrCysGlyTYTPArgGlyValGlyProAlaSerArgAsn 50
Db      70 GGGCCCTGCTGGGGCTGCTCTCTGCTGCTCGGGCGTG-CTGGCCCGGGGTGGCGCTCC 128
QY      51 SerGlyLeu-----TyrAsnIleThrPhe 58
Db      129 CTGGCACTCTCGACCAACCGGGCGGTGTGCTGCCAGCGGGGCTAAACTGCACGCTC 188
QY      59 LysTyraAapCys-----ThrThrTyrlleuAapProValGlyIlyHisValIleAla 76
Db      189 AAGAAATGACTCTCTCGATGACAGCTGCATTCACCT----- 227
QY      77 AapAlaGlnAenIleThr-----IleSerGlnTyraAlaCys 88
Db      228 -----GMAACTGCACCCCTCTCTCCCAAGAGACTGCAGATTCAGCTGCACCTTGGC 281
QY      89 HisAapGln-----ValAlaValThrIleLeuTrpSer---ProGlyAla 102
Db      282 CACACCCAAACAGAGACTGTTCCTCCCGGTGCTCACATGAAATGAGACATGCAAGACAGAC 341

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US-09-949-002-126
Sequence 126, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYOMPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: C1000790
CURRENT APPLICATION NUMBER: US/09/949, 002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 126
LENGTH: 3120
TYPE: DNA
ORGANISM: Human
US-09-949-002-126

Alignment Scores:

Pred. No.:	1,38e-24	Length:	3120
Score:	321.50	Matches:	183
Percent Similarity:	36.0%	Conservative:	107
Best Local Similarity:	22.7%	Mismatches:	356
Query Match:	8.1%	Indels:	161
DB:	3	Gaps:	34

US-10-616-788-2 (1-738) x US-09-949-002-126 (1-3120)

Qy 31 G1AATGATATPGIYAALPThCySGlyTTPArgLyValGIYProLASezArgAsn 50
Db 70 GGCCCTGTGGGGCTGCTCTGCTGCTCTGGGGGTTG-CGGGCCCGGGTGCGCTCC 128
Qy 51 SerGIyLyu-----TyRAnILleThPhe 58
Db 129 CTGCACCTCTCGAACCAACCGGGCGCTGTCTGCCAGCCGGGGCTAAACTGCACGGTC 188
Qy 59 LySTyRAepAnCyS-----ThTThTyLeuAnPProValGIyLysHIAvalIIeAla 76
Db 189 AAGAATGATACCTGCTGGATGACAGCTGCATTCACTC----- 227
Qy 77 AsPAIagInAnILleThr-----ILeserGlnTyRALcyS 88
Db 228 -----GSAACTGAACCCCTCCCTCCCAAGACCTGCAGATCCAAGCTGCACCTTGGCC 281
Qy 89 HIsApGLn-----ValAlaValThrILEuTYPSer--ProGIyAla 102
Db 282 CACACCACAAGAGAGACTGTCCCGGTGGCTCACATCGAATGAGACATGCAGACAGAC 341
Qy 103 LeucLIyleGIunPhelEuLyGIYPheaRGYalIIleuGluGluLeuLYSerGIuGly 122
Db 342 GCCAGCATCTGTGACTCGAGGGGTCAGAGATTATCTGTCTGCAGCTGAACACCAATGAA 401
Qy 123 ArgGInCYseGInGInLeuIIleLyuLaAPProLySGInLeuAnSenSerPheLYARG 142
Db 402 CGTTGTGCGTCAGG-----TTTAGATTCTGTGCCAACTGAGAGCATCACACAGCGCG 455
Qy 143 ThrGIyMeGIuSerGInProPhelEuAnMeLySBpegLUthRAPtyRPheVALlys 162
Db 456 TGGCGTTTACCTTCAGGCACCTTGTG---GTGACCTCGACAGAAATAGAGTAC 512
Qy 163 Val-----ValPProPheProSerILEyASbnLIuSerAnTYRHIsPProPhePhe 180
Db 513 GTTACCAACCTGGCCCAAGCCCATCTCGATGGGAGCAACCAACCAAGTCMAAATTTCC 572
Qy 181 ArgTHRarGaLaCYSAepLeuLeuLeuGInProAsPAnLeuAlaCYSLys----- 197
Db 573 CTGTGGCTGACTGTGAGCAGCCAGATGAAGTAACACGCAATGATGAGTCACTCAGCC 632
Qy 198 ProHeTPHySProARgAnLeu----- 205

Db	653	AGCCGTGGAGACCC---AACAATACCCGTGGAGACCCCTGGAGAGCCCAACAGTGGTGTGG	688
Qy	206	-----AsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis	220
Db	690	AGCTTCAACCCGTGTGGAGCAATCTTACCAATTCACAGATCTGTGTGACCAAGTTTTCGACAC	749
Qy	221	AlaProHisAspPheHisGlyPheAspGlyPheHisGlyLeuHisGlyValLeuHisGlyValGly	240
Db	750	ATGGAGAACCCACAGTTGCTTTGAGACACATGACAC---CACATACCTGGCCGCCAGACAGAA	806
Qy	241	ProPheValGlyValThrCysValGlnGlnGlnInThrThrGlnInThrThrSerCysLeuLeu	260
Db	807	GAGTTTCCACCCAGCATTCACAGTCACTCACTCACTCAAGCAACCTTAAAGGAGTGTGTGGC	866
Qy	261	GlnAsnValSerProGlyAspTyrIleIleGlyLeuValAspAspThr-----Asn	277
Db	867	CACCAAGGACGAGATTCACAGCCCTTGTTCAGAGCTGGCTCAATGATGCTGCTGACATCTCC	926
Qy	278	ThrThrAspGlyValMetHisGlyValLeuValProValHisSerProTyrAlaGlyPro	297
Db	927	GGCACTGTTTCTCTGCCAGAAATGGACACATCCAGATGCTCAACCCGACAGATCAATGCC	986
Qy	298	IleAspAlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPhe	317
Db	987	CTGGGGGTGATCTGTTGATCATACGGGACATCTCACTGTCTGTGGGTGGCTGTCACTCTG	1044
Qy	318	ThrValMetCysValGlyValGlnGlnGlnValAsnIleTyrSerHisValAspGlnGlySer	337
Db	1047	CTCATCTGCTGCATGACCTCGAGGCTAGCTGGGCTGGAAAT-----GAAATAATAC	109
Qy	338	SerGlySerSerThrTyrThrAlaAlaLeuProArgGlnValGluValArgProArgPro---	356
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Qy	357	-----LysValPheLeuCysTyrSerSerIleValAspGlnValAsnHisMetAspVal	373
Db	1158	AAGCCCAAGAAAGGCTGTGATCATCTACCTACCAACC---GACCAACCCCTCTAGCTGAGACGTG	121
Qy	374	ValGlnCysPheAlaTyrPheLeuGlnHisAspPheCysGlyCysGlnValAlaLeuAspLeu	393
Db	1215	GTCTCGAAATTCGCCCAAGTCTCTGTCTCAACGCCCTGGCGACAGAAAGTGGCTGTGACCTG	1277
Qy	394	TyrGlnAspPheSerLeuCysArgGlnGlyGlnArgGlnTyrVal-----Ile	409
Db	1275	CTGGAAAGACGAGCATCTCGAGGACGAGAGTCAATCACTGGTGGTGGCCGTACAGAAAGAG	133
Qy	410	GlnIlyValIleHisGlySerGlnPheIleIleValValCysSerIlyValMetIlyValThr	429
Db	1335	GAGATGTGGAGACCAATCTTAAATGATCATCTCTGTCTCTCCCGGACACGCGC-----	1388
Qy	430	ValAspIlyValAspAspTyrIlyHisIlyValGlyIlyGly-----	441
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Qy	442	ArgGlySerGlyIlyGlyIlyLeuPheLeuValAlaValIleSerAlaIleAlaGlyIlyLeu	461
Db	1443	CACGGAAAGCCCGGTGGGAGCTGTTCATCTGACGACGAAAGATGATCTCCCGGACCTTC	1500
Qy	462	ArgGlnAlaIlyValGlnSerSerSerAlaAlaLeuSerIlyPheIleAlaValIlyPhe---	480
Db	1503	AAGAGG-----CCAGCTGCTTCCGACCTTCAAGTCAAGTCTGTACTTTCAGC	1547
Qy	481	AspTyrSerCysGlnGlyAspValProGlyIlyLeuAspLeuSerThrIlyTyrArgLeu	500
Db	1548	GAGGTCAAGCTTACCGGAGAGTCTCCGACCTGTTCGGCGCGGCGCGGCTACCGCTTC	1607
Qy	501	MetAspAsnLeuProGlnIleCysSerHisIleHisIleSerArgAspHisGlyIlyGlnGlnIly	520
Db	1608	ATGACACAGTTTCAGAGAGGTG-----TACTTCCGATTCACAGACCTGAGATGTTCCAG	1661
Qy	521	ProGlyGlnHisThrArgGlnGly-----SerArgArgAspIlyThrAspSerIlySer	538
Db	1662	CCGGGCGCGATGCACCGGTAGGGAGAGCTGTCCGGGGGACAACTATCTCCGAGCCCGGCG	1721

Qy	539	GLYVRSERLEUITYRVALAIAILECYSAMETHIASGIPHEILEAPRGULUProAsp	558
Db	1722	GCGAGGACGCTCCGGCCGCTTGACAGGTTCCGGGACTGGCAGGTCGGCTCCGAC	1781
Qy	559	TRPHEGU-----LYSGINPHEVALProPHEIASProPro	570
Db	1782	TGGTTTCGAATGTGAACACTCTACTCAGCAGATGACACAGATGCCCGCTCCGTGACGA	1841
Qy	571	PROLEUAIGTRYFAARGGULProVALLEUGULYBPHEAPSERGTYLEUVALLEUAHP	590
Db	1842	GAGGTG--TTTGGAGACCACTGCTGCTCCG--GGAAACGGGATGTGTAAACGGGCG	1895
Qy	591	VALMETCYSLYSPROGILYProGLUSERAPSPHECYSLYUVALYLIALAProVALLEU	610
Db	1896	CCCCGTGGTCCGAG--CTTGCGCTCCAGGCTGCTCGGCAATGAC--CCGCTGCTC	1949
Qy	611	GLYLAATHRGILYProALAASPSEGINHIAGLUSERGINHIA-----	624
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Db	2070	GCGGTGACGCTGGGCCCCCTGCTGACGATGCCGACATCCGCTGGCAGCTGGCGGGAG	2129
Qy	641	ALAIALEUGINProLEUENHIAETHVALYLVALAGLYSerProSERASPMEProARG	660
Db	2130	GCGAGGCGCTGCCGCTGTGGGACGCCGGGCGCTGG-----CGA	2171
Qy	661	ASPSEGTGLYIETRYASPSESERVALProSERSESGILYUENSERGLYProLEMETGLU	680
Db	2172	AATAGCGCTCCCTTC-----CTCCCGTGAACCCGAGAGCTCGCCCTT-----	2216
Qy	681	GLYUENSERTRAPAGLINTHRGILUTHRSERSELEUTHRGILUSERVALSERSESER	700
Db	2217	GCGACGACACCCCATGCGCTCTCTGACCTCTTCCAGAGACGTAG-----	2267
Qy	701	GLYLEUGILYGLUGULINProProALAILEUProSERLYALEUENSERSESGILYSer	720
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Qy	721	LYEALASPGLYCYe	726
Db	2319	CAGGCCACGAGGGGCTGC	2336

RESULT 6
 US-08-620-694A-9
 : Sequence 9, Application US/08620694A
 : Patent No. 5869286
 : GENERAL INFORMATION:
 : APPLICANT: Yao, Zhengbin
 : APPLICANT: Spriggs, Melanie
 : APPLICANT: Fanelow, William
 : TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Immunex Corporation
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: WA
 : COUNTRY: USA
 : ZIP: 98101
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: Apple Power Macintosh
 : OPERATING SYSTEM: Apple Operating System 7.5.5
 : SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/620, 694A

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FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,525
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2693
US-08-620-694A-9

Alignment Scores:
Pred. No.: 1,466-24 Length: 3223
Score: 321.50 Matches: 183
Percent Similarity: 35.9% Conservative: 106
Best Local Similarity: 22.7% Mismatches: 357
Query Match: 8.1% Indels: 161
DB: 2 Gaps: 34

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QY 51 SerGlyLeu-----TyrAsn11eThrPhe 58
189 CTGCGACTCTTGAGACACCGGGCGCTGCTCTGCCACCGGGGGCTMAACTGCACGGCTC 248
QY 59 LysTyrAspAsnCys-----ThrThyTyrLeuAsnProVal1GlyBHisVal11eAla 76
249 AAGAAATAGTACTGCTCTGATGATCAAGCTGATCACTC----- 287
QY 77 AspAlaGlnAsn11eThr-----11eSerGlnTyrAlaCys 88
288 -----CGAAACTGTACCCCTCTCTCCCAAGAGACTGCAGATCTCAGCTGACTTGGCC 341
QY 89 HisAspGln-----Val1AlaVal1Thr11eLeuTyrSer---ProGlyAla 102
342 CACACCCCAACAGAGAGACTCTTCCCGTGGCTCACTCGAATGAGACATGACAGACAGAC 401
QY 103 LeuGly11eGluPheLeuY1eGlyPheArgVal11eLeuGluGlu1eLeuY1eSerGluGly 122
402 GCCAGCACTCTGTAACCTCGAGGGGTGCAGAGTTATCTGCTCGACGCTGAAACACCAATGAA 461
QY 123 ArgGlnCysGlnGlnLeu11eLeuY1eAspProY1eGlnLeuAsnSerSerPheY1eArg 142
462 CGTTTGCGCTCAG-----TTTAGAGTTTCTGTCCAAACTGCAGAGCATCACACAGCGGG 515
QY 143 ThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheVal1Lys 162

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 Qy 181 ArgThrArgIleCysAspLeuLeuGlnProAspAsnLeuIleCysIle----- 197
 Db 633 CTGTGCTGATCTGTAGACAGCGAGATGAAGTAAACAGCCATCATGAGCTCAGGC 692
 Qy 198 ProPheTrpIleProAspAsnLeu----- 205
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 Qy 206 -----AsnIleSerGlnIleGlySerAspMetGlnValSerPheAspHis 220
 Db 750 AGCTTACCCCTGAGACGAAATCATCAAGATCCATGAGTGTGAGCAGATTTTCCGCAC 809
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 Db 810 ATGAGAACACCAAGTTGCTTGAACACATGCAC---CACATACCTGCGCCAGACAGAA 866
 Qy 241 ProPheIleAspTrpIleCysIleGlnGlnIleThrIleThrIleSerCysLeuLeu 260
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 Qy 298 IleArgIleMetAlaIleThrValProLeuValIleSerAlaPheAlaThrLeuPhe 317
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 Db 1449 -----GCCAAGTGGAGCGGCTCTGCTGCGCGGCGGCGCTGCGCGCTGCGTGAC 1502
 Qy 442 ArgGlySerGlyIleGlyLeuPheLeuValAlaValSerAlaIleAlaGlnIleLeu 461
 Db 1503 CAGGAAAGCCCGTGGGAGACTGTTCACTGACGACCATGATGATCTCCCGGAGCTTC 1562
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 Qy 501 MetAspAsnLeuProGlnIleCysSerHisLeuHisSerArgAspHisIleGlnGlnIle 520
 Db 1668 ATGACAGGTTCCAGAGAGT-----TACTTCCGATTCAGACACCTGAGATGTTTCCAG 1721
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 Db 1722 CCGGGCGCATGACCGCGTGAAGGAGCTGTCCGGGAGCAATCACTGACCGGAGCCCGGCG 1781
 Qy 539 GlyArgSerLeuTrpValAlaIleCysAsnMetHisGlnPheIleAspGlnGlnProAsp 558
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RESULT 7
 US-09-022-255-9
 ; Sequence 9, Application US/09022255
 ; Patent No. 6072033
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Farnlow, William
 ; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:

QY 51 SerGlyLeu-----TyrAsnIleThrPhe 58
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 DB 249 AAGAAATGATCTGCTGATGATGACGCTGATTCACCT-----287
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 DB 1956 CCCCTGTGGCGCAG---CCTGTCTCCAGGCGCTGCTGCGCCATAGAC---CCGCTGTG 2009
 QY 611 GlyAlaThrGlyProAlaAspSerGlnHisGluSerGlnHis-----624
 DB 2010 GGGGAGGAAGAGACAGACGATGGCAAGCTGAACTTCACTGACGCCCGGGGTGAG 2069
 QY 624 -----624
 DB 2070 CAGAGCGCGAGCGCTCCACACCTGTGTCTGCGCGGAGAGAGGGCGCTGTGGCC 2129
 QY 625 -----GlyLeuLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640
 DB 2130 GCGGTGAGCGTGGCGCCCTGCTGACAGGTCGCGACGCTCGGCTGACATGCGGGGAG 2189
 QY 641 AlaAlaLeuGlnProLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
 DB 2190 GCGGAGCGCTGCGCTGTGGCGACCGCGGCGCTGGG-----CGA 2231
 QY 661 AspSerGlyLysThrAspSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680

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Db      2232 AATAGCGCTCTTC-----CTCCCGGACGCCGGAGACTGCCTT----- 2276
Qy      681 GtyleSerThraepGlnThrGlutHrserSerleuthrGlnSerValSerSerSer 700
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Db      2277 GGCAAGCACACCCCCCATGCCTCTCCTGACCTCTTCAGAGAGACTAGG----- 2327
Qy      701 GtyleGtlygluglInuProPrAlaleuProSerlySbleuSerSerGlySerCy 720
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2328 -----GAGCACTCGAAGGTGTATGCTCTTGCTTCAGACAGACTGAGCTGC 2378
Qy      721 LysAlaApLeuGlyCy 726
        ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2379 CAGGCCACGGGGGGCTGC 2396

RESULT 9
US-08-978-773-3
; Sequence 3, Application US/08978773
Patent No. 6083906
GENERAL INFORMATION:
APPLICANT: Trout, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978, 773
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052, 525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IL-17R
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2690
US-08-978-773-3

Alignment Scores:
Pred. No.: 1,46e-24 Length: 3223
Score: 321.50 Matches: 183
Percent Similarity: 35.9% Conservative: 106
Best Local Similarity: 22.7% Mismatches: 357

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Query Match:	8.1%	Indels:	161
DB:	3	Gaps:	34
US-10-616-788-2 (1-738) x US-08-978-773-3 (1-3223)			
QY	31	GLYArgLAATPrGlyValAAspThrCysGlyTyrArgGlyValGlyProAlaSerArgAsn	50
DB	130	GGCCCCGCTGGGGCTGCTCTGCTGCTCTCTGGGGCTG-CTGGCCCCGGGGTGGGGCTCC	188
QY	51	SerGlyLeu-----TyrAsnIleThrPhe	58
DB	189	CTGGCAATCTCGAGCAACCGGGCTGGTCTGCTCCAGCGGGGGTAACTGACGGCTC	248
QY	59	LysTyrAspAsnCys-----ThrThyTyrIleAsnProValGlyLysIleValIleLea	76
DB	249	AAGAATAGTACTCTCGATGACAGCTGATGACCTT-----	287
QY	77	AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys	88
DB	288	-----CGAAACTGACCCCTCTCTCCCAAGAACCTCGACAGATCCAGCTGACCTTGGC	341
QY	89	HisArgGln-----ValAlaValThrIleLeuTyrSer--ProGlyAla	102
DB	342	CACACCCCAACAAAGAGACCTGTCCCGTGGCTCAGATCGAATGAGACCTGCACAGAC	401
QY	103	LeuGlyIleGluPheLeuLysGlyPheArgValIleLeuGlnGluLeuLysSerGlnGly	122
DB	402	GCCAGCATCTGTACCTCGAGGGGTGCAGAGTTACTGTCTGCAGCTGAACCCAAATGA	461
QY	123	ArgGlnCysGlnGlnIleuIleLeuLysAspProLysGlnIleuAsnSerPheLysArg	142
DB	462	CGTTGTGCGGCAGG-----TTTGAGTTTCTGTCCAACTGAGGACATCACACAGCGG	515
QY	143	ThrIleMetGlnSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheValLys	162
DB	516	TGGGGTTTACTCTTCAGCCACTTTGTG--GTGACCTCTGCACAGAAATAGAGTGGACC	572
QY	163	Val-----ValProPheProSerIleLysAsnIleuSerAsnTyrGlnPhePhePhe	180
DB	573	GTTACCAACCTGGCCCAAGCCATCTGTAGTGGGACCCCAACCAACCACTGCAAGATTTTC	632
QY	181	ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLys-----	197
DB	633	CTTGTGGCTGACTGTGAGCAACGCAAGATGAGTAAACCAACGCAATGATGAGTCAAGC	692
QY	198	ProPheTyrLysProAlaAsnLeu-----	205
DB	693	AGCCTGTGGAGCCC--AACTATCAACGATGAGAACCTGTGAGGCCAACCACTGCTGTG	749
QY	206	-----AsnIleSerGlnHisGlySerAspMetGlnIleSerPheAspHis	220
DB	750	AGCTTCAACCTGTGGAAACGAACTTACCAATTCACAGATCTGCTGACCAAGTTTTCGGAC	809
QY	221	AlaProHisAsnPheGluPheArgPhePheTyrIleuHisTyrTyrLysLeuLysGlnGly	240
DB	810	ATGGAACAACCAAGTCTTTTGAACACATGAC--CACTACCTGGGCCACAGACAA	866
QY	241	ProPheLysArgLysTyrCysLysGlnGlnIleThrThrGluThrThrSerCysLeuLeu	260
DB	867	GAGTTTCCACAGCATCCAAAGCTCACTCACTCACTTAAGAGGTGCTGTGCG	926
QY	261	GlnAsnValSerProGlnAspTyrIleIleGluLeuValAspArgThr-----Asn	277
DB	927	CACCAATGCAAGATCCAGCCCTTTTCAAGACGCTGCTCAATGATCTGCTCAGACATCC	986
QY	278	ThrThrArgLysValMetHisTyrAlaIleuLysProValHisSerProTyrAlaGlyPro	297
DB	987	GGCACTGTTTCTTCCGCAAAATGCAACCTGCAGAACCAATTCGCGACTACATGCTCC	1046
QY	298	IleArgAlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPhe	317
DB	1047	CTGTGGGTATGACTGTTCAATCAAGGAGATCTCAATCTGTGGTGGGCTGCTGATCTTG	1106


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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2693
US-09-022-253-9

Alignment Scores:
Pred. No.: 1,46e-24 Length: 3223
Score: 321.50 Matches: 183
Percent Similarity: 35.9% Conservative: 106
Best Local Similarity: 22.7% Mismatches: 357
Query Match: 8.1% Indels: 161
DB: Gaps: 34

US-10-616-788-2 (1-738) x US-09-022-253-9 (1-3223)
QY 31 GlyAlaTrpGlyValAspThrCysGlyTrpArgGlyValGlyProAlaSerArgAsn 50
DB 130 GGCCTCTGCTGGGGCTCTCTCTGCTCTGGGCGTG-CTGGCCCGGGGTGGGCGCTCC 188
QY 51 SerGlyLeu-----TyrAsnIleThrPhe 58
DB 189 CTCGCACTCTCGACCAACCGGGCGTGTCTCCAGCCGGGGCTAACTGCACGGTC 248
QY 59 LysTyrAspAsnCys-----ThrThrTyrLeuAsnProValGlyLysHleAla 76
DB 249 AAGAAATGTAACCTGCTCGGTGATGACGTGATTCACCT----- 287
QY 77 AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys 88
DB 288 -----CGAAACCTGACCCCTCTCCCAAGAGACTCGACATCCAGCTGCTTGGCC 341
QY 89 HisAspGln-----ValAlaValThrIleLeuTrpSer-----ProGlyAla 102
DB 342 CACACCCCAAGAGAGACTGTTCCTCCGCTCACATCGAATGACACTGCAGACAGAC 401
QY 103 LeuGlyIleGluPheLeuLysGlyPheArgValIleLeuGluGluLeuLysSerGluGly 122
DB 402 GCCAGCATCTCTGTAACCTCGAGGGTGCAGAGTATCTCTCTGCAGCTGAACACCAAGAA 461
QY 123 ArgGlnCysGlnGlnLeuIleLysAspProLysGlnLeuAsnSerSerPheLysArg 142
DB 462 CGTTTGCGCTCAGG-----TTTGAAGTTCTGTCCAACTGAGGGCATCACACAGCGG 515
QY 143 ThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheValLys 162
DB 516 TGGCGTTTAACTTCAGCCACTTGTG---GTTGACCTTCAGCAAGAAATGAGGTGACC 572
QY 163 Val-----ValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhe 180
DB 573 GTTCACCACTGCTGCCAAGCCATCCCTGATGGGAGCCAAACCACTCAAGTCAAGATTTC 632
QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLys----- 197
DB 633 CTGTGCTGCTGCTGAGCAGCGCAGAGTAGAGTAAACAGGCATCATGAGGTGAGGC 692
QY 198 ProPheTrpLysProArgAsnLeu----- 205
DB 693 AGCCTGTGGAGCC---AACATCACCGTGAAGACCTTGAGGCCACAGCTGCGTGTG 749
QY 206 -----AsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
DB 750 AGCTTCAACCTGTGGAAGCAATCTACCATTAACAGATCTCTGCTGACCAATTTTCCGAC 809
QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuLysGluGly 240
DB 810 ATGGAGAACCAAGATTGCTTTGAGACATGAC---CACATACCTGCGCCAGACAGAA 866
QY 241 ProPheLysArgLysThrCysLysGlnGluGlnThrThrGluThrThrSerCysLeuLeu 260

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DB 867 GAATTCACCAAGGATTCACAGCTCACTCAACGAACTTAAAGGTCTCTGCGC 926
QY 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThr-----Asn 277
DB 927 CACCAAGTGCAATCCAGCCCTTCTTACAGAGCTGCTCAATAGACTGCTCAGACACTCC 986
QY 278 ThrThrArgLysValMetHisTyrAlaLeuLysProValHisSerProTrpAlaGlyPro 297
DB 987 GCGACTGTTTCTGCCCAAAATGCAAGACACTCCAGAAACAAATTCGCACTACATGCC 1046
QY 298 IleArgAlaMetAlaIleThrValProLeuValIleIleSerAlaPheAlaThrLeuPhe 317
DB 1047 CTGTGGGTGTAAGCTTTCATCAACGAGCATCTCATCTGCTGTGGGCTCCGATCTCG 1106
QY 318 ThrValMetCysArgLysLysGlnGlnGlnAsnIleTyrSerHisLeuAspGluSer 337
DB 1107 CTCATGCTGTGACATGACCTGAGGCTAGCTGAGGCTGAAAGT-----GAAATAATAC 1157
QY 338 SerGluSerSerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgPro-- 356
DB 1158 AGTGATGACACCAAAATACACCGATGCGCTGCGGCTGACCTGATCCGCCACGCTG 1217
QY 357 -----LysValPheLeuCysTyrSerSerLysAspGlyGlnAsnHisMetAsnVal 373
DB 1218 AAGCCAGAGAGGTCTGATCATCTACTACGCC---GACCAACCCCTTACGTGACGTG 1274
QY 374 ValGlnCysPheAlaTyrPheLeuGlnAspPheCysGlyCysGlyValAlaLeuAspLeu 393
DB 1275 GTCTCAAAATGCGCCAGATTCCTGCTCACGCGCTGCGGACGGAATGGGCGCTGACCTG 1334
QY 394 TrpGluAspPheSerLeuCysArgGluGlyGlnAspGluTrpVal-----Ile 409
DB 1335 CTGGAAGACAGAGCCATCTCGAGAGGACATGATACCTGGGTGGCGCTCAGAAAGAC 1394
QY 410 GlnLysIleHisGluSerGlnPheIleIleValAlaCysSerLysGlyMetLysTyrPhe 429
DB 1395 GAGATGTGAGAGCACTCTTAAGATCATCTGCTCTGCTCCGCGGACAGCC--- 1448
QY 430 ValAspLysLysAsnTyrLysHisLysGlyGly----- 441
DB 1449 -----GCCAAGTGGAGGCGCTCTGAGCGCGGCGCGCTGTGGCGGTGCGTGCAG 1502
QY 442 ArgGlySerGlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLysLeu 461
DB 1503 CACGGAAGCCCGCTGGGGAGCTGTTCAGCTGCAGCCATGAACATGATCTCCCGAATT 1562
QY 462 ArgGlnAlaLysGlnSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe--- 480
DB 1563 AAGAGG-----CCAGCTGCTTGGCACTTACGTAGTCTGTAATTTCAGC 1607
QY 481 AspTyrSerCysGluGluLysAspValProGlyIleLeuAspLeuSerThrTyrTyrGluLeu 500
DB 1608 GAGGTACGCTGACGCGCACTGCTCCCGACCTTGGCGCGCGCGCGCGCTACCGGCTC 1667
QY 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
DB 1668 ATGACAGAGTTCGAGAGGTG-----TACTTCCGATCCAGACCTGAGATGTTCCAG 1721
QY 521 ProGlyGlnHisThrArgGlnGly-----SerArgAsnTyrThrArgSerLysSer 538
DB 1722 CCGAGCGGATGACACCGCTGAGGAGAGCTGTGGGAGAACTACTGTGGAGGCCGCGG 1781
QY 539 GlyArgSerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGluGluProAsp 558
DB 1782 GCGAGGCACTCGCGCGCGCTGAGCAGATTCCGGAATGGAGAGTCCGCTGTCCGAC 1841
QY 559 TrpPheGln-----LysGlnPheValProPheHisProPro 570
DB 1842 TGGTTCGAATGTGAGAACTTACTACAGAGATGACACAGATGCCCCGCTGAGAGAA 1901
QY 571 ProLeuArgTyrArgGluProValLeuGluLysPheAspSerGlyLeuValLeuAsnAsp 590

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Db      1902  GAGGTG---TTTGAAGGAGCCACTGTGCTGCTCG---GGAACCGGAGTCTGAACGGGGCG 1955
Qy      591  ValMetCyLysProGlyLysPheCysLeuLysValAlaLeuProValLeu 610
      ::::
Db      1956  CCCCTGGTGGCCGAG---CTTGACTCCAGGAGCTCTCGGCATGAC---CCGCTGGTGC 2009
Qy      611  GlyLAlaThrProAlaAspSerGlnHisGlnSerGlnHis----- 624
      |||||
Db      2010  GGGGAGGAAGGAGCAGCAGTGGCAAGCTGAACCTCACTGACAGCCCGGGGCTCAG 2069
      624 ----- 624
Qy      2070  CCAGCGCCGAGCCCTTCACACCTGTGCTCGCCGAGAGAGGGGGCCCTGTGTGCC 2129
Qy      625  -----GlyLysLeuAspGlnAspGlyLysAlaArgProAlaLeuAspGlySer 640
      |||||
Db      2130  GCGGTGAGAGCTGGGGCCCTGAGCGGTGACGATGCCGAGCTGGGCTGACACTGGCGGGGAG 2189
Qy      641  AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
      |||||
Db      2190  GGGCAGGCTGCTCCGCTGTGGGAGCCCGGGGCTGG-----CGA 2231
Qy      661  AspSerGlyLeuLysAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln 680
      |||||
Db      2232  AATAGCGTCTCTTC-----CTCCCCGTGGACCCCGAGAGACTGCCCTT----- 2276
Qy      681  GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSerSer 700
      |||||
Db      2277  GGCAGACACACCCCATGAGCGCTCTCTGACCTCTTCCAGAGAGACTGAG----- 2327
Qy      701  GlyLeuGlyGlnGlnGlnProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
      |||||
Db      2328  -----GAGCACCTGGAAGGCTTGATGCTCTGCTTTCGAGCAGAGTCTGAGCTGC 2378
Qy      721  LysAlaAspLeuGlyCys 726
      ::|||
Db      2379  CAGGCCACGAGGGGCTGC 2396

RESULT 11
US-09-022-260-9
; Sequence 9, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fenslow, William
; TITLE OF INVENTION: No. 6100235e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022.260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

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; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEO ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; type: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTL $\lambda$ 8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693
; US-09-022-260-9

Alignment Scores:
Pred. No.: 1,466-24 Length: 3223
Percent Similarity: 321.50 Matches: 183
Best Local Similarity: 35.9% Conservative: 106
Query Match: 22.7% Mismatches: 357
Gap: 8.1% Indels: 161
DB: 3 Gaps: 34

US-10-616-788-2 (1-738) x US-09-022-260-9 (1-3223)
QY 31 GLYARGALATRPGLVALASPRLHCYSGLYTTPARGLYVALGIPROALAASERGAASN 50
Db 130 GGCGCCGCGGGGCGTCTCCTGCTGTCTCTGGGGTG-CAGGCCCGGGGAGGCCTTC 188
QY 51 SerGlyLeu-----TYRAsnIleThrPhe 58
Db 189 CTCGACTCCTGGACCAACCGGCGCTGCTCTCCAGCCGGGGCTTAACCTGCACGCTC 248
QY 59 LyeTYrAspAsnCys-----ThrlhrTYrLeuAnPrOVAIGLyVSHlValIleAla 76
Db 249 AAGAATAAGTACCTCGCTGGATGACAGCTGAGATTACCCCT----- 287
QY 77 AspAlaGlAsnIleThr-----IleSerGIInTYrAlaCys 88
Db 288 -----GAAACTGTACCCTCCCTCCGCCAAGACCTGCAGATCTCAGCTGACCTTGCC 341
QY 89 HisAspGln-----ValAlaValThrIleLeuTrpSer---ProGlyAla 102
Db 342 CACAACCCAACAAGSAGACCTTTCCCGTGGCTCACATCGAATGAGACATGACAGACAC 401
QY 103 LeuGlyILeGluPhelEuLYseGlyPheArGyallleuGluGluLeuLYserGluGly 122
Db 402 GCCAGACTCTCTGACTCGAAGGATGACAGATTATCTGCTGCAGCTGMAACCAATGAA 461
QY 123 ArgGlnCYseGlnIleuLeuLYAspProLYsglLeuAsnSerPheLYsArg 142
Db 462 CGTTTGTGCTCAGG-----TTTAGATTCTGTCCAAACCTGABGACATACCAACAGCGG 515
QY 143 ThrGlyMetGlnSerGlnProPheLeuAnWetLYsPheGluThrAspTYrPheValLYs 162
Db 516 TGGCGTTTACCTTCAGCACCTTGTG--GTVGACCTGTGACACGAGAAATGAGGTGACC 572
QY 163 Val-----ValProPheProSerIleLYsAbenGlnSerAnTYrHlsProPhePhe 180
Db 573 GTTTCACCATCTGGCCCAAGCCATCTCCCTGATGGGAGCCCAAACCAACAGCTCCAAATTT 632
QY 181 ArgThrArgAlaCYsAspLeuLeuGluInProAspAenLeuAlaCYsLYs----- 197
Db 633 CTGTGCTGACTGTATGACAGCCACGAGATGAAGGTAACTAACCAAGCCATGATGAGCTCAGGC 692

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Db 288 -----CGAAGCTGACCCCTCTCCCAAGAGCTGCAGATCCAGTCTTGCC 341
 Qy 89 HiaArgIn-----ValAlaValThrIleLeuProSer---ProGlyAla 102
 Db 342 CACACCCCAAGAGAGAGCTGTCCCGGTGCTCAGATGAGATGAGACGTGCAGACAGAC 401
 Qy 103 LeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGluGluLeuLeuSerGluGly 122
 Db 402 GCCAGCATCTCTGACTGAGAGGTGAGAGATTATCTCTCTGAGCTGAGACCAAGAA 461
 Qy 123 ArgGlnCysGlnGluLeuIleLeuLysProLysGlnLeuLysSerSerPheLysArg 142
 Db 462 CGTTTGCGCTGACG-----TTTGAGTTTCTGTCCAACTGAGGAGCTACCAAGGCGG 515
 Qy 143 ThrGlyMetLysSerGlnProPheLeuLysMetLysPheGluThrIleArgPheValLys 162
 Db 516 TGGCGTTTACCTTGACGCACTTTGTG---GTTGACCTTGACAGAAATGAGGTGACC 572
 Qy 163 Val-----ValProPheProSerIleLysAlaGlnLysSerValIleProPhePhe 180
 Db 573 GTTCACACACCTGCCCAAGCCCATCTGATGGGAGCCAAACCAACAGTCCAAAGATTTC 632
 Qy 181 ArgThrArgAlaCysArgPheLeuLeuGlnProArgAlaLysLys----- 197
 Db 633 CTGTGCTGACTGTGAGACGCGCAGAGATGAGGTAAACAGCGCATGATGAGCTCAGGC 692
 Qy 198 ProPheTrpLysProLysAlaLeu----- 205
 Db 693 AGCCTGTGGAGCC---AACATCACCTGAGAGACCTGAGAGCCCAACAGCTGCGTGTG 749
 Qy 206 -----AenIleSerGlnIleGlySerArgMetGlnLysSerPheArgHis 220
 Db 750 AGCTTACACCTGTGGAACGAAATTCACCATTCACAGATCTCTGACACAGATTTCGCCAC 809
 Qy 221 AlaProHisAlaPheArgPheArgPheArgPheArgPheArgPheArgPheArgPhe 240
 Db 810 ATGAGAGACACAGATGCTTTGAGCAGACATGCAC---CACATACCTGCGGCCAGACAGAA 866
 Qy 241 ProPheLysArgLysThrCysLysGlnGluGlnThrThrGluThrThrSerCysLeuLeu 260
 Db 867 GAGTTCACACGAGATCCAAAGCTGACACTCACTTACGCAACCTTAAAGGTGCTGTGCG 926
 Qy 261 GlnAlaValSerProGlyArgPheIleIleGluLeuValAlaPheArgPheArgPhe 277
 Db 927 CACCAAGTGCAGATCCAGCCCTTTCAGCAGCTGCTCAATGACTGCTCAGACACTCC 986
 Qy 278 ThrThrArgLysValMetHisTyrAlaLeuLysProValHisSerProTrpAlaGlyPro 297
 Db 987 GCGACTGTTCTGCGCCAGAAATGCCAGACACTCCAGAAACCAATTCCGGACTACATGCC 1046
 Qy 298 IleArgAlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPhe 317
 Db 1047 CTGTGGGTGTAAGTGTTCATTCACGGGCAATCTCCATCTGCTGTGGGCTCGTCATCTCG 1106
 Qy 318 ThrValMetCysArgLysLysGlnGlnGluAlaValIleTyrSerHisLeuAlaPheGluSer 337
 Db 1107 CTGATCTCTGCACTGAGCTGAGGCTAGCTGAGGCTGAGAACT-----GAAAAATAC 1157
 Qy 338 SerGlnSerSerThrTyrThrAlaAlaLeuProArgLysArgLysLeuArgProArgPro 356
 Db 1158 AGTATATACACCAAAATACACGAGTGGCTGCTGCGGTGACATGATCCCGCCACCGCTG 1217
 Qy 357 -----LysValIleLeuLysCysTyrSerSerLysAlaArgLysGlnAlaMetAlaVal 373
 Db 1218 AAGCCAGAGAAAGTCTGATATCTACTACAGC---GACCAACCCCTCTAGTGTGAGGTG 1274
 Qy 374 ValGlnCysPheAlaTyrPheLeuGlnAlaPhePheCysGlnValAlaLeuAlaPheLeu 393
 Db 1275 GTCTGTAATATGCGCGATCTCTCTCAACCGCTGCGGACAGAAATGGCCCTGACCTG 1334
 Qy 394 TrpLysAlaPheSerLeuLysArgGluGlyGlnArgLysVal-----Ile 409
 Db 1335 CTGGAAGAGAGAGGATCTGTGGAAGAGAGATGATGACCTGTGGTGGGCGGTCAAGAGAG 1394

Qy 410 GlnLysIleHisGluSerGlnPheIleIleValIleCysSerLysGlyMetLysTyrPhe 429
 Db 1395 GAGATGTGAGAGAGCACTTAAGATCATCTGTCTGTCTCCGCGGACAGCGC----- 1448
 Qy 430 ValAspLysLysValIleLysLysLysGlyGly----- 441
 Db 1449 -----GCCAAGTGGCAGCGCTCTGGGCGGGGGCGCTGTGGCTGCGCTGCGCTGAC 1502
 Qy 442 ArgGlySerCysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 461
 Db 1503 CAGGAAAGCCCTGGGGGACCTGTTCACCTGACAGCATAAACATGATCTCCCGGACCTTC 1562
 Qy 462 ArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe--- 480
 Db 1563 AAGAGC-----CCAGCTGCTTGGGACCTACCTACTCTGATCTTCCAGC 1607
 Qy 481 AspTyrSerCysGluGlyArgValProGlyIleLeuAlaPheLysSerThrLysTyrArgLeu 500
 Db 1608 GAGTACAGCTGTGACGCGCAGCTCCCGACCTGTTCGGCGCGCGCGGTACCGCGCTC 1667
 Qy 501 MetAspAlaLeuProGlnLeuCysSerHisLysHisSerArgAspHisGlyLeuGlnGlu 520
 Db 1668 ATGAGACAGGTTGAGAGAGGTG-----TACTTCGCGATCCAGGACCTGAGAGATGTTCCAG 1721
 Qy 521 ProGlyGlnHisThrArgGlnGly-----SerArgArgValIleArgSerLysSer 538
 Db 1722 CCGGCGCGACATGACCGCGTGGAGAGCTGTGGGAGACATCACTTGGCGAGCCCGGCG 1781
 Qy 539 GlyArgSerLeuTyrValAlaIleCysAlaMetHisGlnPheIleAspGluProArg 558
 Db 1782 GCGAGCAGCTCGCGCGCGCGCTGAGAGGTTCCGGAATGAGGTCCGCTGCCGAC 1841
 Qy 559 TrpPheGlu-----LysGlnPheValProPheHisProPro 570
 Db 1842 TGGTTCGAATGTGAGAACTTAATCAGAGATGACAGAGATGCCCCGCTCTGAGAGAA 1901
 Qy 571 ProLeuArgTyrArgGluProValLeuGluLysPheAspSerGlyLeuValLeuAlaPhe 590
 Db 1902 GAGGTG---TTTAGAGACCATCTGTCTCTCCG---GAAACCGCATCTGGAAGCGGGCG 1955
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 Qy 624 ----- 624
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 Qy 641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerArgMetProArg 660
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 Qy 661 AspSerGlyIleThrAspSerSerValProSerSerGlyLeuSerLeuProLeuMetGlu 680
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OY	357	-----lyvValPheLeuCyberyserserlyuAaprgylGlnanhiMeLeuVal	373
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OY	374	ValGlnCyPheAlaTyPheLeuGlnAapPheCySGlyCySGluValAlaLeuAapLeu	393
Db	1275	GTCCTGAATTCTGCCAATTCTCTGTCAACCGCTCGGCAAGAAAGTGGCCCTGGACCTG	1334
OY	394	TrpGlnAapPheSerLeuCyAaprgylGlnArgGlnTrpVal-----lle	409
Db	1335	CTGGAAGAGCAGGCGCATCTCGAGGCAAGATCATGACTCGGTGGCGCTGACAAAGCAG	1394
OY	410	GlnlysiLehiAgiuserGlnPheIleValValCysersLyGlyMetLyethrPhe	429
Db	1395	GAGATGTGGAGAGCACTTAAGATGATCGTCTGTCTCTCCCGGCAACGCG-----	1448
OY	430	ValAapLyblyAamTyLehiAlyAaglyGlyGly-----	441
Db	1449	-----GCCAATGGCAGGCGCTCTGGGCGGGGGGCGCTCTGCGGCTGCGCTGCAC	1502
OY	442	ArgGlySerGlyLyblyGlyLeuPheLeuValAlaValSerAlaIleAglulblyLeu	461
Db	1503	CACGGAAGCCCGGTGGGGACCTGTTCACGTGACCATGAACATGATCTCCCGGACCTTC	1562
OY	462	ArgGlnAlaIlybGlnSerSerSerAlaAlaLeuSerLybPheIleAlaValTyPhe---	480
Db	1563	AAGAG-----CCACACTCGCTTCGGCAGCTACTGATGTGTCTACTTTCAGC	1607
OY	481	AapTySerCySGluGlyAapValProGlyIleLeuAapLeuSerThyTyArgLeu	500
Db	1608	GAGCTCACTGTGACGCGGACGTCTCCCAACCTCTTCGGCGGGCGCGCGGTACCGCTTC	1667
OY	501	MetAapLeuLeuProGlnLeuCySberhiAlyeuhisSeraArgAapPheIlyLeuGlnlu	520
Db	1668	ATGACAGAGTTTCAAGAGAGTGT-----TACTTCGCGATCCAGACCTGAGATGTTCCAG	1721
OY	521	ProGlyGlnhiAthrArgGlnGly-----SeraArgAapTyTyPheArgSerLySer	538
Db	1722	CCGGGCCCCCATGACACCGGTAGGGAGGTGTCTGGGGGAACAATCACTTCGGAGCCCGGCG	1781
OY	539	GlyArgSerLeuTyValAlaIleCysAamMetHiAgiPheIleAaprgylGlnuProAap	558
Db	1782	GCGACGACGCTTCGCGCGCGCTTGACAGAGTTCCGGAGCTGGCAGAGTCCGCTGTCCGAC	1841
OY	559	TrpPheGln-----LyGlnPheValProPhehiAProPro	570
Db	1842	TGGTTTCAATGTGAAGAACTCTACTCAGACAGATGACAGAGATGCCCGTCCCTGGACGAA	1901
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Db	1902	GAGGTG---TTTGAGAGACCACTCTGCTCCG---GGAACCGGCAATGTGAAGCGGCG	1955
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Db	1956	CCCCGTGGTGGGAG---CTTGGCTTCCAGGCTCTCTGCGCATGAC---CGGTGGTTC	2009
OY	611	GlyAlaThrGlyProAlaAapSerGlnhiAgiuserGlnhiS-----	624
Db	2010	GGGAGAGAAAGAGAGAGCAGAGTGGCAAACTGAACTCACTGACACCCCGGGGTACG	2065
OY	624	-----	624
Db	2070	CCAGCGCCGAGCCCTCCACACCTGTGTGTCCGCGGAGAGAGGGGCGCTGTGGTGC	2129
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OY	641	AlaAlaLeuGlnProLeuLeuhiAthrValLybAlaGlySerProSerAapMetProArg	660
Db	2190	GCGAGAGGCTGCGCGCTGTGGGAGACCGCGGCGGTGG-----CGA	2231
OY	661	AapSerGlyIleTyAapSerSerValProSerSerGlnLeuSerLeuProLeuMetGln	680

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Qy      701  GlyLeuGlyGlnGlnGluProProAlaLeuProSerLeuLeuSerSerGlySerCys 720
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Qy      721  LySAlaSpLeuGlyCys 726
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RESULT 15
US-08-620-694A-1
Sequence 1, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanelow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: HVS13 receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2715
US-08-620-694A-1

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Alignment Scores:

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Percent Similarity:	38.1%	Conservative:	121
Best Local Similarity:	23.2%	Mismatches:	321
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US-10-616-788-2 (1-738) x US-08-620-694A-1 (1-3288)

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Qy 59 LysrYrAspAsnCysrThrTrpLeuAsnProValGlyLysHISValIleAlaAspAla 78
Db 307 ATCCACCCCAAAAACCTGACCCCGTCTCCCAAAAACATCTATATC----- 354
Qy 79 GluAsnIleThrIleSerGlnTrpAlaCysHISAspGlnValAlaValThr-----Ileu 97
Db 355 ---AATCTTAGTGTCTCTTACCCAGCAGAGAAATTAGTCCGTGTTCATGTTGAG 411
Qy 98 TrpSer---ProGlyAlaLeuGlyIleGluPheLeuYsglyPheArgValIleLeuGlu 116
Db 412 TGGACCTCGCAGACAGATGCCAGCATCTGTACTTCAGAGGCTGCAGAGCTTCGCTCG 471
Qy 117 GluLeuYsSerGlyGlyArgGlnCysGlnGln-----LeuIleLeuYs 131
Db 472 CAGCTGAACCAACATGAGCGGCTGTGTCAAGTTCACAGTTCTGTCTCATCTGCAGCAT 531
Qy 132 AspProYsglnLeuAsnSerSerPheLysArgThrGlyMetGluSerGlnProPheLeu 151
Db 532 CACCGTAGCGGGCGGCTTTTCTTC-----AGCCACTTGTGGTA 573
Qy 152 AsnMetYsPheGlnTrpAspTrpPheValYsValProPheProSerIleYsAsn 171
Db 574 GATCTCGCCGAGAGTATGATGATGACTTTTCAACACCTCCGGAAGCCATCCCTGATCGG 633
Qy 172 GluSerAsnTrpHISProPhePheArgThrArgAlaCysAsp-----LeuLeu 188
Db 634 GACCAACCAACCAATCCAGATCATCTTGTGCTGACTGTGAGCAGACAGACATGAG 693
Qy 189 LeuGlnProAspAsnLeuAlaCysLysProPheTrpLysProArgAsnLeuAsnIleSer 208
Db 694 ATGACTAATCTCATCGTAGCTCAGGACGACCTTGGAGATCC-----AACATCACT 744
Qy 209 GlnHISGlySerAspMetGlnValSerPheAspHISAlaProHISAsnPheGlyPheArg 228
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Qy 407 pValIleGlnLys-----IleHISGluSerGlnPheIleIleValValCysSe 423
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Qy 602 eLeuLysValGlnAla-----ProVa 609
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Qy 609 lLeuGlyAlaIleThrGlyProAlaAspSerGlnHISGluSerGlnHISGlyLeuAspG 629
Db 2085 GCTATG-GCCACAGAGAGAGACTGTGCTCAACACCTCCAAAGATGTGTCTGCAACAG 2143

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 06:07:49 ; Search time 9954 Seconds
(without alignments)
4214.433 Million cell updates/sec

Title: US-10-616-788-2

Sequence: 1 MAFWOLCIVFFVNAACNG.....SCKADGCRSYDELAHAP 738

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs805h
-USER=US10616788 @CGN 1.1 4939 @runat.28022006.160428.14411 -NCPU=6 -ICPU=3
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIS

Result No.	Score	Query Match	Length	DB ID	Description
1	3948	100.0	3083	6	AX251723 Sequence
2	3918	99.2	2341	6	AX364576 Sequence
3	3912	99.1	2724	8	AF458067 Homo sapi

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	FEATURES	CDS
AX251723	Sequence 1 from Patent WO0168859.	AX251723	AX251723.1	GI:15985081			Homo sapiens (human)	Jing, S.	11-17 receptor like molecules and uses thereof	Patent: WO 0168859-A 1 20-SEP-2001; Amgen Inc. (US)	Location/Qualifiers 1..3083 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 22..>2235 /note="unnamed protein product" /codon_start=1 /protein_id="CAC93798.1" /db_xref="GI:15985082"	
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AX364570	Sequence											
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BC038369	Homo sapi											
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AR338364	Sequence											
AX180780	Sequence											
AY358774	Homo sapi											
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AX364582	Sequence											
AF424804	Mus muscu											
CT025426	Xenopus t											
AF364103	Danio rer											
AF401232	Danio rer											
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AC092050	Homo sapi											
AC119550	Rattus no											
AC125152	Mus muscu											
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CR386972	Gallus ga											
BX933449	Gallus ga											
BC066804	Mus muscu											

ALIGNMENTS

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ORIGIN

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US-10-616-788-2 (1-738) x AX251723 (1-3083)

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QY 61 AspAenCysPheThrTyTyrLeuAenProValGlyLeuIleValIleAlaAenAlaGlnAen 80
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QY 121 GluGlyAArgGlnCysGlnGlnLeuIleLeuLeuAaPProLeuArgGlnLeuAenSerPhe 140
Db 382 GAGGAAAGAGAGTGCACAACTGATTTCTAAAGATCCGAAAGAGCTCAACAGAGCTTC 441
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Db 562 AGAAGCCGAGCTGTGACTGTGTGTTACAGCCGAGCAATCTAGCTGTATAAACCCTTCTGG 621
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LOCUS      Sequence 7 from Patent WO0208259.
ACCESSION      AX364576
VERSION      AX364576.1 GI:18696536
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ORGANISM      Homo sapiens
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Pred. No.: 3,09e-300
Score: 3918.00
Percent Similarity: 99.6%

Length: 2341
Matches: 734
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ACCESSION AP458067
VERSION AP458067.1 GI:21779862
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Hominoidea; Homo.
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1. (bases 1 to 2724)
AUTHORS Gilbert J.M. and Gorman D.M.
TITLE Identification of novel IL-17 related receptors
JOURNAL Unpublished
REFERENCE
2. (bases 1 to 2724)
AUTHORS Gilbert J.M. and Gorman D.M.
TITLE Direct Submision
JOURNAL Submitted (13-DEC-2001) Genomics, DNAX Research Inc., 901
California Ave., Palo Alto, CA 94304, USA

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US-10-616-788-2 (1-738) x AP458067 (1-2724)

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Qy	501	MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu	520
Db	1501	ATGAGCAATCTTCTCAAGCTGTGTCTCCACTGCTACCTCCGAGACACAGGCTCCAGAG	1560
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 (IL17RM) mRNA, complete cds; alternatively spliced.
 ACCESSION AF494208

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VERSION      AF94208.1  GI:21667503
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ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE    1 (bases 1 to 4477)
AUTHORS      Xiong, S., Zhao, Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S.,
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TITLE        hSet Inhibits PC-12 Cell Differentiation by Interfering with
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JOURNAL      J. Biol. Chem. 278 (50), 50273-50282 (2003)
PUBMED       12958313
REFERENCES   2 (bases 1 to 4477)
AUTHORS      Xiong, S.O., Huang, G.R., Zhao, Q.H., Chen, P.L., Rong, Z.L., Ye, X.Y.,
              Chen, Y., Liu, L., Fu, X.Y., and Chang, Z.Z.
TITLE        Direct Subcellular
JOURNAL      Submitted (22-MAR-2002) Tsinghua Institute of Genome Research,
              Department of Biological Sciences and Biotechnology, and School of
              Medicine, Tsinghua University, Beijing 100084, P.R. China
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ORIGIN
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Percent Similarity: 99.5%      Conservative: 2
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 VERSION AX364573.1 GI:18696533
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 REFERENCE
 1 Presnell,S.R., Kuestner,R.E. and Gao,Z.
 AUTORS Human cytokine receptor
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 JOURNAL ZymoGenetics, Inc. (US)
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ORIGIN

Alignment Scores:

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Query Match:	98.6%	Indels:	14
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US-10-616-788-2 (1-738) x AX364573 (1-2383)

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DB 1166 CTCCCAAGAGAGAGCTCG 1225
QY 367 GlyIleAsnHisMetAsnValAlaGlnCysPheAlaTyPheLeuGlnIleAspPheCysGly 386
DB 1226 GGCAGAAATCAATGAAATGCTGCAAGTTCCTGCTTCTCTTCCAGAACTTCTGTGGC 1285
QY 387 CysGlnValAlaLeuAspLeuTrpGlnAspPheSerLeuCysArgGlnIleGlnArgGln 406
DB 1286 TGTGAGTGGCTCTGGACCTGTGGGAGACTTCAAGCTCTGTATGAGAGAGGAGAGAGAA 1345
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QY 427 TyrTyTrpPheValAspIleValAsnTyIleValIleValIleValIleValIleValIle 446
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QY 467 SerSerSerAlaAlaLeuSerIleValIleValIleValIleValIleValIleValIle 486
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QY 487 AspValProGlyIleLeuAspIleSerThrIleTyIleValIleMetAspAsnLeuProGln 506
DB 1586 GACGTCCCGCGGTATCTTACCTGATCACTGATCAAGTACAGACTCATGTGCAATCTTCCGAC 1645
QY 507 LeuCysSerHisIleuHisSerArgAspHisGlyLeuGlnGlnIleProGlyIleHisIleThrArg 526
DB 1646 CTCTGTTCCCACTGACCTCCGAGACACAGCCCTTCCAGAGACCCGGGAGACAGACGCA 1705
QY 527 GlnGlySerArgArgAsnTyPheArgSerIleValArgSerIleValAlaIle 546
DB 1706 CAGGGCAGAGAAAGAACTTCTCCGAGCAAGTCAAGCGGCTCTTATACCTGCGCATTT 1765
QY 547 CysAsnMetHisGlnPheIleAspGlnIleProArgTrpPheGlnIleValIlePro 566

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Db      1766 TGCACATGACACGATTATTGACAGAGAGCCGAGCTGTTCCAAAAAGCAGTTCC 1825
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Db      1826 TTCATCTCTCTCCACGCGCTACCGGAGCCAGTCTTGAGAAATTTGATTCGGGCTTG 1885
Qy      587 ValLeuAsnAspValMetCysLysProGlyProGlyUserAspPheCysLeuLysValGlu 606
Db      1886 GTTTTAATATATGTCATGTCGCAACGAGGCTCGAGAGTACCTTCCCTAAAGGTAGAG 1945
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Qy      647 LeuHisThrValLysAlaGlySerProSerAspMetProArgAspSerGlyIleTyrAsp 666
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Qy      667 SerSerValProSerSerGlyLeuSerLeuProLeuMetGluGlyLeuSerThrAspGln 686
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Qy      687 ThrGluThrSerSerLeuThrGluSerValSerSerSerGlyLeuGlyGluGluGlu 706
Db      2186 ACAGAAACGCTTCCCTCGAGGAGAGGTCTCTCTTCAAGCCCTGGGTGAGAGGAA 2245
Qy      707 ProProAlaLeuProSerLysLeuLeuSerSerGlySerCysLysAlaAspLeuGlyCys 726
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Qy      727 ArgSerThrThrAspGluLeuHisAlaValAlaPro 738
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RESULT 7
LOCUS   CS083243              4392 bp      DNA      linear      PAT 18-MAY-2005
DEFINITION
Sequence 15 from Patent EP1529843.
ACCESSION
CS083243
VERSION
CS083243.1 GI:66349785
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Edmonds, B.T., Micanovic, R., Ou, W., Su, E.W., Tschang, S.H. and
Wang, H.
Novel secreted proteins and their uses
Patent: EP 1529843-A 15 11-MAY-2005;
JOURNAL
Eli Lilly & Company (US)
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ORIGIN

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Alignment Scores:
Pred. No.:      4, 87e-295      Length:      4392
Score:          3857.00          Matches:      732
Percent Similarity: 98.8%          Conservative: 1
Best Local Similarity: 98.7%          Mismatches: 5
Query Match:      97.7%          Indels:      4
DB:               6              Gaps:         0

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US-10-616-788-2 (1-738) X CS083243 (1-4392)

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Qy      21 SerGlnLeuAlaValAlaAlaGlySerGlyArgAlaTTrpGlyValAspThrCysGly 40
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Qy      41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLysTyr 60
Db      121 TGGAGGGGAGTGGGGCGACCGCAGAAACAGTGGGCTGTACACATCACTTCAAAATAT 180
Qy      61 AspAsnCysThrThrTyrLeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsn 80
Db      181 GACAAATTGTACCACTTCAATGATCCAGTGGGGAAGCAATGATGCTGACCCCGAAT 240
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Db      241 ATCAACCATGACGCAAGTATCTTGCCATGACAGATGCGACTCAACATTTTGGTCCCA 300
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Qy      181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
Db      541 AGAAACCGGAGCTGTGACCTGTGTGTTACGCGGACAACTTGCTTGAACCTTCTG 600
Qy      201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
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Qy      221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuLysHisGluGly 240
Db      661 GCAACGCAACATTTGGGCTTCCGTTTCTTATCTTCACTAACAAGTCAAGACGAAAGGA 720
Qy      721 CTTTCAACGGAAGACCTGTAAAGAGGAGCAAACTACAGACGACGACGCTGCTCTT 780
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Qy      520 LysPro-GlyGlnHisThrArgGlnGly-SerArgArgAsnTyrPheArgSerLysSerG 539
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Qy      679 tGluGlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSe 699
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LOCUS DEFINITION Sequence 15 from Patent WO0214358.
ACCESSION AX392973
VERSION AX392973.1 GI:19701020
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 Edmonds, B.T., Micanovic, R., Ou, W., Su, E.W., Tschang, S.H. and
AUTHORS Wang, H.
TITLE Novel secreted proteins and their uses
JOURNAL Patent: WO 0214358-A 15 21-FEB-2002;
ELI LILLY AND COMPANY (US)
FEATURES
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Percent Similarity: 98.8% Conservative: 1
Best Local Similarity: 97.7% Mismatches: 5
Query Match: 97.7% Indels: 4
DB: 6 Gaps: 0

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RESULT 9

CS135272
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 DEFINITION Sequence 9 from Patent WO2005065711.
 ACCESSION CS135272
 VERSION CS135272.1 GI:72067723
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 1. Garmen, D.M.
 Mammalian receptor proteins, related reagents and methods
 Patent: WO 2005065711-A 9 21-JUL-2005;
 Schering Corporation (US)
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US-10-616-788-2 (1-738) x CS135272 (1-2786)

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DEFINITION Sequence 13 from Patent WO0190358.
ACCESSION AX350979
VERSION AX350979.1 GI:18616355

KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
AUTHORS 1
TITLE Gorman, D.M.
JOURNAL Mammalian receptor proteins; related reagents and methods
Patent: WO 0190358-A 13 29-NOV-2001;
SCHERING CORPORATION (US)
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 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodegren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Boutard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smallus, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)
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 NIH MGC Project
 Direct Submission
 Submitted (01-OCT-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Niklos Palakovic, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Louieged, H.,
 Kowis, C.R., Speed, A.J., Martin, R.G., Muzny, D.M., Manavati,
 A.N., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
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ORIGIN

Alignment Scores:
 Pred. No.: 7,366-284
 Score: 3716.00
 Percent Similarity: 99.9%
 Best Local Similarity: 99.7%
 Query Match: 94.1%

Matches: 4490
 Conservative: 1
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US-10-616-788-2 (1-738) x BC038369 (1-4490)

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US-10-616-788-2 (1-738) x AY489047 (1-2364)

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RESULT 13
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 LOCUS AX747904
 DEFINITION Sequence 1429 from Patent EP1308459.

ACCESSION AX747904
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 1
 Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
 Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
 Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
 Masuko, Y.
 TITLE
 JOURNAL Full-length cDNA sequences
 Patent: EP 1308459-A 1429 07-MAY-2003;
 Helix Research Institute (JP) ; Research Association for
 Biotechnology (JP)
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ACCESSION AK093074.1 GI:21751823
VERSION c1.90 capping, fis (full insert sequence).
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SOURCE Homo sapiens
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Homidae; Homo.
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Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohtsuka, M., Nishi, T., Shibahara, T., Tanaka, T.,
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Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A.,
Sasaki, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A.,
Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Terashima, N., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukumizu, Y., Fujimori, Y., Komiyama, M.,
Tashiro, A., Tanigami, A., Fujimura, T., Ono, T., Yamada, K., Fujii, Y.,
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Ohtani, R., Kawakami, T.,
Nojima, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togsashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isegaki, T., and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)

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PUBMED 14702039
REFERENCE
AUTHORS Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
Arita, M., Musashino, K., Yuki, H., Hara, H., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Iehi, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsumura, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B.,
Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and
Isegaki, T.
TITLE MEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2894)
AUTHORS Isegaki, T. and Yamamoto, J.
TITLE Direct Substitution
JOURNAL Submitted (04-JUN-2002) Takao Isegaki, FLJ Project (HRI Team); 2-6-7
Kazusa-Kametani, Kisei, Chiba 292-0812, Japan
(E-mail:genominfo@kai.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
MEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4478)
 AUTHORS Xiong,S., Zhao,Q., Rong,Z., Huang,G., Huang,Y., Chen,P., Zhang,S.,
 Liu,L., Fu,X. and Chang,Z.
 TITLE hsf inhibits PC-12 Cell Differentiation by Interfering with
 Ras-Mitogen-activated Protein Kinase MAPK Signaling
 JOURNAL J. Biol. Chem. 278 (50), 50273-50282 (2003)
 PUBMED 12958313
 REFERENCE 2 (bases 1 to 4478)
 AUTHORS Xiong,S., Zhao,Q., Huang,G., Chen,P., Rong,Z., Ye,X., Chen,Y.,
 Liu,L., Fu,X. and Chang,Z.
 TITLE Direct Submision
 JOURNAL Submitted (22-MAR-2002) Tsinghua Institute of Genome Research,
 Department of Biological Sciences and Biotechnology, and School of
 Medicine, Tsinghua University, Beijing 100084, P.R. China
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ORIGIN

Alignment Scores:

Pred. No.: 4,54e-283 Length: 4478
 Score: 3706.00 Matches: 694
 Percent Similarity: 99.7% Conservative: 2
 Best Local Similarity: 99.4% Mismatches: 0
 Query Match: 93.9% Indels: 0
 DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x AF494211 (1-4478)

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 06:07:20 ; Search time 973 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21	3690	93.5	2319	10	ADAA3240 Human int
22	3690	93.5	2319	10	ADAA3240 Human int
23	3690	93.5	2319	10	ADAA3240 Human int
24	3690	93.5	2319	12	ADAA3240 Human int
25	3690	93.5	2319	12	ADAA3240 Human int
26	3594	91.0	4450	8	AAAS1235 Human IL-
27	3382	85.7	2443	6	ABA95037 Human REM
28	3345	84.7	2224	13	ADW6587 House mou
29	3248	82.3	3948	6	ABZ11243 Human pol
30	3248	82.3	3948	12	ADMA43761 Novel hum
31	3085	78.1	2217	6	ABA95036 Human Zcy
32	3069	77.7	2259	6	ABA95032 Human Zcy
33	3059	77.5	2259	6	ABA95034 Human Zcy
34	3009.5	76.2	2214	6	AAAS18135 Human DCR
35	2671.5	67.7	2134	13	ADW21235 DNA encod
36	2649	67.1	2217	6	ABA95038 Human int
37	1595.5	40.4	1620	13	ADX01629 Murine cy
38	1329	33.7	960	4	AAAS16201 5' portio
39	670	17.0	453	9	Ach39213 Human fce
40	321.5	8.1	2601	14	ADVA42775 Human pay
41	321.5	8.1	3120	10	ADW25545 Binding d
42	321.5	8.1	3120	10	ADK61414 Ovarian c
43	321.5	8.1	3120	12	ADP09696 Human int
44	321.5	8.1	3120	12	ADP09696 Human int
45	321.5	8.1	3223	2	AAAT33801 Human int

ALIGNMENTS

RESULT 1	AAAS15346	standard; cDNA; 3083 BP.
ID	AAAS15346	
XX	AAAS15346	
AC	AAAS15346	
XX	13-FEB-2002 (first entry)	
DT	13-FEB-2002 (first entry)	
XX	DNA encoding human Interleukin 17 (IL-17) receptor like protein.	
DE	DNA encoding human Interleukin 17 (IL-17) receptor like protein.	
XX	Interleukin 17, IL-17 receptor like protein; immunomodulatory;	
KW	anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;	
KW	hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;	
KW	anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;	
KW	vascular; cytostatic; anti-leukemic; anti-fertility; ophthalmological;	
KW	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;	
KW	bone disease; vascular disorder; eye disorder; cancer; human; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX		
FX	Key	Location/Qualifiers
FT	CDS	22..2235
FT		/tag = a
FT		/product = "Interleukin 17 (IL-17) receptor like protein"
FT		/partial
XX		/notes "No stop codon given"
PN	W0200168859-A2.	

XX 20-SEP-2001.
XX 15-MAR-2001; 2001KO-US008678.
XX 16-MAR-2000; 2000US-0189816P.
XX 28-NOV-2000; 2000US-00724460.
XX (AMGE-) AMGEN INC.
XX Jinq S;
XX MPI; 2001-611392/70.
XX P-PSDB; AAU09904.
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX Claim 1; Page 147-148, 150-151; 158pp; English.
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cyostatic, anti-leukemic, anti-infectivity and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin diseases
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also be used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The anti-
XX IL17rp antibodies and antagonists may also be used to down regulate
XX expression and activity. This sequence encodes the human interleukin 17
XX (IL-17) receptor like protein described in the method of the invention
XX
XX Sequence 3083 BP; 782 A; 807 C; 767 G; 727 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 3083
XX Score: 3948.00 Matches: 738
XX Percent Similarity: 100.0% Conservative: 0
XX Beat Local Similarity: 100.0% Mismatches: 0
XX Query Match: 100.0% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-616-788-2 (1-738) x AAS15346 (1-3083)
XX
XX 1 MetAlaProThrLeuGlnLeuCySerValPhePheThrValAsnAlaCysLeuAsnGly 20
XX 22 ATGGCCCCGGGCGCGAGCTCTGCTCTCTTTACGGTCAACGGCTCTCAACGGC 81
XX 21 SerGlnLeuAlaValAlaAlaGlySerGlyValArgAlaTrpGlyValAspThrCysGly 40
XX 82 TCGCAGCTGGCTGTGGCGCTGGCGGGTCCGGCCGCGCTGGCGCTGCACACTGTGGC 141
XX 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuValTrpAsnIleThrPheLeuTyr 60
XX 142 TGGAGGGGAGTGGGGCGACGCCAGCAAGTGGGCTGTAAACATCACTTCAATAT 201

Qy AspAsnCySerThrThrTyrLeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsn 80
Db GACAAATTGTACCACTTGAATCCAGTGGGGAACATGTATCTCTACCGCCAGAAAT 261
Qy IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
Db ATCACCATCAGCAGATATGCTTGCATGACCAAGTGGCAGTCCACTTCTTGGTCCCCA 321
Qy GlyAlaLeuGlyTyrIleGlnPheLeuLysGlyPheArgValIleLeuGlnGlnLeuLysSer 120
Db GGGGCCCCCTGGCATTCGAATTCCTGAAGAGATTTGGGTAATCTGGAGAGCTGAAGTGG 381
Qy GluGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
Db GAGGAGAGACAGTGGCAACACATGATTCCTAAAGAGATCCGAGAGAGCTCAACAGTACTTC 441
Qy LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe 160
Db AAAAGAACTGGAATGAAATCTCAACCTTCTGAAATATGAAATTTGAAACGGATATTTTC 501
Qy ValLysValValProPheProSerIleLysAsnGlnSerAsnTyrThrIleProPhePhe 180
Db GTAAAGTGTCTCTTTCTTCCATTAAACGAAGCAATTAACCACTTCTTCTTT 561
Qy ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysPProPheTrp 200
Db AGAACCCGAGCGCTGTACCTGTTTACAGCCGGAACATAGTCTTGAACCTTCTG 621
Qy LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
Db AAGCCCTGGAACTGAACATCAAGCCAGTGGCTCGCAATGACAGGTGCTTCGACGAC 681
Qy AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuLysHisGlnGly 240
Db GACCCGCAACACTTGGCTTCCGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 741
Qy ProPheLysArgGlyThrCysLysGlnGlnGlnThrThrGluThrThrSerCysLeuLeu 260
Db CTTTCAAGCGAAGACCTGTAAAGCAGAGCAACATCAAGAGACGACGCTCCCTT 801
Qy GlnAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrAsnThrArg 280
Db CAAGAAGTTTCTCCAGGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 861
Qy LysValMetHisTyrTrpAlaLeuLysProValHisSerProTrpAlaGlyProIleAspAla 300
Db AAGTATGATGATTATATCTTAAAGCAGTCACTCCCGTGGCGCCGACCAAGAGCC 921
Qy MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
Db ATGGCCATCAGACGTGCACTGTGATGATATGCGCATTTGCGACGCTCTTCACTGATG 981
Qy CysArgLysLysGlnGlnGlnLeuAsnIleTyrSerHisLeuAspGlnGlnSerSerGlnSer 340
Db TGGCGCAAGAGCAACAAATAATATATATATCACTTGAATGAGAGAGCTCTGAGTCT 1041
Qy SerThrTyrThrAlaLeuProArgGlnLysArgGlnProArgProLysValPheLeu 360
Db TCCACATACCTGCACACCTCCCAAGAGAGAGCTCCGCGCGCGAAGGCTTTTCTC 1101
Qy CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
Db TGTATTTCCAGTAAATATGGCCAGATTCATGAAATGTGTCCAGTGTTCGCTACTTTC 1161
Qy LeuGlnAspPheCysGlyCysGlyValAlaLeuAspLeuTrpGlnAspPheSerLeuCys 400
Db CTCAGAGACTCTGTGTGTGAGTGGTGGCTTGGACCTGTGGGAGAACTTCAAGCTGTGT 1221
Qy ArgGlnGlyGlnArgGluTrpValIleGlnLysIleHisGlnSerGlnPheIleIleVal 420
Db AGAGAAAGGCGAGAGAAATGGGTCAATCCAGAAAGTCCAGAGATCCAGATTCATCATTTGG 1281
Qy ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGlyGly 440

QY 21 SerGlnLeuAlaValAlaIleAGlyGlySerGlyValArgAlaTrpGlyValAspThrCysGly 40
 DB 82 TCCAGAGCTGCTGGCGCTGGCGGGCTCCGGCCGGCGGTGGAGCTGACACTGCGGC 141
 QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyArgAsnIleThrPheIleGlyTyr 60
 DB 142 TGGAGGGGAGTGGGGCCAGCGACAGAAACAGTGGGCTGTACAAACATCACCTTCAATAT 201
 QY 61 AspAsnCySerThrThrTyLeuAsnProValGlyLeuIleValIleAlaAspAlaGlnAsn 80
 DB 202 GACATTTGTACCACTTCTTGATTCAGTGGGAAAGCATGTGATGCTTGACGCCCAAT 261
 QY 81 IleThrIleSerGlnTyAlaCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
 DB 262 ATCACCATCAGCCAGTATGGCTGGCCATGACCAAGTGCAGTCAACATTTCTTGGTCCCA 321
 QY 101 GlyAlaLeuGlyIleGlyPheLeuLeuGlyPheArgValIleLeuGlyIleLeuIleGlySer 120
 DB 322 GGGGCCCTCGGACATCGAAATTCGTGAAAGATTCGGGTAAATACTGGAGAGCTGAAGTCC 381
 QY 121 GlnGlyValArgGlnCysGlnGlnIleLeuIleAspProIleGlyIleLeuAsnSerSerPhe 140
 DB 382 GAGGAAAGACAGTGCACAACTGATTTCAAAGGATCCGAAGCGTCAACAGTACGCTTC 441
 QY 141 LysArgThrGlyMetGlySerGlnProPheLeuAsnMetLysPheGlyIleThrAspTyrPhe 160
 DB 442 AAAAGAACTGGAAATGGAAATCTCAACCTTCTGTGAATGTGAATTGAAACGGAATTATTTTC 501
 QY 161 ValIleValValIleProPheProSerIleLysAsnGlySerAsnTyArgIleProPhePhe 180
 DB 502 GTAAAGGTGTGCTCTTTCTTCATTAAACGAAAGCAATTAACCCCTTTCTCTTT 561
 QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysIleProPheTrp 200
 DB 562 AGAACCCGAGCTGTGACCTGTGTGTACAGCCGACATCTAGCTGTAAACCTTTCTGG 621
 QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValIleSerPheAspHis 220
 DB 622 AAGCTTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCAGACAC 681
 QY 221 AlaProHisAsnPheGlyPheArgPheArgPheTyLeuHisGlyIleLeuLeuValHisGlyGly 240
 DB 682 GCACCGGACAACTTCGGCTTCCTGTCTCATCTTCAACAGCTCAAGCGACGAAAGGA 741
 QY 241 ProPheLysArgLysThrCysIleGlnGlnIleThrGlnIleThrThrSerCysIleLeu 260
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 QY 261 GlnAsnValSerProGlyAspTyrIleIleGlyLeuValAspAspThrAsnThrArg 280
 DB 802 CAATAATGTTCTCCAGGGGATTAATATATGAGCTGTGATGACATTAACAACAAGA 861
 QY 281 LysValMetHisGlyTyrAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAla 300
 DB 862 AAAGTATGATTAATGCTTAAAGCCAGTCACTCCCGTGGCGCGGCCCATCAGAGCC 921
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrIlePheThrValMet 320
 DB 922 ATGGCCATCAAGGCACTGTGATGATATGGCATTCGGAGAGCTTTCACATGTGATG 981
 QY 321 CysArgLysLeuGlnGlnIleAsnIleTyrSerHisLeuAspGlnGlySerSerGlySer 340
 DB 982 TGGCGCAAGAGCAACAAGAAATATATATTCAATTAGATGAAGAGACTCGAGTCT 1041
 QY 341 SerThrTyThrAlaAlaLeuProArgGlyIleArgLeuArgProArgProLysValPheLeu 360
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 QY 361 CysTySerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyPhePhe 380
 DB 1102 TGCATTATCCAGTAAAGATGGCCAGAAATCACTGATATGTCTGCTTCCGCTACTTTC 1161
 QY 381 LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTrpGluAspPheSerLeuCys 400

DB 1162 CTCACAGACTTCTGTGGCTGTGAGGTGGCTGGACCTGTGGGAAGACTTCAAGCTCTGT 1221
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 DB 1222 AGAGAAAGGACAGAAATGGGTCAATCCAGAAAGTCCAGAGTCCAGTTCATCATTTGTG 1281
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 DB 1282 GTTTGTTCAGAGATGTGAAGTACTTTGTGACAGAGAAAGATCTACAAACAAGAGAGGT 1341
 QY 441 GlyArgGlySerGlyLysGlyGlyLeuPheLeuValAlaValSerAlaIleAlaGlyLys 460
 DB 1342 GGCCGAGGCTCGGGAAAGAGAGCTTCTGTTGGCGGTGTCAAGCTTCCGCAAAAG 1401
 QY 461 LeuArgGlnAlaIleGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyPhe 480
 DB 1402 CTCGCGCAAGCCAGAGAGTTCGTCCGGCGCTCAGAAAGTTATTCGCGCTTACTTT 1461
 QY 481 AspTySerCysGlyGlyValAspValProGlyIleLeuAspLeuSerThrLysTyArgLeu 500
 DB 1462 GATTATTCCTCGAGGGAACGTCCCGGTATCTTAGACTGATACAAAGTACAGACTC 1521
 QY 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGly 520
 DB 1522 ATGCAATCTTCTCAGCTGTGTTCCCACTGCACTCCGAGACCAAGCGCTCCAGAG 1581
 QY 521 ProGlyGlnHisThrArgGlnGlySerArgArgArgArgTyPheArgSerLysSerGlyArg 540
 DB 1582 CCGGGGACACACGGGACAGGCGACAGAGAGAACTACTTCCGAGCAAGTCAAGCGCCG 1641
 QY 541 SerLeuTyValAlaIleCysAsnMetHisGlnPheIleAspGlyGlyIleProAspTrpPhe 560
 DB 1642 TCCCTATAGCTGCCCATTTGCAACATGACACAGTTTATTTGACGAGGAGCCGACTGTTC 1701
 QY 561 GlyLysGlnPheValProPheHisProProProLeuArgTyArgGlyIleProValLeuGly 580
 DB 1702 GAAAGCAGTGTGCTTCCTTCATCTCTCCACTGCGCTACCGGAGGACAGCTTGGAG 1761
 QY 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyIleProLysAsp 600
 DB 1762 AAATTTGATTCGGGCTGTGTTTAAATGATGTCAATGTGAACAGAGGCTTGAAGTGAAC 1821
 QY 601 PheCysLeuLysValGlyAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620
 DB 1822 TTCTGCTTAAAGGTAGAGCGCTGTCTTGGGGCAACGGACAGCCGACTCCAGCAC 1881
 QY 621 GlySerGlnHisGlyGlyLeuAspGlnAspGlyGlyAlaArgProAlaLeuAspGlySer 640
 DB 1882 GAGAGTCAGCATGGGGGCTGGACCAAGACGGGAGAGCGCGCTGCTTGAACGGTAGC 1941
 QY 641 AlaAlaLeuGlnProLeuLeuHisThrValLysValAGlySerProSerAspMetProArg 660
 DB 1942 GCGGCCCTTCAACCCCTGTGACACAGGTGAAGCGGAGGCCCTCGGACATGCGCGCG 2001
 QY 661 AspSerGlyIleTyArgAspSerValProSerSerGlyLeuSerLeuProLeuMetGly 680
 DB 2002 GACTCAGGATCTATACCTGTCTGTGCGCTCATCCGAGCTGTCTGCACTGATGGA 2061
 QY 681 GlyLeuSerThrAspGlnThrGlyIleThrSerSerLeuThrGlySerValSerSerSer 700
 DB 2062 GAGCTCTCAGCGGACAGACAGAAAGTCTCTCCCTGACGGAAGCGTGTCTCTTCA 2121
 QY 701 GlyLeuGlyGlyGlyIleProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
 DB 2122 GGCCTGGGTGAAGAGAACTCTGTGCTTCTTCCAACTCTCTTCTTGGGTATGC 2181
 QY 721 LysAlaAspLeuGlyCysArgSerTyThrAspGlyLeuHisAlaValAlaPro 738
 DB 2182 AAAGCAATCTTGTGTTGCCGACGTAAGTGAATCAACGCGGTCCGCTT 2235
 RESULT 3
 ABA95035

ID ABA95035 standard; DNA; 2341 BP.
 AC ABA95035;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE Human cytokine receptor, zcytor18 splice variant nucleotide sequence.
 XX
 KW Cytokine receptor; zcytor18; cell proliferation; antiproliferic; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 86..2305
 FT /*tag= a
 FT /product= "zcytor18 splice variant"
 XX
 XX MO200208259-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001MO-US023253.
 XX
 PR 26-JUL-2000; 2000US-0220747P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Kuestner RE, Gao Z;
 XX
 DR WPI, 2002-217048/27.
 DR P-PSDB; ABB07628.
 XX
 PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor growth,
 PT and modulating immune system by binding to endogenous zcytor18 ligand.
 XX
 PS Claim 5; Page 102-106; 119pp; English.
 XX
 CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 splice variant nucleotide sequence
 XX
 SQ Sequence 2341 BP; 550 A; 668 C; 625 G; 498 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 0 Length: 2341
 Score: 3918.00 Matches: 734
 Percent Similarity: 99.6% Conservative: 1
 Best Local Similarity: 99.5% Mismatches: 3
 Query Match: 99.2% Indels: 0
 DB: Gaps: 0
 US-10-616-788-2 (1-738) x ABA95035 (1-2341)
 QY 1 MetAlaProTTrpLeuGlnLeuCySerValPhePheThrValAlaAlaCysLeuAlaGly 20
 DB 86 ATGGCCCGGCGGCGAGCTCTGCTCGCTCTTACGGGTCAACGGCTCCTCAACGGC 145
 QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAlaTrpTrpGly 40

DB 146 TCGCAGCTGGCTGTGGCCGCTGGCGGGGTCCGCCGCCGCCGCCGCCACACTGTGGC 205
 QY 41 TTPATGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLeuTyr 60
 DB 206 TGGAGGGGAGTGGGGCGAGCGACAGAAAACAGTGGGCTGTACAACTCACTTCAATAT 265
 QY 61 AspAsnCyThrThrThrTyrLeuAsnProValGlyValAlaIleAlaAspAlaGlnAsn 80
 DB 266 GACAAATGTACCACTTACCTTGAATCCAGTGGGAGCAATGTGATGCTGACGCCAGAAAT 325
 QY 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrSerPro 100
 DB 326 ATCAACATCAGCCAGATGCTTGGCATGACCAAGTGGCATCACTTCTTGTGCCCA 385
 QY 101 GlyAlaLeuGlyTleGluPheLeuLeuGlyPheArgValIleLeuGlnGluLeuLeuSer 120
 DB 386 GGGGCCCTCGGCATTCGAATTCCTGAAAGAGATTTCCGGTAAATCTGAGGAGCGTGAAGTCG 445
 QY 121 GlnGlyArgGlnCysGlnGlnGlnIleLeuIleLeuValAspProGlnLeuAsnSerSerPhe 140
 DB 446 GAGGAAAGACAGTGCACCAACTGATTTCAAGAGATCCAGAGAGCTCAACAGTACCTTC 505
 QY 141 LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe 160
 DB 506 AAAAGAACTGGAAATGGAATCTCAACTTCTCGAATATGAAATTTGAACGGATTTATTC 565
 QY 161 ValLysValValProPheProSerIleLysAsnGlnSerAsnTyrHisProPhePhe 180
 DB 566 GTAAAGTTGTCCCTTTCTCTTCTTCAATTAAGAAAGAAATATCAACCTTCTTCTT 625
 QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLysPProPheTrp 200
 DB 626 AGAACCCGAGCCGTGATCCGTGTGTTACAGCCGCAACATCTTACTGTGAACCTTCTTG 665
 QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 DB 686 AAGCTTCGAACTGAACTGAACATCAACGACATGCTCGGACATGAGGTCTCTTCAACAT 745
 QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisIleTyrLysLeuLysIleGly 240
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 QY 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrGlnThrThrSerCysLeuLeu 260
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 QY 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrArg 280
 DB 866 CAAATGTTTCTCCAGGGAGATTTATATTTGAGCTGTGATGACATTAACACAAAGA 925
 QY 281 LysValMetHisIleTyrAlaLeuLysProValHisSerProTyrAlaGlyProIleArgAla 300
 DB 926 AAAGTATCATTTATTCCTTAAAGCAGGCACTCCCGTGGGCCGAGCATCAAGGC 985
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 DB 986 GTGGCCATCAAGTGCACGTGATGATCATATGCGCATTCGCGACGCTCTTCACTGTGAGT 1045
 QY 321 CysArgLysLysGlnGlnGlnIleLeuAsnIleTyrSerHisLeuAspGlnGlnSerSerGly 340
 DB 1046 TGGCGAAGAGAGCAAGAAATATATATTCATCATTTAGATGAGAGAGCTGTGAGTCT 1105
 QY 341 SerThrTyrThrAlaAlaLeuProArgGlnArgLeuArgProArgProLysValPheLeu 360
 DB 1106 TCCACATACACGACGACATCCCAAGAGAGAGGCTCCGCGCGGCGGAGAGGCTTCTTC 1165
 QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
 DB 1166 TGTCTATTCCAGTAAGATGCGCAGATCATCAAGAAATGCTGTCCAGTGTTCCTTCACTTC 1225
 QY 381 LeuGlnAspPheCysGlyCysGlyValAlaAlaAspLeuTrpGlnAspPheSerLeuCys 400
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QY 401 ArgGluGlnArgGluTTPValIleGlnIleHisGlnPheIleIleVal 420
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QY 421 ValCysSerIleGlyMetLeuTyrPheValAspIleValAsnTyrIleHisGlyGly 440
Db 1346 GTTGTGTTCCAAAGGTATGAAGTACTTTGTGGACAAAGAACTCAAAACCAAGAGGT 1405
QY 441 GLYArgGlySerGlyLeuGlyGlnPheLeuValAlaValSerAlaIleGlnGly 460
Db 1406 GGCCGAGCTCGGGGAAAGAGAGACTCTCTGTTGGCGGTGTCAGCATTTGCCGAAAG 1465
QY 461 LeuArgGlnAlaIleGlnSerSerSerAlaIleLeuSerPheIleAlaIleTyrPhe 480
Db 1466 CTCGCGCCAGGCGCAAGCAGAGTCTCCGCGCGCTCGACAAATTTCACCGCTTACTTT 1525
QY 481 AspTyrSerCysGluGlnIleAspValProGlyIleLeuAspLeuSerThrIleTyrArgLeu 500
Db 1526 GATTATTCCTGCGAGGAGAGCTCCCGGTATCTTAACCTGAGTACCAAGTACAGACTC 1585
QY 501 MetAspAsnLeuProGlnIleCysSerHisGlnHisGlnSerArgAspHisGlyLeuGlnGlu 520
Db 1586 ATGACACATCTTCTCCAGCTCTGTTCCACTTGCACTCCGAGACACGCGCTCCAGAG 1645
QY 521 ProGlyValIleHisThrArgGlnGlySerArgArgAsnTyrPheArgSerIleSerGlyArg 540
Db 1646 CCGGGGAGAGACAGCGACAGGGGAGAGAAAGAACTACTTCGAGCAAGTCAAGCCGG 1705
QY 541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGlnIleProAspTyrPhe 560
Db 1706 TCCCTATACCTGCGCATTTTGCACATGCAACAGTTTATTGACGAGAGCCGCACTGTTTC 1765
QY 561 GlnIleGlnPheValProPheHisProProProLeuArgTyrArgGluProValIleGln 580
Db 1766 GAAAGAGAGTTCCTCCCTCCATCCCTCCCACTGGGCTACCGGGAGCCAGTCTTGAG 1825
QY 581 LysPheAspSerGlyLeuValIleAsnAspValMetCysIleProGlyProGlySerAsp 600
Db 1826 AATTTGATTCGGGCTTGTTGTTTAATGATGTCAATGTGCAACAGGAGCTTGAGAGTGAC 1885
QY 601 PheCysLeuLysValGlnAlaProValIleGlnIleAlaThrGlyProAlaAspSerGlnHis 620
Db 1886 TTCGCTTAAGGTAGAGGGCGGTCTTGGGGCAACCGGACGAGCTCCAGCAC 1945
QY 621 GluSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
Db 1946 GAGAGTCAGATGGGGGCTGTCGACCAAGACGGGGAGGCCGCGCTTGACCGGTAGC 2005
QY 641 AlaAlaLeuGlnProLeuLeuHisThrValIleValIleGlySerProSerAspMetProArg 660
Db 2006 GCGGCTTGCAACCCCTGTCGACACGGTAAAGCCGCGAGCCCTTGACATGCGCGG 2065
QY 661 AspSerGlyIleTyrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln 680
Db 2066 GACTCAGGACATATGATGCTGTGTCCTCCATCCGAGCTGTCTGCCATGATGAA 2125
QY 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGluSerValIleSerSerSer 700
Db 2126 GGACTTCGACGAGCAGACGAAACCTCTTCCTTCGACGAGCGGTCTCTCTTCA 2185
QY 701 GlnLeuGlnIleGlnIleProProAlaLeuProSerIleLeuLeuSerSerGlySerCys 720
Db 2186 GGCTTGAGTAAAGAGAACTCTGCGCTTCTTCAGAGCTCTCTTCTTGAGTACATGC 2245
QY 721 LysAlaAspLeuGlyCysArgSerTyrThrAspGlnLeuHisAlaValAlaPro 738
Db 2246 AAGGACATCTTGTTGCGGACGTAACATGATGAATCCACGCGGTGCGCCCT 2299

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AC ADU69241;
XX
XX 10-FEB-2005 (first entry)
DT
XX
XX Human SEF gene SEQ ID NO:1.
DE
XX
XX de; gene; fibroblast growth factor; SEF; similar expression of FGF genes;
KW cytotatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
KW vasotropic; hypertensive; nephrotropic; gene therapy; diagnosis;
KW prognosis; proliferative disorders; cardiovascular disorders;
KW renal disease; glomerular disease.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 90..2309
FT /tag= a
FT /product= "SEF"
XX
XX US2004235104-A1.
XX
XX 25-NOV-2004.
XX
XX 07-MAY-2004; 2004US-00842006.
XX
XX 08-MAY-2003; 2003US-0469522P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Yang R;
XX
XX WPI; 2004-821320/81.
XX P-PDB; ADU69242.
XX
XX New isolated SEF nucleic acid and polypeptide, useful for monitoring,
PT treating, or diagnosing proliferative and/or differentiative disorders,
PT e.g. ovarian cancer, breast cancer, or cardiovascular disorder including
PT arteriosclerosis.
XX
XX Claim 1, SEQ ID NO 1; 46pp; English.
XX
XX The invention relates to a novel isolated SEF (similar expression of FGF
XX genes) nucleic acid molecule (I). An SEF of the invention has cyostatic,
XX cardiovascular-gen., antiarteriosclerotic, cardiant, vasotropic,
XX hypotensive, and nephrotropic activity, and may have a use in gene
XX therapy. The SEF nucleic acids and polypeptides can be used for
XX diagnostic assays, prognostic assays, and monitoring clinical trials.
XX They can also be used for treating a subject at risk of or susceptible to
XX a disorder or having a disorder associated with aberrant or unwanted SEF
XX expression or activity. The SEF molecules can also be used for
XX monitoring, treating, or diagnosing proliferative and/or differentiative
XX disorders, e.g. ovarian cancer, breast cancer, colon cancer, prostatic
XX cancer, FGF related disorder, cardiovascular disorder including
XX arteriosclerosis, coronary artery disease, ischemia, reperfusion injury,
XX restenosis, arterial inflammation, hypertension, endothelial disorders,
XX and a kidney disorder, e.g. glomerulonephritis, vascular nephropathy,
XX renal failure, or glomerular disease. The SEF molecules can also be used
XX as markers of disorders or disease states, as markers for precursors of
XX disease states, as markers for predilection of disease states, as
XX markers of drug activity, or as markers of the pharmacogenomic profile of
XX a subject. The present sequence represents the SEF nucleic acid molecule
XX of the invention.
XX
XX Sequence 4477 BP; 1133 A; 1086 C; 1141 G; 1117 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 4477
XX Score: 3908.00 Matches: 732
XX Percent Similarity: 99.5% Conservative: 2
XX Best Local Similarity: 99.2% Mismatches: 4
XX Query Match: 99.0% Indels: 0
XX DB: 13 Gaps: 0

```


QY 721 LysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
DB 2250 AAGGAGATCTTGTGGTCCGACGTAACATGATGAATCCACCGGGTCCGCCCT 2303

RESULT 5
ADM23599
ID ADM23599 standard; DNA; 4477 BP.
XX
AC ADM23599;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human IL-17RLM DNA.
XX
KM Neuroprotective; Immunosuppressive; Cytostatic; IL-17RLM;
XX rheumatoid arthritis; asthma; carcinoma; ds; gene.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS /tag= a
FT /product= "IL-17RLM"
XX
PN CN1463982-A.
XX
PD 31-DEC-2003.
XX
PF 28-JUN-2002; 2002CN-00123447.
XX
PR 28-JUN-2002; 2002CN-00123447.
XX
PA (UYOI) UNIV QINGHUA.
XX
PI Xiong S, Chang Z, Fu X;
XX
DR MPI; 2004-248693/24.
XX P-PSDB; ADM23600.
XX
PT New polynucleotide encoding IL-17RLM polypeptide, useful in preparing a
PT composition for treating e.g., neurological or autoimmune disease, such
PT as rheumatoid arthritis or asthma, or kidney- or testis-related
PT carcinoma.
XX
PS Disclosure; SEQ ID NO 1; 14pp; Chinese.
XX
CC The present invention relates to a new isolated IL-17RLM polynucleotide.
CC The polynucleotide encoding the IL-17RLM polypeptide is useful in
CC preparing a composition for treating an individual in need of an
CC increased or decreased level of IL-17RLM polypeptide, e.g. neurological
CC or autoimmune disease, such as rheumatoid arthritis or asthma, or kidney-
CC or testis-related carcinoma. The present sequence represents human IL-
CC 17RLM DNA.
XX
SQ Sequence 4477 BP; 1133 A; 1086 C; 1141 G; 1117 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 4477
Score: 3908.00 Matches: 732
Percent Similarity: 99.5% Conservative: 2
Best Local Similarity: 99.2% Mismatches: 4
Query Match: 13 Indels: 0
DB: 13 Gaps: 0

US-10-616-788-2 (1-738) x ADM23599 (1-4477)

QY 1 MetAlaProTyrLeuGlnLeuCysSerValPhePheThrValAlaMetAlaCysLeuAangly 20
DB 90 ATGGCCCCCGGTGCGACGCTCTGCTCTTCTTTACGCTCAACGCTCTCAACGGC 149

QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAlaAspThrCysGly 40
DB 150 TCGCAGACTGGCTGTGGCCGCTGGCGGGGTCCGGCCGCGCGGGGCGCGCACTCTGTGGC 209

QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLeuTyr 60
DB 210 TGGAGGGAGATGGGGGCGACCCAGCAAGAACAGTGGCTGTACACACTCACTCAATAT 269

QY 61 AspAsnCysThrThrThrTyrLeuAsnProValGlyValHisValIleAlaAspAlaGlnAsn 80
DB 270 GACAAATTGTACCACTTACTGAATCCAGTGGGAGACATGATGATCTGACCGCCAGAAAT 329

QY 81 IleThrIleSerGlnThrValaCysHisAspGlnValAlaValThrIleLeuTyrSerPro 100
DB 330 ATCACCATCAGCAGATATCTTGCACATGACCAAGTGGCAGTCAACATTTTGTGCTCCA 389

QY 101 GlyAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGlnGluLeuLeuSer 120
DB 390 GGGGCGCTCGGACATCAATCTCGAAGAGATTTCCGGGTAACTGGAGAGAGCTGAAGTGG 449

QY 121 GluGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
DB 450 GAGGAGAGACAGTGGCCACACATGATTTAAAGATCCGAAAGCAGTCAACAGTACCTTC 509

QY 141 LysArgThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe 160
DB 510 AAAAGAACTGGAAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTTC 569

QY 161 ValLysValValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhe 180
DB 570 GTTAAGCTTGTCCCTTTCTTCCATTAAAGAAAGCAATTACCACTTTCTTCTTT 629

QY 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
DB 630 AGAACCCGAGCCTGTGACCTGTGTGTAAGCCGAGCAATCTGAGTTAAACCTTCTG 689

QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
DB 690 AAGCCTCGGAACCTGGAACATCAGCCAGCATGCTCGAATCGAGGTGCTTCGACGAC 749

QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisGlyTyrLeuLeuHisGlyGly 240
DB 750 GCAACGCAACACTTGGCTTCCGCTTCTTCTTCACTTCACTCAAGCTCAAGCAGAGAA 809

QY 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGlnThrThrSerCysLeuLeu 260
DB 810 CTTTCAAGCGAAGAACTGTGAGCAGAGCAAACTACAGATGACAGTGGCTCTCTT 869

QY 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrArg 280
DB 870 CAATAATGTTCTCCAGAGGATTAATATATGAGCTGTGTGATGACCTAACACAAACAGA 929

QY 281 LysValMetHisGlyAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAla 300
DB 930 AAGATATGATTAATATCTTTAAAGCCAGTGCCTCCCGTGGGCGGCGCCATCAGAGCC 989

QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
DB 990 GTGGCATCAGATGTCAGTGGATGATATGCGGATTCGCGACGCTTCACTGTGATG 1049

QY 321 CysArgLysLysGlnGlnGlnAsnIleTyrSerHisLeuAspGluGluSerSerGlySer 340
DB 1050 TGCCTCGAAGAACACAAACAAATATATATTTCACTTGTGAAGAAAGAGCTCTGAGTGT 1109

QY 341 SerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgProArgValPheLeu 360
DB 1110 TCCACATACCTGCGACATCTCCAGAGAGAGAGCTCCGCGCGCCGAGAGCTTTCTTC 1169

QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
DB 1170 TGTATTTCCAGTAAAGATGGCCAGATCACTGAATGTGTCCAGTGTTCGCTCACTTC 1229

QY 381 LeuGlnAspPheCysGlyCysGlyValAlaAlaLeuAspLeuTrpGluAspHisSerLeuCys 400
DB 1230 CTCACAGACTCTGT 1289

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QY 401 ArgGluGlyValArgGluTrpValIleGlnIleValIleHisGluSerGlnPheIleIleVal 420
DB 1290 AAGGAGGCGAGAGAAATGGGTCAATCCAGAAATCCAGATTCCTCATCATTTG 1349
QY 421 ValGlySerIleValGlyMetIleValPheValAspIleValAsnIleValIleValGly 440
DB 1350 GTTGTTCAGAAAGTATGAAGTACTTGTGACAGAAAGAACTACAAACCAAGAGG 1409
QY 441 GlyValGlySerGlyIleValGlyValPheValIleValSerAlaIleValGlyVal 460
DB 1410 GCGCGAGGCTCGGAGAAAGAGAGCTCTCTGTGTGCGGTGACGATTCGCGTAAAG 1469
QY 461 LeuArgGlnAlaValGlnIleSerSerAlaAlaLeuSerIlePheIleAlaValIlePhe 480
DB 1470 CTCGCGCAGGCGCAGAGAGAGTCTGCGCGGCTGACGAGTTATTCGCGTCACTT 1529
QY 481 AspIleSerCysGluGlyValAspValProGlyIleLeuAspLeuSerThrIleValIleVal 500
DB 1530 GATTATTCCTCGAGGAGAGAGCTCCCGGTATCTAGACTGAGTACAGTACAGACTC 1589
QY 501 MetAspAsnLeuProGlnLeuValCysSerHisLeuHisSerArgAspHisGlyLeuGlnIle 520
DB 1590 ATGCAAAATCTCTCTGAGCTCTGTTCCACCTGACCTCCGAGACCAAGCGCTCCAGAG 1649
QY 521 ProGlnIleHisThrArgGlnIleValSerArgArgAsnIlePheArgSerIleValSerGly 540
DB 1650 CCGGGGCGAGACCGGAGACGAGGCGAGAGAGAACTACTTCGAGAGCAAGTACAGCGCG 1709
QY 541 SerLeuValAlaIleCysAsnMetHisGlnPheIleAspGluGlnProAspTrpPhe 560
DB 1710 TCCCTATGCTGCTCCCTTTCAGACATGACCACTTATTCAGAGAGAGCGCGCTGTT 1769
QY 561 GlyValGlnPheValProPheHisProProLeuArgGlyValGlnProValIleGlnIle 580
DB 1770 GAAAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1829
QY 581 LysPheAspSerGlyLeuValIleLeuAspValMetCysIleAspProGlyProGluSerAsp 600
DB 1830 AATTTGATTCGGGCTGTGTTTAAATGATGATGCAAAACAGGCGCTGAGAGTGAAC 1889
QY 601 PheCysLeuValIleGlnAlaProValIleGlnAlaThrGlyProAlaAspSerGlnHis 620
DB 1890 TTCTGCTTAAAGTAAAGCGGCTGTTCTTGGGCGAACCGACCACTCCAGCAC 1949
QY 621 GluSerGlnHisGlyIleLeuAspGlnAspGlyIleAlaIleProAlaLeuAspGlySer 640
DB 1950 GAGAGTCAGCATGGGGGCTGGACCAAGAGCGGAGCGCGCTGACCGTGAAC 2009
QY 641 AlaAlaLeuGlnProLeuLeuHisThrValIleGlySerProSerAspMetProArg 660
DB 2010 GCGCGCTCTCAACCTCTGTCGACAGGTGAAGCGGCGCGCTCTGAGCATGCGCGG 2069
QY 661 AspSerGlyIleThrAspSerSerValProSerSerGluLeuSerIleProLeuMetGln 680
DB 2070 GACTCAGGCACTTATGATCTGCTGTGCTCTCAATCCGAGCTGTCTCTGCACTGATGAA 2129
QY 681 GlyLeuSerThrAspGlnThrGlnThrSerSerIleThrGluSerValSerSerSer 700
DB 2130 GAGCTCTCAAGCAGACAGAGAAAGTCTCTGACGAGAGCGGTCTCTCTTCA 2189
QY 701 GlyLeuGlyIleGlnIleProProAlaLeuProSerIleValLeuSerSerGlySerCys 720
DB 2190 GCGCTGGGTGAAGAGAACTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2249
QY 721 LysAlaAspLeuGlyCysArgSerIleThrAspGluLeuHisAlaValAlaPro 738
DB 2250 AAGGCAATCTTGTGTGCGGCACTGATGAATCTCAAGCGGTGCGCCCT 2303

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RESULT 6
ABA95031
ID ABA95031 standard; DNA; 2383 BP.
XX
AC ABA95031;

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XX 20-MAY-2002 (first entry)
DT
XX Human cytokine receptor, Zcytor18 nucleotide sequence.
DE
XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;
XX erythroleukemia; chromosome 3p14.3; gene therapy; de.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 86..2347
FT /tag= a
FT /product= "Zcytor18"
XX
PN WO200208259-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023253.
XX
PR 26-JUL-2000; 2000US-0220747P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Kuestner RE, Gao Z,
XX
DR WPI; 2002-217048/27.
XX
DR P-PDB; ABB07626.
XX
PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX
PS Claim 5; Page 85-90; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumor growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial
XX periodic fever and erythroleukemia, and erythroleukemia associated with
XX CC polymorphisms of cytokine receptors. The present sequence represents a
XX human Zcytor18 nucleotide sequence
XX
SQ Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 2383
Score: 3901.00 Matches: 734
Percent Similarity: 97.7% Conservatve: 1
Best Local Similarity: 97.6% Mismatches: 3
Query Match: 98.8% Indels: 14
DB: 6 Gaps: 1
US-10-616-788-2 (1-738) x ABA95031 (1-2383)
QY 1 MetAlaProTrpLeuGlnIleuValPhePheThrValAsnAlaCysLeuAsnGly 20
DB 86 ATGGCCCCGCTGCTGAGCTCTGCTCTCTTTCAGGTCAAGCCCTGCTCAACCGC 145
QY 21 SerGlnLeuAlaValAlaIleGlySerGlyArgAlaTrpGlyValAspThrCysGly 40
DB 146 TCGCAGCTGCTGTGCGCGCTGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
QY 41 TrpArg-----GlyValGlyPro 46

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|||||
Db 206 TGGAGGATGAAAGCGCTGCCGACCCCGCTTGTGTTGCTAATGAGGAGTGGGGCCA 265
|||
Qy 47 ALaSerArgAsnSerGlyLeuTyrAsnIleThrPheLeuTyrAspAsnGlyThrThrTyr 66
Db 266 GCGAGCGAAAGAGTGGCTGTACCAATCACCTTCAAAATATAGCAATTTATCCACTTAC 325
Qy 67 LeuAsnProValGlyLeuSerHisValIleAlaAspAlaGlnAsnIleThrIleSerGlnTyr 86
Db 326 TTGAATCCAGTGGGGAGAGCATGTGATGTCGACCCCGAATATACCACTCACCGCATAT 385
Qy 87 ALaCysHisAspGlnValAlaValThrIleLeuTyrSerProGlyValAlaGlyIleGlu 106
Db 386 GCTTGCATGACCAAGGCGAGTCACCACTTGTGGTCCCGAGGGGCGCTCGGCATGAA 445
Qy 107 PheLeuLeuGlyPheArgValIleLeuGluGluLeuLeuSerGluGlyValArgGln 126
Db 446 TTCCCTGAAGAGATTTCCGGTAATATCGAGAGCTGAAGTCGAGGGAGACAGTGCAG 505
Qy 127 GlnLeuIleLeuLeuAspProLeuGlnLeuAsnSerSerPheLeuArgThrGlyMetGlu 146
Db 506 CAACATGATTTAAAGATCCGAGAGCACTCAACATGCTTCAAAAGACTGGAAATCGAA 565
Qy 147 SerGlnProPheLeuAsnMetLeuPheGluThrAspTyrPheValIleValProPhe 166
Db 566 TCTCAACCTTCTCGAATATGAATTTGAAACGGATATTTCGTAAGGTTGCTCCCTTT 625
Qy 167 ProSerIleLeuAsnGluSerAsnTyrHisProPhePheArgThrArgAlaCysAsp 186
Db 626 CTTTCCATTAAAGCAAGAACCAATTCACACCTTTCTTTAGAACCCAGGCTGTGAC 685
Qy 187 LeuLeuLeuGlnProAspAsnLeuAlaCysLeuProPheTyrPheProArgAsnLeuAsn 206
Db 686 CTCTTGTTCACGCCGAGCAATCTAAGCTTGTAAACCTTCTGGAAGCTCCGAACTCGAAC 745
Qy 207 IleSerGlnHisGlySerAspMetGlnValSerPheAspHisAlaProHisAsnAspGly 226
Db 746 ATCAGCCAGCATGGCTCGGACATGACAGGTGCTCTTCGACCATGACCGGCAACTTCGCG 805
Qy 227 PheArgPhePheTyrLeuHisGlyTyrLeuLeuHisGlyGluProPheLeuValGlyThr 246
Db 806 TTCCGGTTCTTCACTCTCACTCAAGCTCAAGCAACAGAACCTTTCAGGCGAAAGACC 865
Qy 247 CysLeuGlnGluGlnThrThrGluThrThrSerCysLeuLeuGlnAsnValIleSerProGly 266
Db 866 TGTAAAGAGAGCAACTACAGAGACACAGCTGCTCTTCAAAATGTTTCTCCAGGG 925
Qy 267 AspTyrIleIleGluLeuValAspAspThrAsnThrThrArgLeuValMetHisGlyAla 286
Db 926 GATTATATATATTGAGCTGGTGATGACACTAACACAAAGAAAGTGCATTATAGCC 985
Qy 287 LeuLeuProValHisSerProTyrAlaGlyProIleArgAlaMetAlaIleThrValPro 306
Db 986 TTAAAGCCAGTGCATCCCGGTGGCGGGCCCATCGAGCCGTGGCATCAACAGTGC 1045
Qy 307 LeuValValIleSerAlaPheAlaThrLeuPheThrValMetCysArgLeuGlyGln 326
Db 1046 CTGGTATGCTATTCGGCATTCGGAGCGCTTCACTGTATGTCCGCAAGAAAGCAACAA 1105
Qy 327 GlnAsnIleTyrSerHisLeuAspGluGluSerSerGluSerSerThrTyrThrAlaAla 346
Db 1106 GAAATATATATATTCACTTAAATGAAAGAGAGCTGTAGTCTTCAACATACCTGAGCA 1165
Qy 347 LeuProArgGluArgLeuArgProArgProLeuValPheLeuGlyTyrTyrSerLeuAsp 366
Db 1166 CTCCCAAGAGAGGCGCTCCGGCGCGGCGCAAGGTCTTCTCTGTCTAATTCAGATAAGAT 1225
Qy 367 GlnGlnAsnHisMetAsnValIleGlnCysPheAlaTyrPheLeuGlnAspPheCysGly 386
Db 1226 GGCAGATACATGAATGTGTCAGAGTTCGCTTCTTCCAGGACCTTGTGGC 1285
Qy 387 CysGlnValAlaLeuAspLeuTyrGluAspPheSerLeuCysArgGluGlyGlnArgGlu 406
|||||

Db 1286 TGTAGGTGGCTCTGAGCCTGTGGAGAGACTTCAGCCTCTGTAGAGAGGAGAGAA 1345
Qy 407 TTPValIleGlnLeuValIleHisGluSerGlnPheIleIleValValCysSerLeuGlyMet 426
Db 1346 TGGGTATCCAGAAAGATCCAGAGTCCAGTTTCATATGTGTGTTTGTTCGAAAGTTAG 1405
Qy 427 TyrTyrPheValAspLeuValAsnTyrLeuHisGlyGlyGlyValArgGlySerGlyLeu 446
Db 1406 AGTATCTTTGTGGACAAAGAACTACAAACCAAGAGAGGTGGCGGAGCTCGGGGAAA 1465
Qy 447 GlnGluLeuPheLeuValAlaValSerAlaIleAlaGluLeuLeuArgGlnAlaGlyGln 466
Db 1466 GAGAGCTTCTCTGTGTGGCGGTGTCCAGCATTTGCGGAAAGCTCCGACAGGCGAAG 1525
Qy 467 SerSerSerAlaLeuSerLeuPheIleAlaValTyrPheAspTyrSerCysGluGly 486
Db 1526 AGTTGTCGCGGCGCTTCAGCAGATTTATCGCGCTTACTTTGATTTATTCCTGCGAGGA 1585
Qy 487 AspValProGlyIleLeuAspLeuSerThrLeuValArgLeuMetAspAsnLeuProGln 506
Db 1586 GACGTCCCGGATCTTACAGCTGAGTACCAAGTACAGATCAGATCATGACATCTTCTCAG 1645
Qy 507 LeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGluProGlyGlnHisGlyArg 526
Db 1646 CTCTGTTCACATTCACCTCCGAGACACAGGCTTCAGAGAGCCGGGCGAGCACAGCGCA 1705
Qy 527 GlnGlySerArgArgAsnTyrPheArgSerLeuSerGlyArgSerLeuTyrValAlaIle 546
Db 1706 CAGGGACAGAAAGAACTACTTCCGAGACAGTCAAGCCGCTCTTATACCTCGCATT 1765
Qy 547 CysAsnMetHisGlnPheIleAspGluGluProAspTyrPheGluLeuGlnPheValPro 566
Db 1766 TGGAAATCAGACCAAGTTTATTGACAGAGAGCCGAGCTGTTGCAAAAGAGTTCGTTCCC 1825
Qy 567 PheHisProProLeuArgTyrArgGluProValLeuGluLeuPheAspSerGlyLeu 586
Db 1826 TTCCATCTCTTCCATCTGCGCTACCGGAGCCAGTCTTGAGAAATTTATTCGCGGCTTG 1885
Qy 587 ValLeuAsnAspValMetCysLeuProGlyProGluSerAspPheCysLeuValGlu 606
Db 1886 GTTTAAATGATGTCATGTGCAACAGGAGCTCGAAGATGATCTTGTGCTTAAGGTAGAG 1945
Qy 607 AlaProValLeuGlyValaThrGlyProAlaAspSerGlnHisGluSerGlnHisGlyGly 626
Db 1946 GCGGCTGTTCTTGGGCAACCGGACAGCGCACTCCACACAGAGTCAAGATGGGGG 2005
Qy 627 LeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySerAlaAlaLeuGlnProLeu 646
Db 2006 CTGGACCAAGAGCGGGAGGCGCGCTGCGCTTGAAGGTAGCGCGCTCGCAACCCCTG 2065
Qy 647 LeuHisThrValLeuValaGlySerProSerAspMetProArgAspSerGlyIleTyrAsp 666
Db 2066 CTGCACAGGTGAAGCCGGAGCGCCCTCGAGATGCCCGGGATTCAGGACATCTATAGAC 2125
Qy 667 SerSerValProSerSerGluLeuSerLeuProLeuMetGluGlyLeuSerThrAspGln 686
Db 2126 TGCTGTGTCCTTCATCCGAGGTGCTCTGCACTGATGAAAGACTTCGACGAGCAAG 2185
Qy 687 ThrGluThrSerSerLeuThrGluSerValSerSerSerSerGlyLeuGluGluGlu 706
Db 2186 ACAAGAAACGTCTTCCCTGACGAGAGCGGTGCTCTCTTCAGGCGCTGGGTGAGAGAA 2245
Qy 707 ProProAlaLeuProSerLeuValLeuLeuSerSerGlySerCysLeuValaAspLeuGlyCys 726
Db 2246 CTTCTGCGCTTCTTCCAAAGCTCTCTTCTTGGGTGACAGCAAGATCTTGTGTGC 2305
Qy 727 ArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
Db 2306 CGAGCTACATGATGAATCTCAAGCGGTGCGCCCT 2341
|||||

RESULT 7
ABA95033
ID ABA95033 standard; DNA; 2383 BP.


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QY 387 CyGGLuValAlaLeuAapLeuTrpGluAapPheSerLeuCyAaArgGluInaArgGlu 406
DB 1286 TGAGAGTGCTCTGAGCCTGTGGAGAGACTTCAAGCTCTGTAGAGAGAGGCGAGAGAA 1345
QY 407 TrpValIleGlnuValIleHISGluSerGlnPheIleIleValValCysSerLyGlyMet 426
DB 1346 TGGGTCTCCAGAGAGATCCAGAGTCCAGTTCATCTTGCTGGTTGTTGTTCCAAAGGTATG 1405
QY 427 LysTyrPheValAapLySlyAanTyrLysHISGlyGlyValGlyAaArgLySerGlyLys 446
DB 1406 AAGGACTTGTGGCAAGAGAACTACAAACAAAGAGAGTGGCCAGAGCTCGGGGAAA 1465
QY 447 GLyGlyLeuPheLeuValAlaValSerAlaIleAaGluLysLeuAaArgGlnAlaLysGln 466
DB 1466 GAGAGAGTCTTCTGGTGGGCGGTCTCAAGCTTCCGAAAAGCTCCCGCCAGGCCAACAG 1525
QY 467 SerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAapTyrSerCyGlyGly 486
DB 1526 AGTTCCGTCGCGGCGCTCAAGATTATCGCGCTTCACTTGTATTTCTCTCGAGAGGA 1585
QY 487 AapValProGlyIleLeuAapLeuSerThrLysTyrArgLeuMetAapAanLeuProGln 506
DB 1586 GAGGTCCTCCGATCTTGAAGCTGAGTACCAAGTACAGACTCAATGACAAATCTTCTCAG 1645
QY 507 LeuCySerHISaLeuHISaSerAaAaPheHISGlyLeuGlnGluProGlyGlnHISThrArg 526
DB 1646 CTCTGTTCCACCTGCACTCCCGAGACCAAGCTTCCAGAGAGCGGGGCGAGCACAGCGGA 1705
QY 527 GlnGlySerArgArgAanTyrPheArgSerLysSerGlyAaArgSerLeuTyrValAlaIle 546
DB 1706 CAGGGCAGCAGAAAGAACTACTTCCGAGCAGAGTCAAGCGGTCCTATACGTCGCATTT 1765
QY 547 CysAanMetHISGlnPheIleAapGluGluProAapTrpPheGlnuLysGlnPheValPro 566
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QY 567 PheHISProProProLeuAaArgTyrArgGluProValLeuGlnuLysPheAaPserGlyLeu 586
DB 1826 TTTCATCTCTCTCACTCGCCCTACCGGAGACCACTTGTGAGAAATTTGATTCGGCGTTG 1885
QY 587 ValLeuAanAapValMetCyLysProGlyProGluSerAapPheCyLeuLysValGlu 606
DB 1886 GTTTTAATGATGATGATGTCACAAACCGAGGCTGACAGTACCTTGCCTAAAGGTAGAG 1945
QY 607 AlaProValLeuGlnAlaThrGlyProAlaAapSerGlnHISGluSerGlnHISGlyGly 626
DB 1946 GCGGCTGTTCTTGGGCAACCGGACCGGACCTCCAGCAACGAGTCAAGCATGGGAGGC 2005
QY 627 LeuAapGlnAapGlyGluAlaArgProAlaLeuAapGlySerAlaAlaLeuGlnProLeu 646
DB 2006 CTGACCAACAGACGGGAGAGCGCCGCTTGAACGTGACCGCCGCTGCAACCCCTG 2065
QY 647 LeuHISThrValIysAlaGlySerProSerAaPheProArgAapSerGlyIleTyrAap 666
DB 2066 CTCACACCGGTGAAGCGCGGACCCCTCGACATGCGCGGAGCTCAGACATCTATGAC 2125
QY 667 SerSerValProSerSerGlyLeuSerLeuProLeuMetGluGlyLeuSerThrAapGln 686
DB 2126 TCGTCTGTGCTCCATCCGAGCTGTCTCTCCACTGATGAGAGACTTGTGAGGAGACAG 2185
QY 687 ThrGluThrSerSerLeuThrGlnuSerValSerSerSerSerGlyLeuGlyGluGlu 706
DB 2186 ACGAAACGCTTCTCCGAGCGAGAGGCTGTCTCTCTTCAAGGCTCGGAGTGAGAGAA 2245
QY 707 ProProAlaLeuProSerLysLeuLeuSerSerGlySerCyLysAlaAapLeuGlyCys 726
DB 2246 CTCCTGCGCTTCTCTTCAAGCTCTCTCTTGTGGGTCAAGCAAGAGCATTTGTTGTC 2305
QY 727 ArgSerTyrThrAapGluLeuHISAlaValAlaPro 738
DB 2306 CGCAGCTACACTGATGAATCTCAACGCGCGCCCT 2341

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ABK62082
ID ABK62082 standard; cDNA; 4392 BP.
XX
AC ABK62082;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human cDNA encoding novel secreted protein LP253.
XX
KW Human; sex; gene; secreted protein; cancer; autoimmune disease; arthritis;
KW osteoporosis; Alzheimer's disease; Parkinson's disease; meningitis;
KW encephalitis; neoplasia; trauma; ischemia; infection; mania; stroke;
KW cardiovascular disease; atherosclerosis; sepsis; anaemia;
KW rheumatoid arthritis; hypothyroidism; allergic response; liver failure;
KW multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder;
KW autism; panic disorder; learning disability; feeding disorder;
KW sleep pattern disorder; balance; perception; Th1-dependent insulinitis;
KW adult respiratory distress syndrome; ARDS.
XX
OS Homo sapiens.
XX
PN WO200214358-A2.
XX
PD 21-FEB-2002.
XX
PF 30-JUL-2001, 2001MO-US021124.
XX
PR 11-ANG-2000; 2000US-0224642P.
XX
PR 19-OCT-2000; 2000US-0241779P.
XX
PA (ELIL) LILLY & CO ELL.
XX
PI Edmonds BT, Micanovic R, Ou W, Su EM, Tschang SR, Wang H;
XX
DR WPI; 2002-304057/34.
XX
DR P-PSDB; AA091330.
XX
PT Novel polypeptides and polynucleotides of secreted proteins useful for
PT treating various diseases such as multiple sclerosis, cancer, autoimmune
PT diseases, osteoporosis, Alzheimer's disease and Parkinson's disease.
XX
PS Claim 1; Page 166-171; 235pp; English.
XX
XX
CC The invention relates to a novel human secreted polypeptide having
CC sequence 90% identical to the polypeptide sequences of LP105, LP61,
CC LP224, LP240, LP239(a), LP243(a), LP243(b), LP253, LP218), LP251(a),
CC LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP255(b), or
CC LP223(b). Also included are the nucleic acids encoding the LP proteins
CC (including complement, fragments encoding mature forms of the polypeptide
CC or variant), a vector comprising the nucleic acid, a host cell comprising
CC the vector, the preparation of the protein, an anti-LP antibody,
CC anti/agonists of LP and anti-LP-encoding mRNA ribozymes. The secreted
CC protein or its agonist is useful in the manufacture of a medicament for
CC treating a mammal suffering from a disease (and in diagnosis), condition
CC or disorder associated with aberrant levels of the secreted protein e.g.
CC cancer, autoimmune diseases, arthritis, osteoporosis, Alzheimer's
CC disease, Parkinson's disease, meningitis, encephalitis, neoplasia,
CC trauma, ischemia and infection, mania, stroke, cardiovascular disease,
CC atherosclerosis, rheumatoid arthritis, hypothyroidism, anaemia, sepsis,
CC allergic response, multiple sclerosis, liver failure, haemorrhages,
CC paranoia, obsessive compulsive disorder, autism, panic disorder, learning
CC disabilities, ALS (amyotrophic lateral sclerosis) psychoses, disorders
CC in feeding, sleep patterns, balance, and perception. Th1-dependent
CC insulinitis, adult respiratory distress syndrome (ARDS). The secreted
CC protein is further useful for identifying compounds that bind to the
CC secreted protein. The present sequence encodes a novel secreted protein
CC of the invention
XX
SQ Sequence 4392 BP; 1125 A; 1050 C; 1101 G; 1116 T; 0 U; 0 Other;

```

Alignment Scores: 0 Length: 4392
Pred. No.: 3857.00 Matches: 732

QY 699 rsergyleuglgluglupproalaaleuproserglyleuensergerglyse 719
 DB 2101 rTCAAGGCTGGGAGAGAGAACTCTGCCCTCTCTCCAGCTCTCTCTGAGCTC 2160
 QY 719 rCyblyalaaspleuglycyasargserlyrthaspglyleuhsialaValaapro 738
 DB 2161 ATCAAGACGAGCTTGTGGTGGCGGACGCTACGAGTGAATCCACGGGTGGCCCT 2218
 RESULT 9
 AAS18134
 ID AAS18134 standard; cDNA; 2786 BP.
 XX AAS18134;
 AC AAS18134;
 XX 26-MAR-2002 (first entry)
 DT
 XX Human DNAX cytokine receptor subunit 8 (DCRS8) cDNA.
 XX Human DNAX cytokine receptor subunit 8; DCRS8: phosphate labelling; ss;
 KM gene therapy; protein therapy; immunological disorder.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS /tag= a
 FT /product= "Human DCRS8"
 FT
 XX MO200190358-A2.
 XX 29-NOV-2001.
 XX 23-MAY-2001; 2001MO-US016767.
 XX 24-MAY-2000; 2000US-0206862P.
 PR (SCHE) SCHERING CORP.
 PA Gorman DM;
 PI WPI; 2002-106198/14.
 DR P-PSDB; AAU11355.
 XX
 PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
 PT useful for detecting antibodies generated in response to presence of
 PT increased protein levels or immunological disorders.
 XX
 PS Claim 16; Page 21-25; 148pp; English.
 XX
 CC The invention relates to primate and rodent DNAX cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents cDNA encoding the human
 CC DCRS8 polypeptide
 XX
 SQ Sequence 2786 BP; 673 A; 760 C; 709 G; 637 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.: 0 Length: 2786
 Score: 3835.50 Matches: 722
 Percent Similarity: 98.2% Conservative: 3
 Best Local Similarity: 97.8% Mismatches: 12
 Query Match: 97.2% Indels: 1
 DB: 6 Gaps: 1

US-10-616-788-2 (1-738) x AAS18134 (1-2786)
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 DB 70 ATGGCCCGCTGGGTGAGCTGTCTCCGCTCTTACCGGTCAACCCCTGGCCCAACGGC 129
 QY 21 SerGlnLeuAlaValAlaIaGlyserGlyATGAlaTfPglValAAspThCybGly 40
 DB 130 TCGACAGTGGCTGTCGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGC 189
 QY 41 TrpArgGlyValGlyProAlaSerArgAAspSerGlyLeuTyAsnIleThrPheLeuTy 60
 DB 190 TGGANGGAGGTGGGGCGACCGACGACGACGACGACGACGACGACGACGACGACGACGAC 249
 QY 61 AspAAspCybThrThrTyLeuAAspProValGlyValAlaIaAspAlaGlnAAsn 80
 DB 250 GACAAATTTGATCCACCTTACCTTGAATCCAGGGGAGACATGTGATTCACCGCCGAAAT 309
 QY 81 IleThrIleSerGlnTyAlaCybHisAAspGlnValAlaValThrIleLeuTfPserPro 100
 DB 310 ATCACCATGACGACGATGATGCTTGCATGACCAAGTGGCAGTCAACATCTTGGTCCCA 369
 QY 101 GlyAlaLeuGlyIleGlnPheLeuLeuGlyPheArgValIleLeuGlnGlnLeuLeuSer 120
 DB 370 GGGGCCCTGGGATGGAATTCCTGAAAGGATTTCCGGTAAATCTGGAGGAGGTGAAGTGG 429
 QY 121 GlnGlyArgGlnCybGlnGlnLeuIleLeuValAAspProGlyGlnLeuAAspSerPhe 140
 DB 430 GAGGGAAGACAGAGCCCAACCTGATTCAGAGATCCCAACAGAGTCAACAGTACCTTC 489
 QY 141 LysArgThrGlyMetGlnSerGlnProPheLeuAAspMetLysPheGlnThrAspTyPhe 160
 DB 490 AAAGAACTGAAATGGAATCTCACTTCTGAAATATGAATTTGAAACGATTAATTTTC 549
 QY 161 ValLysValValProPheProSerIleLysAAspGlnSerAspTyPhePhePhePhe 180
 DB 550 GTAAAG---TGTGCTTCTTCTTCAATTAAGAAAGCAATTACACACCTTCTTCTTT 606
 QY 181 ArgThrArgAlaCybAAspLeuLeuGlnProAAspAAspAlaCybLysProPheTfP 200
 DB 607 AGAACCAGAGCTGTGACCTGTGTTGTAACGGGACCAATCTGACTTGAACCTTCTG 666
 QY 201 LysProArgAAspLeuAAsnIleSerGlnHisGlySerAspMetGlnValSerPheAAsp 220
 DB 667 AAGCTCTGGAACCTGAACATCAGCCAGCATGGCTGGAATGAGGTGCTTCCAGCAC 726
 QY 221 AlaProHisAAspPheGlyPheArgPhePheTyLeuHisTyLeuLeuLysHisGlnGly 240
 DB 727 GACCCGACAACTTGGCTTCCGTTCTTCTTCTTCACTTCACTTCAAGCTCAAGCAAGGA 786
 QY 241 ProPheLysArgLysThrCybLysGlnGlnInThrGlnThrThrSerCybLeuLeu 260
 DB 787 CTTTCAACCGAAAGCTGTAAAGCGAGGACCAACTACAGATGACGAGCTGCCCTCTT 846
 QY 261 GlnAAspValSerProGlyAspTyPheIleIleGlnLeuValAAspAAspThrAAsnThrArg 280
 DB 847 CAAGAGTTTCTCCAGGGGAGTTATATATGACTGTGATGACCTTACACACACAAAG 906
 QY 281 LysValMetHisTyLeuAlaLeuLysProValHisSerProTfPAlaGlyProIleArgAla 300
 DB 907 AAAGTATGATTAATTCCTTAAAGCCAGTGCACCTCCGTTGGGGCGGGCCATCAAGGC 966
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 DB 967 GTGGGCATCATCAGTGCACGTGATGATCATATGCGCATGCGCGCTTCACTGGAAG 1026
 QY 321 CybArgLysLysGlnGlnGlnAAsnIleTySerHisAAspGlnGlnSerGlySer 340
 DB 1027 TGGCCGAAAGACAAAGAAATATATATTCACATTATGATGAAAGAGCTGTGAGCTT 1086
 QY 341 SerThrTyThrAlaAlaLeuProArgGlnArgLeuArgProArgProLysValPheLeu 360

Db 1087 TCCACATACACTGACGACCTCCCAAGAGAGGCTCCGGCCGCGGCAAGGTCTTCTC 1146
 Qy 361 CysTyrSerSerIysAspGlyGlnAsnHisMetAsnValValGlnCysPheIleTyrPhe 380
 Db 1147 TGCATATTCAGTAAGATGCGCAGAAATCACATGATGTCCTCCAGTCTTCCGCTTACTTC 1206
 Qy 381 LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTyrGluAspPheSerLeuCys 400
 Db 1207 CTCACGACCTTCTGTGCTGTAGTGGCTTGGACTTGGAGAAAGCTTCAAGCTTCTGT 1266
 Qy 401 ArgGlnGlyGlnArgGlnTyrValIleGlnLysIleHisGlnSerGlnPheIleIleVal 420
 Db 1267 AGAAGAGGCGAGAGATGGGTCAATCCAGAAATCCACAGATCCCAAGTTCATCATTTGTC 1326
 Qy 421 ValCysSerIysGlyMetIleTyrPheValAspLysLysValSerTyrLysHisGlyGly 440
 Db 1327 GTTGTGTTCCAAAGATGAAATCTTGTGTGACAAAGAAATCAAAACCAAGAGAGT 1386
 Qy 441 GLYArgGlySerGlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLys 460
 Db 1387 GGCCTGAGCTCGGGGAAAGAGACTTCTCTGGTGGGTGTCAGCCATTGCCAAAG 1446
 Qy 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 Db 1447 CTCGCGCAGGCGCAAGAGATTCGTCCGCGCGCTCAGCAAGTTTATCGCGCTTACTTT 1506
 Qy 481 AspTyrSerCysGluGlyAspValProGlyTyrLeuAspLeuSerThrLysTyrArgLeu 500
 Db 1507 GATTATTTCTCGCAGGAGAGAGCTCCCGGTATCTTAACCTGAGTACCAAGTACAGACTC 1566
 Qy 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
 Db 1567 ATGACACATTTCTCTAGCTGTCTTCCACCTGACTCCGAGACCAAGCGCTCCAGAGAG 1626
 Qy 521 ProGlyGlnHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540
 Db 1627 CCGGGGAGAGACACGCGACAGGAGAGAGAAAGAACTACTTCCGACCAAGTCAAGCGCG 1686
 Qy 541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGluProAspTyrPhe 560
 Db 1687 TCCCTATACCTCGCATTTGCAACATGACCAAGTTTATGACAGAGAGCGGACTGGTTTC 1746
 Qy 561 GlnLysGlnPheValProPheHisProProProLeuArgTyrArgGluProValLeuGlu 580
 Db 1747 GAAAGAGAGTTCCTTCCCTTCCATCTCCCTCCACTGGCTACCGGAGAGCACTTGGAG 1806
 Qy 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGlyLysSer 600
 Db 1807 AATTTGATTCGGGCTTGGTTTAAATGATGTCAATGTGCANACAGGCGCTGAGAGTGCAC 1866
 Qy 601 PheCysLeuLysValGluAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620
 Db 1867 TTCTGCTTAAAGATGAGAGCGGCGTCTTGGGGCAACCGGACAGCGACTCCAGCAC 1926
 Qy 621 GluSerGlnHisGlyLysLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640
 Db 1927 GAGAGTCAAGATGGGGCTTGGACCAAGAGCGGAGCGGCTGCTTGGACGCTGAGC 1986
 Qy 641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
 Db 1987 GCGGCGCTGAAACCCCTGCTGCACAGGTAAAGCCCGGAGCCCTTGCACATGCCCGCG 2046
 Qy 661 AspSerGlyTyrThrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGlu 680
 Db 2047 GACTCAGGAGCATATGATCGTCTGTGCTCCCTCAACGAGCTGTCTGCCACATGATGAA 2106
 Qy 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSerSer 700
 Db 2107 GGACTCTCGACGAGCAAGCAAAACCTTCTCCCTGACGAGAGCGGTCTCTCTTCA 2166
 Qy 701 GlyLeuGlyGlnGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
 Db 2167 GGCCTGGGTGAGAGAACTCTGCGCTTCTTCCAGCTCTCTTCTTGGGTCTATGC 2226

Qy 721 LysAlaAspLeuGlyCysAspSerTyrThrAspGluLeuHisAlaValAlaPro 738
 Db 2227 AAAGCAGATCTTGTGCGCAGACTTACCTGATGAATCCACGCGGTGCGCCCT 2280
 RESULT 10
 ID AEB55653
 AC AEB55653 standard; cDNA; 2786 BP.
 XX
 XX AEB55653;
 XX
 XX 22-SEP-2005 (first entry)
 DE Human DCR8 polypeptide encoding cDNA.
 KW Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
 KW DCR8; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
 KW interstitial lung disorder; asthma; allergy; atherosclerosis;
 KW gastrointestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;
 KW antipneumatic; antiarteriosclerotic; respiratory-Gen.; immunosuppressive;
 KW antitumor; DCR9 agonist; DCR9 antagonist; IL-17C antagonist;
 KW IL-17C agonist; human; DCR8; gene; ss; antisense therapy; RNAi therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 70..2286
 FT /*tag= b
 FT /product= "DCR8"
 FT /transl_except= (pos: 169..171, aa: Xaa)
 FT /transl_except= (pos: 193..195, aa: Xaa)
 FT /transl_except= (pos: 442..444, aa: Xaa)
 FT /transl_except= (pos: 475..478, aa: Xaa)
 FT /transl_except= (pos: 517..519, aa: Xaa)
 FT /note= "Xaa = unknown"
 FT sig_peptide 70..117
 FT /*tag= a
 FT mat_peptide 118..2283
 FT /*tag= c
 PN MO2005065711-A2.
 XX
 XX 21-JUL-2005.
 PD
 XX
 XX 22-DEC-2004; 2004MO-US042935.
 PF
 XX
 XX 29-DEC-2003; 2003US-00749144.
 PR
 XX
 XX (SCHER) SCHERING CORP.
 PA
 XX
 XX Gorman DM;
 PI
 XX
 XX WPI: 2005-506792/51.
 DR P-PDB; AEB55654.
 XX
 XX
 XX Modulating activity of cell, involves contacting cell with an agonist or
 PT antagonist of DNAX cytokine receptor subunit.
 PS Example 5; SEQ ID NO 9; 130bp; English.
 XX
 XX The invention relates to modulating (M1) activity of cell, by contacting
 CC cell with an agonist or antagonist of DNAX cytokine receptor subunit
 CC (DCR9) or of interleukin (IL)-17C where the cell modulates psoriasis,
 CC inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or
 CC allergy, or atherosclerosis. Also provided are methods for treating (M2)
 CC the disorders which involves administration of the modulator and
 CC diagnosing (M3) a disorder as mentioned above that involves contacting a
 CC sample from a test subject with a binding composition that specifically
 CC binds to a polypeptide or nucleic acid of DCR9 or IL-17C. (M1) is useful
 CC for modulating an activity of a cell. (M2) is useful for treating a
 CC subject suffering from a disorder such as psoriasis, IBD, interstitial
 CC lung disorder, asthma or allergy, or atherosclerosis, where the
 CC interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic

CC granuloma, or hypersensitivity pneumonitis. The IBID is Crohn's disease or
CC ulcerative colitis. The present sequence represents a human DCMS8
CC polypeptide encoding cDNA.

XX Sequence 2786 BF; 673 A; 760 C; 709 G; 637 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	Length:	2786
Score:	3835.50	Matches: 722
Percent Similarity:	98.2%	Conservative: 3
Beet Local Similarity:	97.8%	Mismatches: 12
Query Match:	97.2%	Indels: 1
DB:	14	Gaps: 1

US-10-616-788-2 (1-738) x AEB55653 (1-2786)

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QY 1 MetAlaProTTrpLeuGlnLeuCySerValPhePheThrValAlaMetAlaCyValLeuMetGly 20
Db 70 ATGGCCCCCTGGGCTGAGCTCTGCTCCGTCCTTTACGGTCAACGCTGCTCAACGGC 129
QY 21 SerGlnLeuAlaValAlaAlaGlySerGlyValArgAlaTrpGlyValAspThrCysGly 40
Db 130 TCCAGCTGGCTGTGTCGCTGGCGGGGTCCGGCCGCGCGCGCCGACCTGTAGC 189
QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyraAsnIleThrPheLeuTyr 60
Db 190 TGGAGGAGATGGGGCCAGCCAGCAGAAACAGTGGCTGTACAAACATCACTTCAAAATAT 249
QY 61 AspAsnCySerThrThyTyrLeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAsn 80
Db 250 GACAATGTATCCACTTGAATCCAGTGGGAAAGCATGTGATGTGACGCCCAAGAT 309
QY 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrPro 100
Db 310 ATCAACCATCGCAAGATAGCTGTGCATGACCAAGTGCAGTCAACATTTCTTGGTCCCA 359
QY 101 GlyAlaLeuGlyIleGlnPheLeuLeuGlyPheArgValIleLeuGlnGlnLeuLeuSer 120
Db 370 GGGGCCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAATCTGGAGAGCTGAACTCG 429
QY 121 GlnGlyValArgGlnCysGlnGlnLeuIleLeuValAspProLeuGlnLeuAsnSerPhe 140
Db 430 GAGGGAAGACAGAGCCCAACATGATTTCTAAAGGATCCGAAGCAGTCAACATGACTTC 489
QY 141 LysArgThrGlnMetGlySerGlnProPheLeuAsnMetLysPheGlnTrpArgTyrPhe 160
Db 490 AAAAGAACTGGAAATGGAAATCTCAACCTTCTGAAATATGAAATTTGAAAGGAAATATTTC 549
QY 161 ValLysValValProPheProSerIleLysAsnGlnSerAsnTyrHisProPhePhe 180
Db 550 GTAAAG---TTGTCCTTTCTTCAATTAAAGCAAAATTAACCACTTTCTTCTTT 606
QY 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTyr 200
Db 607 AGAAGCCGAGCTGTGACTGTGTTTACAGCCGCAACATCTAGCTGTATAAACCTTCTG 656
QY 201 LysProAspAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAsnHis 220
Db 667 AACCTCTGGAACTGAAACATACAGCAGCATGCTCGGACATGACGAGGTCTTCTGACAC 726
QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuLeuHisGlnGly 240
Db 727 GCACCCGACAACTTCGGCTTCGGTTCTTCTTCACTTCAACAGCTCAAGCAGAAAGA 786
QY 241 ProPheLysArgLysThrCysLysGlnGlnIleThrThrGlnIleThrThrSerCysLeu 260
Db 787 CCTTCAAGGGAAGACCTGAAGCAGAGCAAACTACAGAGATGACACACTGCTCTCTT 846
QY 261 GlnAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrAsnThrThrArg 280
Db 847 CAAAAGTGTCTCTCAGGGGATTAATATAATGAGCTGTGTGATGACATTAACAAACAA 906
QY 281 LysValMetHisTyrAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAla 300

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Db 907 AAAGTATCATTAATCTTTAAAGCAGTGCATCCCGCTGGGCCAGGCATCAAGGCC 966
QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
Db 967 GTGGCCATCAACAGTGCAGCTGTGATGATAGTGGCAATTCGCAAGCTTTCATGTGAATG 1026
QY 321 CysArgLysLeuGlnGlnIleLeuAsnIleTyrSerHisLeuAspGlnGlnSerSerGlnSer 340
Db 1027 TGGCGAAGAAAGCAACAAABAAATATATTTCACTTGAATGATGAAAGAGCTTGAGTCT 1086
QY 341 SerThrTyrThrAlaAlaLeuProArgGlnArgLeuArgProArgProLysValPheLeu 360
Db 1087 TCCACATACATCGACACATCCCAAGAGAGAGGCTCCGGCGCGCGCAAGGCTTTCTC 1146
QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
Db 1147 TGCTATTTCCAGTAAAGATGGCCAGAAATCAATGAATGTGTGTCCAGTGTTCCTACTTC 1206
QY 381 LeuGlnAspPheCysGlyCysGlnValAlaLeuAspLeuTrpGlnAspPheSerLeuCys 400
Db 1207 CTCAGAACTTCTGTGCTGTAGAGTGTGCTTGAACTGTGGAGAACTTCAGCTCTGT 1266
QY 401 ArgGlnGlyGlnArgGlnTrpValIleGlnLysIleHisGlnSerGlnPheIleIleVal 420
Db 1267 AGAAGAGGCGAGAGAAATGGGTCAACAGAAATCCAGAGTCCAGTTCATCATTTGTG 1326
QY 421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGly 440
Db 1327 GTTGTGTCCAAAGATATGAAGTACTTTGTGACAAAGAACTCAACAAACAAAGAGGT 1386
QY 441 GlyArgGlySerGlyLysGlyGlnLeuPheLeuValAlaValSerAlaIleAlaGlnLys 460
Db 1387 GGGCGAGGCTCGGGGAAAGAGAGCTTCTGTGTGGCTGTGACCATTTGCCGAAAG 1446
QY 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
Db 1447 CTCGCGCAGGCCAAGCAGAGTGTGTCCGGCGGCTCAGCAAGTTATTCGCCGTACTTT 1506
QY 481 AspTyrSerCysGlnGlyAspValProGlyIleLeuAspLeuSerThrTyrTyrArgLeu 500
Db 1507 GATTATTTCTGGAGGGAACGTCCCGGTATCTTAGACTGATCAACAAAGTACAAACTTC 1566
QY 501 MetAspAsnLeuProGlnLeuCysSerHisLysHisSerArgAspHisGlyLeuGlnGln 520
Db 1567 ATGCAAACTTCTCTAGCTGTGTCCACTGTCACTCCGAGACCAAGGCTTCCAGAG 1626
QY 521 ProGlyGlnHisThrArgGlnLysArgArgAsnTyrPheArgSerLysSerGlyArg 540
Db 1627 CCGGGGCAACACACGCGCAGGCGAGCAGAAAGAACTATTCGAGAGCAAGTCAAGCCG 1686
QY 541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGlnGlnProAspTrpPhe 560
Db 1687 TCCCTATAGCTGCCATTGTGCAACAGTGTATTTAGAGAGGAGGCCACATGAGTTTC 1746
QY 561 GlnLysGlnPheValProPheHisProProLeuArgTyrArgGlnProValLeuGln 580
Db 1747 GAAAGCAATGCTTCTTCACTCTTCACTGCGGTACCGGAGGCAAGCTTTGGAG 1806
QY 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGlnSerAsp 600
Db 1807 AATTTGATTCGGGCTGTGTTTAAATGATGATGATGCAATGCAACAGGCGCTGAGAGT 1866
QY 601 PheCysLeuLysValGlnAlaProValLeuGlyValThrGlyProAlaAspSerGlnHis 620
Db 1867 TTCTGTCTTAAAGGTAAAGCGGCTGTCTTGGGGCAACCGGACCAAGCTTCCAGCAC 1926
QY 621 GlnSerGlnHisGlyLysLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
Db 1927 GAGAGTCAACATGGGGGCTGTGACCAAGAGCGGGAGGCCCGGCTTGTGAGGTAGC 1986
QY 641 AlaAlaLeuGlnProLeuLeuHisThrValLysValGlySerProSerAspMetProArg 660

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Db      870 CAAAAGTTCTCCAGGAGGATTAATATAGCTGGTGGATGACATTAACAACAAGA 929
Qy      281 LysValMetHisThrAlaLeuValHisSerProTrpAlaGlyProIleAla 300
Db      930 AAGGTATGATTAATGCTTAAGCCAGTCACTCCCGTGGCGCCCATCAGAGCC 989
Qy      301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
Db      990 GTGGCCATCACTGACCTGGTATGATATCCGCAATCCGAGCGCTCTTCACTGTATG 1049
Qy      321 CysArgLysLysGlnGlnGlnAlaMetLysSerHisLeuAspGluGluSerSerGluSer 340
Db      1050 TGCAGAGAGAGCAACAAGAAATATATATACATTAGTAGAAGAGAGCTCGAGTCT 1109
Qy      341 SerThrThrThrAlaAlaLeuProArgGluArgLeuArgProArgProLysValPheLeu 360
Db      1110 TCCACATACACTCGACAGCTCCCAAGAGAGAGCTCCGCGCGCGCAAGGTCTTCTC 1169
Qy      361 CysTyrSerSerLysAspArgLysGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
Db      1170 TGCATTTCCATTAAGATGCGCAGATCACTGAATGCTGCTCCAGTCTTCCGCTACTTC 1229
Qy      381 LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTrpGluAspPheSerLeuCys 400
Db      1230 CTCAGGACTTCTGTGGCTGTGAGGTGGCTCTGGACCTGTGGAGAGCTTCAAGCTCTGT 1289
Qy      401 ArgGluGlyGlnArgGluTrpValIleGlnLysIleHisGluSerGlnPheIleVal 420
Db      1290 AGAGAAAGGAGAGAGATGGTCTATCCAGAAAGATCCACAGAGTCCCAAGTTCATCTTGTG 1349
Qy      421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGlyGly 440
Db      1350 GTTTGTTCCAAAGTATGAAGTACTTTGTGACAAAGAAAGATCTCAAAAGAGAGGT 1409
Qy      441 GlyArgGlySerGlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLys 460
Db      1410 GCGCGAGGCTCGGGAAGAGAGAGCTCTCTGGTGGCGGTGCAGCCATTTGCCGAAAG 1469
Qy      461 LeuArgGlnAlaLysGlnSerSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
Db      1470 CTCGCGCAGGCGCAAGAGAGTGTCTCGCGCGCTCGCAAGATTTAATCGCGCTACTTT 1529
Qy      481 AspTyrSerCysGluGluAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500
Db      1530 GATTATTCCTGCGAGGAGAGAGCTCCCGGTATCTTAACCTGAGTACCAAGTACAGACTC 1589
Qy      501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
Db      1590 ATGGACATCTTCTCTAGCTCTGTCCACCTGCACTCCGAGAGCCAGGCTCCAGAGAG 1649
Qy      521 ProGlyGlnHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540
Db      1650 CCGGGGAGAGACACGCGACAGGGGAGAGAAAGAACTTCCGAGCAAGTCAAGGCGCG 1709
Qy      541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGluGluProArgPhe 560
Db      1710 TCCCTATACGTCGCAATTCGACATGACACAGTTTATTAACAGAGAGCCGACTGGTTC 1769
Qy      561 GluLysGlnPheValProPheHisProProProLeuArgTyrArgGluProValLeuGlu 580
Db      1770 GAAAGAGAGTTCGTTCCCTTCATCTCCCTCCACTGGGCTACCGGAGGACGACTTGGAG 1829
Qy      581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGluSerAsp 600
Db      1830 AATTTGATTCGCGGCTGTGTTTAAATGATGTCTATGTGCAAAACGAGGCGCTGAGAGTGC 1889
Qy      601 PheCysLeuLysValGluAlaProValLeuGlyValaThrGlyProAlaAspSerGlnHis 620
Db      1890 TTTCGCTTAAGGTAAAGGAGCGGCTGTTCTTGGGGCAACCGGACCGGACTCCAGACAC 1949
Qy      621 GluSerGlnHisGlyGlyLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640

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Db      1950 GAGAGTCAAGATGAGGGGCTTGACCAAGAGGGGAGCCCGGCTTCCTTGAAGGTAGC 2009
Qy      641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
Db      2010 GCGGCTTCACACCTTCGTGACACGTTGAAGCCGAGAGCCCTCGGACATGCGCGG 2069
Qy      661 AspSerGlyIleTyrAspSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680
Db      2070 GACTCAGGATCATATACCTGTCTGTGCCCTATACCGACTGTCTTGCACATGAGAA 2129
Qy      681 GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSer 700
Db      2130 GGACTTCGACGAGACAGACAGAAAGTCTTCCTTACCGAGAGCGTGTCTCTCTTCA 2189
Qy      701 GlyLeuGlyGluGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySer 720
Db      2190 GGCCTGGTGAAGAGAGACCTTCGCTTCTTCACAGCTCTCTTCTGTGGTATGC 2249
Qy      721 LysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
Db      2250 AAGCAGATCTTGTTGGCGGAGTACACTGATGAACCTCAGCGGCTGCCCT 2303

RESULT 12
ADM7619 standard; DNA; 4508 BP.
ID
XX
AC ADM7619;
XX
DT 24-MAR-2005 (first entry)
XX
DE Human Interleukin-17 (IL-17) receptor DNA.
XX
KM Interleukin-17 receptor; IL-17 receptor; ds; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 553..2340
FT /tag= a
FT /product= "Human Interleukin-17 (IL-17) receptor protein"
XX
PN CN1465592-A.
XX
PD 07-JAN-2004.
XX
PF 01-JUL-2002; 2002CN-00123540.
XX
PR 01-JUL-2002; 2002CN-00123540.
XX
PA (UYOI ) UNIV QINGHUA.
XX
PI Xiong S, Chang Z, Fu X;
XX
XX WPI; 2004-248799/24.
DR P-PSDB; ADM76620.
XX
PT Human Interleukin-17 receptor sample protein, coding gene and its uses.
XX
PS Claim 3; SEQ ID NO 1; 14pp; Chinese.
XX
CC The invention relates to a novel human interleukin-17 (IL-17) receptor
CC protein, the coding gene and application. The current sequence is that of
CC the human interleukin-17 receptor DNA of the invention.
XX
SQ Sequence 4508 BP; 1175 A; 1061 C; 1141 G; 1131 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 4508
Score: 3706.00 Matches: 694
Percent Similarity: 99.7% Conservative: 2
Best Local Similarity: 99.4% Mismatches: 2
Query Match: 93.9% Indels: 0
DB: Gaps: 13

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US-10-616-788-2 (1-738) x ADM76619 (1-4508)

QY 41 TTPARGLYVALGYPVALASERARGASNSERGLYLEUTYRANILLETHERPHELYTYR 60
 DB 241 TGGCAGGAGTGGGGCCAGCCAGCAAGAGTGGGCTGTACCAACATCACCTTCATAATAT 300
 QY 61 AAGASNCYETHRTYRLEUASPPOVALGLYVYHISVALIILEALAAPALAGLASN 80
 DB 301 GACAAATGTACCACTTACTTGAATCCAGTGGGAGAAATGTGATGTGACGCCCAAT 360
 QY 81 ILETHERLIESERGLNYRALACYSNHSASPGLINVALALAVALTHTRILETUTPSERPRO 100
 DB 361 ATGACCATGACCCAGCATGTGCTTCCATGACCAACATGGCAGCATTCCTTGGTCCCCA 420
 QY 101 GLVALALEUGLYLIEGLUPHEULEUYEGLYPHEARGVALIILEUGLUGLULEUYSER 120
 DB 421 GGGGGCCCTCGGCAATCGAATTCCTGAAAGAAATTCGGGTAAATACGAGAGAGCTGAAGCTCG 480
 QY 121 GLUGLYARGGLNCYSGINGLNULEULILEULYASPPROLYSGILEUASNSESSERPHE 140
 DB 481 GAGGAGAAAGACATGACCAACATGATCTAAAGGATCCGAGACGCTCAACAGTAGCTTC 540
 QY 141 LYSARGTHRGLYMETGLUSERGLNPROPHLEUASNMETLYSPHEGLUTHTNAPRYTYPHE 160
 DB 541 AAAAGAACTGGAATGGAATCTCAACCTTCTGAAATGTGAATTTGAAACGGAATATTTC 600
 QY 161 VALLYVALVALPROPHEROSERTIELYASNGLUSERANTRYRHISPROPHEPHE 180
 DB 601 GTAAAGGTTCCTTCCTTCTTCAATTAAACGAAGCAATTACCAACCTTCTTCTT 660
 QY 181 ARGTHRARGALACYSAAPLEULEUGLNPPOASPSNLEULIACYVLYSPROPHETYP 200
 DB 661 AGAAGCCGAGCTGTGACCTGTGTACACCCGAGCAATCTAGCTTTAAACCTTCTGG 720
 QY 201 LYSPPROARGASNLEUASNILIESERGLNHSGLYSEASPMETGLINVALSERPHEASPHIS 220
 DB 721 AAGCTTCGAACTGAACTGAACTGACCAATGCTCGGACATGACGATGCTTCCTTCACAC 780
 QY 221 ALAPROHISANPHEGLYPHEARGPHEPHETYRLEUHIISTYRILYVLEULYSHISGLUGLY 240
 DB 781 GACCCGACAACTTCGGCTTCCTGTTCTTCATCTTCACTACAAAGCTCAAGCAGAGAGA 840
 QY 241 PROPHELYARGLYSTHYRQVLYSGINGLUGLINTHTHRGLUTHRTHSERQVLEULEU 260
 DB 841 CCTTTCAAGGAGAAAGACCTGTAGCAGAGCAAACTACAGATGACAGCTGCTCTCT 900
 QY 261 GLASNVALSERPROGLYASPRYRILIEILEGLULEUVALASPARHTHRANHTHRARG 280
 DB 901 CAHAATGTTCTCCAGGGGAAATATATATATGAGCTGTGATGACACTTAACACAAACAGA 960
 QY 281 LYSVALMETHISTYRALALEULYSPROVALHISERPROTPRALAGLYPROILEARGALA 300
 DB 961 AAAGTAGTAGATATGCTTAAAGCCAGTGCATCCCCGTGGCGGGCCCATACAGGCC 1020
 QY 301 METALILETHRYVALPROLEUVALVALIILESERALAPHEALATHRLEUPHERTHVALMET 320
 DB 1021 GTGGCCATCAAGGCGCACTGTATGATATCGGCATTCGCGAGCTCTTCACTGATG 1080
 QY 321 CYAARGLYLYSGINGLNULEULILETYRSETHISTEUPSPGLUGLUSERSESGLUSER 340
 DB 1081 TGGCGCAGAGGACCAAGAAATATATATATCAATTGAATGAAGAGCTCGAAGCTCT 1140
 QY 341 SETHTYRTHRALALALEUPROARGLUAARGLEUARGPROARGPROLYSVALPHELEU 360
 DB 1141 TCCACATACACTGAGACACTCCCAAGAGAGAGCTCGCGCGCGCGAGAGCTTTCTC 1200
 QY 361 CYETYSERSESLYASPRGLYGLINASNHISMETASNVALVALGLINQVSPHEALATYPHE 380
 DB 1201 TGGCATTTCCAGTAAAGATGCGCAAGATCAATGAATGCTCCAGTGTTCGCTACTTC 1260
 QY 381 LEUGLASPHECYSGLYCYSGIUVALLALEUASPRLEUTRGLUASPPHESERLEUCYS 400

DB 1261 CTCACAGACTTCTGTGGCTGTGAGGTGGCTGTGGAACCTGTGGGAAGACTTCAGCTCTGT 1320
 QY 401 ARGGLUGLYGLNARGGLUTTPVALIILEGLINLYELLHISGLUSERGLNPHLEIILEVAL 420
 DB 1321 AGAAGAGGGCAGAGAAATGGGTTCATCCAGAAATCCACAGATCCCAAGTTCATCATTTGTG 1380
 QY 421 VALCYSESLYSGLYMETLYSTYRPHLEVALASPLYSELVSNANTYRILYSHISLYSGLYGLY 440
 DB 1381 GTTTGTTCCAAAGGTATGAATGACTTTGTGCAAGAAAGAACTACAAACCAAGAGAGGT 1440
 QY 441 GLYARGGLYSEGLYLYSGIUGLEUPHELEUVALALAVASERALILEALAGLULYS 460
 DB 1441 GGCAGAGGCTCGGGGAAAGAGAGCTTCTCTGTGGCGGTGTGACCATTTGCCGAAAG 1500
 QY 461 LEUARGGLNALYSGINSESSERSEVALALEUUSERLYSPHEIILEALATYPHE 480
 DB 1501 CTCGCGCAGGCCAAGACAGATTCGTCCGCGCCCTCAGCAAGTTATTCGCGCTACTCTT 1560
 QY 481 ASPTYRSECYSGIUGLYASPRVALPROGLYIILEUASPLEUSERTHRYSTYRARGLEU 500
 DB 1561 GATTAATCTTCGAGAGGAGACGTCCCGGTATCTGACTGAGTACCAATACAGACTC 1620
 QY 501 METASPSNLEUPROGLINLEUCYSERHISLEUHIISERARGASPHISGLYLEUGLNU 520
 DB 1621 ATGAGCAATCTTCTCAGCTCTGTTCCACTGCACTCCGAGACCAAGCCCTCCAGAG 1680
 QY 521 PROGLYGLNHSITHRARGINGLYSERARGARGASNTRYRPHARGSERLYSSEGLYARG 540
 DB 1681 CCGGGCAGACACAGCGCACAGGCGACAGAAAGAACTACTCCGAGCAAGTCAAGCGCGG 1740
 QY 541 SERLEUTYRVALIILECYSAEMETHISGLNPHLEASPRGLUGLUPROASPTTPHE 560
 DB 1741 TCCCTATACCTGCCCATTTGCAACATGACACAGATTATTAACAGAGGCCGAGCTGGTTC 1800
 QY 561 GLULYGLINPHEVALPROPHENISPROPROPROLEUARGTYRARGLUPROVALLEUGLU 580
 DB 1801 GAAGAAGAGTTCCTTCTTCATCTCTCCACTGCGCTACCGGAGCCAGTCTTGAG 1860
 QY 581 LYSPPHEASPSERGLYLEUVALLEUASNAPVALMETCYSLYASPROGLYPROGLUSERASP 600
 DB 1861 AAATTTGATTCGGGCTTGTTTAAATGATGTATGTCAGTGCAAACAGGGCTGAGAGAGGAC 1920
 QY 601 PHECYLEULYVALGLUALAPROVALLEUGLYALATHRGLYPROLAAASERGLNHS 620
 DB 1921 TTCTGCTTAAAGGTAGAGGGGCTGTCTTGGGCAACCGGACAGCTCCACAGCAC 1980
 QY 621 GLUSERGLNHSGLYGLYLEUASPRGLINASPRGLYGLUALARGPROLALASAPGLYSER 640
 DB 1981 GAGATGACGATGGGGCTGTGACCAAGACGGGAGAGCCCGGCTTGACGSTRAGC 2040
 QY 641 ALALALEUGLNPPOLEULEUHIISTHRVALLYVALAGLYSERPROSEASPMETPROARG 660
 DB 2041 GCGCCCTGCAACCCCTGCTGACACAGGTGAAGCCGGGAGCCCTTCGACATGCCGCGG 2100
 QY 661 ASPSERGLYLETYRASPSESERVALPROSESERGLILEUUSERLEUPROLEUMETGLU 680
 DB 2101 GACTCAGGCATCTATGACTGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACATGAGAA 2160
 QY 681 GLYLEUSERTHRAPGLNTHRGUTHRTHSERSESLYTHRGJUSERYVALISERSESSER 700
 DB 2161 GACCTTCGACGAGACCAAGCAAGAAAGCTTCTCTTAAGCAGAGGCTGTCTCTCTTCA 2220
 QY 701 GLYLEUGLYGLUGLUPROPROLALALEUPROSERLYLEULEUSERSESGLYSERQVS 720
 DB 2221 GGCCTGGGTAGAGAGAACTCTGCTTCCTTCCAAAGCTCTCTCTTGTGGGTATGC 2280
 QY 721 LYSALASAPLEUGLYCYARGSERTYRTHRAPGLILEUHIISALAVALLAPRO 738
 DB 2281 AAAGCAGATCTTGTGGCGCACTACATGAAACTCCACCGCGGTGCCCT 2334
 RESULT 13
 ABX71363
 ID ABX71363 standard; cDNA; 2406 BP.

QY 500 LeuMetAspAenLeuProGlnLeuCySeSerHisLeuHisSerArgAspHisGlyLeuGln 519
 DB 1411 CTATGACACATCTTCTCCAGCTCTGTTCCACCTGACCTCCGAGACACGGCTCCAG 1470
 QY 520 GluProGlyGlnHisThrArgGlnGlySerArgArgArgArgArgArgArgArgArgArg 539
 DB 1471 GACCCGGGAGGACACACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1530
 QY 540 ArgSerLeuTyrValAlaIleCyAspMetHisGlnPheHisGlnGluProAspTyr 559
 DB 1531 CGGTCTCTATACGTCGCTTCATTCATTCCTTCATTCCTTCATTCCTTCATTCCTTCG 1590
 QY 560 PheGluLeuGlnPheValProPheHisProProPheLeuArgTyrArgGlnProValLeu 579
 DB 1591 TTGAAAGAGAGGATTCCTTCCTTCATTCCTTCATTCCTTCATTCCTTCATTCCTTCG 1650
 QY 580 GluLeuPheAspSerGlyLeuValLeuAspHisValMetCysLeuProGlyProGluSer 599
 DB 1651 GAGAAATTTGATTCGGCTTGGTTTAAATGATTCATTCGCAACCGAGGCTTGAGAGT 1710
 QY 600 AspPheCysLeuLeuValGluAlaProValLeuGlyValThrGlyProAlaAspSerGln 619
 DB 1711 GACTTCTGCTAAAGAGAGAGGCGCTGTTCTTGAGGCAACCGAGCCGACTCCAG 1770
 QY 620 HisGluSerGlnHisGlyLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGly 639
 DB 1771 CAGGAGAGTACAGATGGGGGCTGGAGCAGAGACGGGAGGCGCGCTGCTTGAGCGT 1830
 QY 640 SerAlaAlaLeuGlnProLeuLeuHisThrValValAlaGlySerProSerAspMetPro 659
 DB 1831 AGGCGCGCTTCGACACCCCTGCTGACACCGGTAAACCGGACCGCTTCGACATCCG 1890
 QY 660 ArgAspSerGlyTyrAspSerSerValProSerSerGluLeuSerLeuProLeuMet 679
 DB 1891 CGGAGACTCAGGACATCTATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1950
 QY 680 GluGlyLeuSerThrArgGlnThrGlnThrSerSerLeuThrGluSerValSerSerSer 699
 DB 1951 GAAGGACTCTCGACGAGCAGACAGAAACGCTCTCTGACGAGCGTCTCTCTCTCTCT 2010
 QY 700 SerGlyLeuGlyGluGluProProAlaLeuProSerSerSerSerSerSerSerSer 719
 DB 2011 TCGAGCTGAGTGAAGAGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2070
 QY 720 CysLeuAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
 DB 2071 TGCAGACGACATCTTGGTTCCGAGCTACATGATGATCCACGCGGTGCGCCCT 2127
 RESULT 14
 AAS09517
 ID AAS09517 standard; cDNA; 2319 BP.
 AC AAS09517;
 XX
 DT 24-OCT-2001 (first entry)
 DE Human cDNA encoding Interleukin 17 receptor, IL-17RH4.
 XX
 KM Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; ss;
 KM PRO20026; DNA 154095-2998; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; diabetes mellitus;
 KM allergic disease; asthma; demyelinating disease;
 KM degenerative cartilaginous disorder; transplantation associated disease.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..2255
 FT /tag= a
 FT /product= "IL-17RH4"
 XX
 PN MO200146420-A2.

XX PD 28-JUN-2001.
 XX PF 20-DEC-2000; 2000MO-US034956.
 XX PR 23-DEC-1999; 99US-0172096P.
 PR 30-DEC-1999; 99MO-US031274.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 22-JUN-2000; 2000US-0213807P.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 24-OCT-2000; 2000US-0242837P.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000MO-US032678.
 XX
 PA (GENTH) GENENTECH INC.
 PI Chen J, Filvaroff R, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vanden RL;
 PI Watanabe CK, Williams PM, Wood WI, Yaneura DG;
 DR WPI; 2001-451708/48.
 DR P-PSDB; AAU04958.
 XX
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 PT arthritis and diabetes.
 PS Claim 1; Fig 17; 188bp; English.
 XX
 CC The sequence (DNA 154095-2998) encodes a PRO polypeptide (PRO20026) which
 CC is the human Interleukin 17 receptor, IL-17RH4. A composition containing
 CC ant/agonists to the PRO polypeptides or individual components are useful
 CC for treating a mammal with an immune related disease, e.g. systemic lupus
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a
 CC demyelinating disease, an autoimmune or immune-mediated skin disease,
 CC contact dermatitis, an allergic disease e.g. food hypersensitivity,
 CC asthma, a transplantation associated disease, or a chronic inflammatory
 CC demyelinating polynuropathy. Treating a degenerative cartilaginous
 CC disorder comprises administering a PRO1031 or PRO112 polypeptide
 CC agonist, or antagonist to the mammal. Numerous examples of the diseases
 CC and disorders are given in the specification
 XX
 SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 2319
 Score: 3690.00 Matches: 702
 Percent Similarity: 96.0% Conservative: 2
 Best Local Similarity: 95.8% Mismatches: 11
 Query Match: 93.5% Indels: 18
 DB: 4 Gaps: 3
 US-10-616-788-2 (1-738) x AAS09517 (1-2319)
 QY 24 AlaValAlaAlaGlyGlySerGlyArg-----AlaTrpGlyValAsp-----Thr 38
 DB 52 GCGGTGAGAGGGGAGAGATGCCAGCGCTTCTGCTCAGGATCTCTCGCTGTTGTC 111
 QY 39 CysGlyTyrArgGlyValGlyProAlaSerArgAspSerGlyLeuTyrAsnIleThrPhe 58
 DB 112 AGTGAAGACAGAGGATGGGGCCAGCCACAGAAACAGTGGCTGTACAAACATCACCTTC 171

QY 59 LysTyrAspAsnCyserThrThrTyrLeuAsnProValGlyLysHileValIleAlaAspAla 78
 Db 172 AAlATATGACATGTGTACCACTTACTTGAATCCAGTGGGAGAGATGATGTGTGACGCC 231
 QY 79 GlnAsnIleThrIleSerGlnTyrAlaCyserHleAspGlnValAlaValThrIleLeuTyr 98
 Db 232 CAGAAATATCCATCAGCCAGTATGCTGTGCATACCAAGTGGCAGTCAATCTTTGG 291
 QY 99 SerProGlyValAlaLeuGlyIleGluPheLeuLysGlyPheArgValIleLeuGlnGluLeu 118
 Db 292 TCCCCAGGGGCGCTCGGCATCGAATTCCTGAAGAGATTCGGGTAATACTGGAGAGCTG 351
 QY 119 LysSerGlnGlyYargGlnCyserGlnLeuIleLeuLysAspProLysGlnLeuAsnSer 138
 Db 352 AAGTCGAGGAGAGACAGTGTCCAACTGATTTCTAAAGATTCGAAGCAGCTCAACAGT 411
 QY 139 SerPheLysArgThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAsp 158
 Db 412 AGCTTCAAAAGAACTGGAAATGGAAATCTCAACTTCTGAAATAGAAATTTGAAACGGAT 471
 QY 159 TyrPheValLysValValProPheProSerIleLysAsnGluSerAsnTyrHleAspPhe 178
 Db 472 TATTTGTAAGGTGTGTCTCTTTCTTCATTAAAAAGAAAGCAATTACCACTTTC 531
 QY 179 PhePheArgThrArgAlaCyserPheLeuLeuGlnProAspAsnLeuAlaCyLysPro 198
 Db 532 TTCTTTAGAACCCGAGCGCTGTGACTGTGTTCACAGCCGAGCAATCTAGCTTTAAACC 591
 QY 199 PheTrpLysProArgAsnLeuAsnIleSerGln----- 209
 Db 592 TTCTGGAAGCTCGGAACCTGAACATCAGCAGCATGCTCGGACATGCAAGTGTCTTC 651
 QY 210 -----HileGlySerAspMetGlnLysSerPheAspHleAlaProHleAsnPhe 225
 Db 652 GACCAACGACCGGATGCTGTGACATGACAGTGTCTTCGACCAAGCAAGCACTTC 711
 QY 226 GlyPheArgPhePheTyrLeuHileTyrLysLeuLysHileGluGlyProPheLysArgLys 245
 Db 712 GGTTCGCTTCTTCTTACTTCACTCACTCAAGCTCAAGACGAGAGACCTTTCAGCGAAAG 771
 QY 246 ThrCyLysGlnGlnGlnThrThrGluThrThrSerCyLeuLeuGlnAsnValSerPro 265
 Db 772 ACCTGTAGACGAGCAACTACAGAGATGACAGCGCTCTCTCAAAATGTTCTCCA 831
 QY 266 GlyAspTyrIleIleGlnLeuValAspAspThrAsnThrThrArgLysValMetHileTyr 285
 Db 832 GGGGATTTATATATGAGCTGTGTGATGACACTTAACAAAGAAAGATGACTAT 891
 QY 286 AlaLeuLysProValHleSerProTyrAlaGlyProIleArgAlaMetAlaIleThrVal 305
 Db 892 GCTTAAAGCAATGCACTCCCGTGGCCGGGCCATCAAGCCGTCGGCATCAACGTG 951
 QY 306 ProLeuValValIleSerAlaPheAlaThrLeuPheThrValMetCyAspArgLysGln 325
 Db 952 CCACTGTAGTCAATATCGGCATTGCGAGCGCTCTTCACTGTGATGTGCCCAAGAGCAA 1011
 QY 326 GlnGlnAsnIleTyrSerHileAspAspGluGluSerSerGluSerSerThrTyrThrAla 345
 Db 1012 CAAGAAATATATATTCACATTAGATGAGAGAGAGCTGTGATCTTCCATATCACCTGCA 1071
 QY 346 AlaLeuProArgGluArgLeuArgProArgProLysValPheLeuCyserTyrSerSerLys 365
 Db 1072 GCATCTCCAGAGAGAGAGCTCCCGCCCGCCGAGAGTCTTTCTGTCTATTTCCAGTAA 1131
 QY 366 AspGlyGlnAsnHileMetAsnValValGlnCyserPheAlaTyrPheLeuGlnAspPheCys 385
 Db 1132 GATGGCCAGAGATCACTGAATGTGTCTCAAGTGTTCGCTCACTTCCAGAGACTTGTGT 1191
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 Db 1192 GGTGTGAGGTGTCTGTGAGCTGTGTGGAAGACTTCAGCTCTGTGTAGAGAGAGAGAGA 1251
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Db 1252 GAATGGTCATCCAGAAATCCACAGAGTCCAGTTCATATGTGTGTCTCAAGGT 1311
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 Db 1312 ATGAAGTACTTTGTGTGACAAAGAACTACAAACAAAGAGAGTGGCCGAGCTGGGG 1371
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RESULT 15

ACA89858

ID ACA89858 standard, cDNA, 2319 BP.

XX ACA89858;

DT	10-JUL-2003	(first entry)
DE	Human cDNA encoding PRO20026.	
XX		
XX	Human; ss; gene; interleukin 17, IL-17, IL17 receptor; angiogenesis;	
XX	T-Lymphocyte proliferation; inflammatory cell infiltration;	
XX	immune related disorder; systemic lupus erythematosus; osteoarthritis;	
XX	rheumatoid arthritis; spondyloarthritis; systemic sclerosis;	
XX	Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia;	
XX	thyroiditis; diabetes mellitus; immune-mediated renal disease;	
XX	demyelinating diseases; Guillain-Barre syndrome; hepatobiliary disease;	
XX	hepatitis; inflammatory bowel disease; Multiple's disease; psoriasis;	
XX	immune-mediated skin disease; erythema multiforme; contact dermatitis;	
XX	allergic disease; asthma; atopic dermatitis; food hypersensitivity;	
XX	urticaria; immunologic disease of the lung; eosinophilic pneumonia;	
XX	idiopathic pulmonary fibrosis; transplantation associated disease;	
XX	graft-versus-host disease.	
OS	Homo sapiens.	
XX		
XX	US2003003546-A1.	
XX		
PD	02-JAN-2003.	
XX		
PF	22-MAR-2001; 2001US-00816744.	
XX		
PR	15-MAY-1998; 98US-0085579P.	
PR	23-DEC-1998; 98US-0113621P.	
PR	08-MAR-1999; 99WO-US005028.	
PR	21-APR-1999; 99US-0130232P.	
PR	26-APR-1999; 99US-0131022P.	
PR	14-MAY-1999; 99US-00311832.	
PR	14-MAY-1999; 99US-0134287P.	
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PR	09-JUN-1999; 99US-0138387P.	
PR	23-DEC-1999; 99US-0172096P.	
PR	30-DEC-1999; 99WO-US031274.	
PR	11-JAN-2000; 2000US-0175481P.	
PR	18-FEB-2000; 2000WO-US004341.	
PR	01-MAR-2000; 2000WO-US005601.	
PR	02-MAR-2000; 2000WO-US005841.	
PR	21-MAR-2000; 2000US-0191007P.	
PR	21-MAR-2000; 2000WO-US007532.	
PR	02-JUN-2000; 2000WO-US015264.	
PR	22-JUN-2000; 2000US-0213807P.	
PR	24-AUG-2000; 2000WO-US023328.	
PR	24-OCT-2000; 2000US-0242837P.	
PR	26-OCT-2000; 2000US-0244072P.	
PR	10-NOV-2000; 2000WO-US030873.	
PR	28-NOV-2000; 2000US-0253646P.	
PR	01-DEC-2000; 2000WO-US032678.	
PR	20-DEC-2000; 2000WO-US04956P.	
PR	28-FEB-2001; 2001WO-US006520.	
XX		
XX	(GETH) GENENTECH INC.	
XX		
PI	Chen Y, Filvaroff E, Fong S, Goddard A, Godowski P, Grimaldi C,	
PI	Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;	
PI	Watanabe C, Williams PM, Wood WT, Yansura D;	
DR	WPI; 2003-428843/40.	
DR	P-PSDB; AB089705.	
XX		
PT	New PRO polypeptides and polynucleotides homologous to interleukin-17,	
PT	useful for treating e.g. systemic lupus erythematosus, rheumatoid	
PT	arthritis, osteoarthritis, juvenile chronic arthritis, or systemic	
PT	sclerosis.	
XX		
XX	Claim 2; Fig 17; 12pp; English.	
XX		
CC	The invention relates to a nucleic acid having similarity to interleukin-17	
CC	(IL-17) or IL-17 receptor comprises at least 80% nucleic acid sequence	
CC	identity to a nucleotide sequence which: (a) encodes a polypeptide having	

CC	a sequence of appearing as ABUS9697-ABUS9700 and ABUS9702-ABUS9705 (P1-
CC	p8), lacking or having its associated signal peptide; (b) encodes an
CC	extracellular domain of P1-p8 lacking its associated signal peptide; (c)
CC	consists of a sequence of appearing as ACA89850-ACA89853 and ACA9855-
CC	ACA9858687; or (d) consists of the full-length coding sequence of
CC	selected from SI-58, and of the cDNA deposited under ATCC accession
CC	number 209866, 203557, PTA-1185, PTA-2108, PTA-202, PTA-155, PTA-1082 or
CC	PTA-2531. Also included are expression vectors, host cells, encoded
CC	proteins, chimeric proteins, antibodies, ant/agonists, compounds
CC	inhibiting the expression of SI-58 or activity (or mimicking the activity
CC	of) of P1-p8, stimulating/inhibiting the proliferation of T-lymphocytes
CC	using the polypeptides or ant/agonists, enhancing the infiltration of
CC	inflammatory cells into a tissue of a mammal by administering a PRO1031
CC	polypeptide, its an agonist or antagonist, and inhibiting angiogenesis
CC	induced by a PRO1031 polypeptide or its agonist in a mammal by
CC	administering a PRO1031 polypeptide, its ant/agonist or an anti-PRO1031
CC	antibody. The proteins, antibodies, ant/agonists and compounds are useful
CC	for treating an immune related disorder such as systemic lupus
CC	erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC	arthritis, a spondyloarthritis, systemic sclerosis, an idiopathic
CC	inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC	sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC	thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC	thyroidal disease of the central or peripheral nervous system,
CC	idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a
CC	chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC	disease, infectious or autoimmune chronic active hepatitis, primary
CC	biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC	inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC	disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC	disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC	disease, asthma, allergic rhinitis, atopic dermatitis, food
CC	hypersensitivity, urticaria, an immunologic disease of the lung,
CC	eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC	pneumonitis, a transplantation associated disease, graft rejection or
CC	graft-versus-host disease. The present sequence encodes an IL17 or IL17
CC	receptor homologue of the invention
XX	
SQ	Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	0 Length: 2319
Score:	3690.00 Matches: 702
Percent Similarity:	96.04 Conservative: 2
Best Local Similarity:	95.88 Mismatches: 11
Query Match:	93.54 Indels: 18
DB:	8 Gaps: 3
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QY	24 AAlaValAlaAlaGlyGlySerGlyArg-----AlaTrpGlyValAlaSer-----Thr 38
DB	52 GCGGTTGAGAGGGGAGGAGATGCGACGCGTTCTGCTCAGGTGTTCTCGTGTTC 111
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DB	112 AGTGAGAGCAGGAGGTGGGCGCACCGACAGCAAlaCAGTGGCGCTGTACAACATCACCTTC 171
QY	59 LysGlyTArPArAenCyethrThyrTytleuAenProValGlyLysHlsvAlIleAlaPAla 78
DB	172 AAATVTGACAAATGTGACCACTTACTTGAATCCAGTGGGAGACGANTGTGATGTGTACGCC 231
QY	79 GluAenIleThrIleSerGlnTyranIaCyHlAspGlnValAlaValThrIleLeuTrp 98
DB	232 CAGATATTCACCATGACGACAGTATGCTTGCCATGACCAAGTGGACGTCAACATCTTTGG 291
QY	99 SerProGlyAlaLeuGlyTlIeGlnPheLeuLysGlyPheArgValIleLeuGlnGluLeu 118
DB	292 TCCCGAGGGGCGCCCTCGGCATCGAAATTCCTCGAAAGGATTTCCGGGTATATCTGAGGAGCTG 351
QY	119 LysSerGlnGlyArgGlnCyGlnGlnIleuIleLeuLysAAspProGlyGlnIleuAAsenSer 138
DB	352 AAGTCGAGGGGAAAGCAGTGGCCAAACATCGATTTCAAAGATTCGAAAGCAGCTCAACAGT 411

QY 139 SerPheValArgThrGlyMetGlySerGlnProPheLeuAsnMetLeuPheGluThrAsp 158
 DB 412 AGCTTCAAAAGAACTGGAAATGAAATCTCAACCTTCTGAAATATGAATTTGAAACGAT 471
 QY 159 TyrPheValIleValValProPheProSerIleLeuAsnGluSerAsnTyrHisProPhe 178
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 QY 179 PhePheArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysIlePro 198
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 QY 210 -----HISerAspMetGlnValSerPheAspHisAlaProHisAsnPhe 225
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 DB 1132 GATGGCCAGAAATCAATGAATGTGTCAAGTGTTCCTACTTCTCCAGAACTTGT 1191
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 DB 1192 GGTGTAGGTGGTGTCTGACCTGTGGAAAGACTTCAGCTCTGTATGAAGAGGCAAGA 1251
 QY 406 GluTrpValIleGluIleValIleHisGluSerGlnPheIleIleValValCysSerLeuGly 425
 DB 1252 GAATGGGTATCCAGAAATCCAGAGTCCCAAGTTCATGTGGTGTTCCTCAAGGT 1311
 QY 426 MetLeuTyrPheValAspLeuValAspValTyrLeuHisIleArgGlyValArgGlySerGly 445
 DB 1312 ATGAAGTACTTTGTGGACAAAGAACTACAAACAAGAGGTGGCCAGAGTCCGGG 1371
 QY 446 LysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLeuArgGlnAlaLeu 465
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QY 486 GlyAspValProGlyIleLeuAspLeuSerThrTyrArgLeuMetAspAsnLeuPro 505
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 Job time : 1064 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 06:19:54 ; Search time 7487 Seconds
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Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2858.5	72.4	1677	10	AY408490 Homo sapi
4	2355	59.7	1674	10	AY408491 Pan trogl
5	1522	38.6	908	7	CJ025168 Mus muscu
6	1481	37.5	856	8	CJ025168 Mus muscu
7	1470	37.2	851	8	DN282586 DN282586
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8	1183	30.0	724	3	BP154750
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43	702	17.8	636	2	BG985614
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ALIGNMENTS

RESULT 1
LOCUS HSM805220 2406 bp mRNA linear HTC 20-JAN-2005
DEFINITION Homo sapiens mRNA; cDNA DKFp434L0320 (from clone DKFp434L0320).
ACCESSION AL833913
VERSION AL833913.1 GI:21739453
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1 (bases 1 to 2406)
Ockenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaupp,A.,
Mewes,H.W., Weill,B., Amid,C., Oesanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German cDNA Consortium
Submitted (20-JAN-2005) MIPB, Ingolstaedter Landstr.1, D-85764
Neuerberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing Consortium of the German Genome Project.
This clone (DKFp434L0320) is available at the RZPD Deutsches
Resourcentzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for Ordering:
http://www.rzpd.de/cgi-bin/product/ci.cgi?cloneID=DKFp434L0320
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/
Location/Qualifiers

FEATURES

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GPBESDFCLKVEAAVAGATGPADSOHSGQGLDQGEARPALDGAALQPLHATKA
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ORIGIN

Alignment Scores:

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Score:	3698.00	Matches:	694
Percent Similarity:	99.6%	Conservative:	2
Best Local Similarity:	99.3%	Mismatches:	3
Query Match:	93.7%	Indels:	0
DB:	4	Gaps:	0

US-10-616-788-2 (1-738) x HSM605220 (1-2406)

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DB 31 GGAAGACAGGAGTGGGGCCAGCCAGCAAGACAGTGGCTGTAAACATCAACCTTCAA 90
QY 60 T|YAspAsnC|YserThr|YLeuAsnProValG|YLeuSH|sValI|leAlaAPAlaG|n 79
    : : :
DB 91 TATGACATTTGATCACTTCTTGAATCCAGTGGGAGAGCATGTGATGCTGACGCCAG 150
QY 80 AsnI|eThrI|eSerG|nTYrAlaCYsH|sAspG|nValAlaValI|ThrI|eLeuTYrSer 99
    : : :
DB 151 AATATACCATCAATGACAGTATGCTTGCCATGACCAAGTGGCAATTCCTTGGTCC 210
QY 100 ProG|YAlaLeuG|YI|leG|YLeuLeu|YsG|YPheArgYAlI|leLeuG|nG|uLeu|Ys 119
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DB 211 CCAAGGGCCCTCGGATCGAATTCGTAAGATTCGAGTAAATACGAGGAGCTGAAG 270
QY 120 SerG|uG|YArgG|nCYsG|nG|nLeuI|eLeu|YsAspPro|YsG|nLeuAsnSerSer 139
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DB 271 TCGGAGGAGAGACAGTCCCAACATGATTTCTAAAGATCCGAAGCACTCAACAGTAGC 330
QY 140 Phe|YsArgThrG|YMetG|uSerG|nProPhe|LeuAsnMet|YsPheG|uThrAspTYr 159
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DB 331 TTCAAAAGAACTGGAATGGAATCTCAACCTTCTCTGAATATGAATTTGAAAGGATTAAT 390
QY 160 PheVal|YsVal|YAlaProPheProSerI|e|YsAsnG|uSerAsnTYrH|sProPhePne 179
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DB 391 TTCGTAAAGGTGTCCCTTTCTTCATTAATAAAGCAAAAGCAATTAACACCTTTCTTC 450

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QY 180 PheArgThrArgAlaCYsAspLeuLeuG|nProAspAsnLeuAlaCYsYsProPhe 199
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QY 200 T|Y|YsProArgAsnLeuAsnI|eSerG|nH|sG|YSerAspMetG|nValSerPheAsp 219
    : : :
DB 511 TGGAAAGCTCGGAACCTGAACATCAAGCCAGTGGCTCGGAACATGACGAGTGTCTTCGAC 570
QY 220 H|sAlaProH|sAsnPheG|YPheArgPhePheTYrLeuH|eTYrYsLeuYsH|sG|u 239
    : : :
DB 571 CAGGACCGGACAACTTCGAGCTTCGTTCTTCTATCTTCACTCAAGCTCAAGCAAGAA 630
QY 240 G|YProPhe|YsArgYsThrCYsYsG|nG|nG|nThrG|uThrThrSerCYsLeu 259
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DB 631 GGAACCTTCAAGGAAGAAAGCTGTAAAGCAAGGAAACCTCAAGAGATGACCAAGCTCCTC 690
QY 260 LeuG|nAsnValSerProG|YAspTYrI|eI|leG|uLeuValAspAspThrAsnThr 279
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DB 691 CTTCAAAATGTTTCTCCAGGGGATTAATATATGAGCTGTGATGACATAACACACAA 750
QY 280 ArgYsValMetH|eTYrAlaLeuYsProValH|sSerProThralaG|YProIleArg 299
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DB 751 AGAAAGTATGATATATCTTAAAGCAAGTCACTCCCGGCGGCGCCATCAAG 810
QY 300 AlameAlaI|eThrValProLeuValI|eSerAlaPheAlaThrLeuPheThrVal 319
    : : :
DB 811 GCGGTGGCATCAAGTGCACATGATGATATGATGATGATGATGATGATGATGATGATG 870
QY 320 MetCYsArgYsLeuG|nG|nG|nG|nG|nG|nG|nG|nG|nG|nG|nG|nG|nG|nG|nG 339
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QY 340 SerSerThrThrThralaIleuProArgG|uArgYsArgProArgProArgValPhe 359
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QY 360 LeuCYsTYrSerSerYsAspG|YG|nAsnH|sMetAsnValIaG|nCYsPheAlaTYr 379
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DB 991 CTCTGTATATTCAGTAAAGATGAGGCAAGATCAATGAATGTGTCCAGTGTTCGCTAC 1050
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DB 1051 TTCCTCCAGACTCTGTGTGCTGTGAGTGGCTGTGACCTGTGGGAACATTCAGCCTC 1110
QY 400 CYsArgG|uG|YAlaArgG|uThrValI|eG|nYsI|eH|sG|uSerG|nHelle 419
    : : :
DB 1111 TGTAGAAAGGCGAGAGAAATGGTCAATCAAGAGATCAAGAGTCCAGATTCATCAT 1170
QY 420 ValIa|CYsSerYsG|YMetYsTYrPheValAspYsLeuAsnTYrYsH|sYsG|Y 439
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DB 1171 GTGGTTTGTCCAAAGATATGAAGTACTTTGTGACAAAGAAACCTACAAACAAAGGA 1230
QY 440 G|Y|YsArgG|YSerG|Y|YsG|YLeuLeuPheLeuValAlaValSerAlaI|eAlaG|u 459
    : : :
DB 1231 GGTGGCGGAGGCTCGGGGAAAGAGAGCTCTCTGTGCGGCTGCAACCTTCGCGAA 1290
QY 460 YsLeuArgAlaIaYsG|nSerSerSerAlaIaIaLeuSerYsPheI|eAlaValTYr 479
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DB 1291 AAGCTCGGCAAGGCAAGAGATGCTCGGGGCGCTCAAGCAAGTTATCGCGCTTAC 1350
QY 480 PheAspTYrSerCYsG|uG|YAspValProG|YI|eLeuAspLeuSerThrTYrArg 499
    : : :
DB 1351 TTTGATTAATCTCGAGAGGAGACGTCCTCGGATCTTGAAGCTGATCAAGTACAA 1410
QY 500 LeuMetAspAsnLeuProG|nLeuCYsSerH|sVleuH|sSerArgAspH|sG|YLeuG|n 519
    : : :
DB 1411 CTCATGACAAATCTCTCAGCTGTGTTCCACTGCACTCCCGAAGCAAGCGCTCCAG 1470
QY 520 G|uProG|YG|nH|eThrArgG|nG|YSerArgArgAsnTYrPheArgSerYsYsG|Y 539
    : : :
DB 1471 GAGCGGCGGACACACGGAACGGGCAAGAAAGAACTACTTCCGAGCAAGTACAGGC 1530
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Db      1591 TTGGAAGACAGATTCTTCCCTTCATCTCCCTCCACTGGCTGACCGGAGCCAGTCTTG 1650
Qy      580 GluValPheAspSerGlyLeuValLeuAspValMetCysValProGlyProGlyIser 599
Db      1651 GAGAAATTTGATTGGGCTTGTTTAAATGATGATGCAACAGGAGCCGAGAGT 1710
Qy      600 AspPheCysLeuValGluValProValLeuGlyValThrGlyProAlaAspSerGln 619
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Qy      620 HisGluSerGlnHisGlyLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGly 639
Db      1771 CACGAGAGTCAGCATGGGGCTGAGACCAAGACGGGAGGCCCGGCTTGACGGT 1830
Qy      640 SerAlaAlaLeuGlnProLeuLeuHisThrValLeuAlaGlySerProSerAspMetPro 659
Db      1831 AGGCGCCCTGACACCCCTGTCGACACGGTAAAGCCGCGACCCCTCGACATGCCG 1890
Qy      660 ArgAspSerGlyLeuTyrAspSerSerValProSerSerGlyLeuSerLeuProLeuMet 679
Db      1891 CGGAGCTCAGGACATCTATGACTGCTGTCGCTCCCTCATCCAGCTGCTCTGCCACTGATG 1950
Qy      680 GluGlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSer 699
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Qy      700 SerGlyLeuGlyGluGluGluProProAlaLeuProSerGlyLeuLeuSerSerGlySer 719
Db      2011 TCAGGCTCGGAGGAGGAACTCTGCGCTTCTTCACAGCTCTCTCTTGAGGTCA 2070
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DEFINITION Genomic survey sequence.
ACCESSION AY408489
VERSION AY408489.1 GI:39764460
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1677)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
2 (bases 1 to 1677)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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US-10-616-788-2 (1-738) x AY408489 (1-1677)

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Qy      165 ProPheProSerIleValAsnGluSerAsnTyrHisProPhePheAspThrArgAla 184
Db      61 CTTTTCCTTCCATTAAAAACGAAAGCAATTACACCTTCTTCTTGAACCCGAGTC 120
Qy      185 CysAspLeuLeuGlnProAspAsnLeuAlaCysValProPheThrIysProArgAsn 204
Db      121 -----TGGAAAGCTCGGAAC 135
Qy      205 LeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHisAlaProHisAsn 224
Db      136 CTGAACATAGCAGCATGGCTCGGACATGCAAGTGTCCTTGACCATCAGCCGCAAC 195
Qy      225 PheGlyPheArgPhePheTyrLeuHisTyrTyrLeuValHisGluGlyProPheIysArg 244
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Qy      245 TyrThrCysValGlnGluGlnThrThrGluThrThrSerCysLeuLeuGlnAsnValSer 264
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Qy      265 ProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrThrArgIysValMetHis 284
Db      271 -----CTGGTGAATGACACTCAACAAAGAAAGATGATGCAAT 309
Qy      285 TyrAlaLeuValProValHisSerProTyrAlaGlyProIleArgAlaMetAlaIleThr 304
Db      310 TATGCTTAAAGCAGTGCACTCCCGTGGCCGCGCCATCAGAGCCGTGGCCATCACA 369
Qy      305 ValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMetCysArgIysVal 324
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Qy      385 CysGlyCysGluValAlaLeuAspLeuTyrGluAspPheSerLeuCysArgGluGln 404
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Qy      405 ArgGluTyrValIleGlnIysIleHisGluSerGlnPheIleIleValValCysSerIys 424
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Qy	445	GlyLysGlyValIleuPheLeuValAlaValSerAlaIleAlaGlyLysLeuArgGlnAla	464
Db	790	GGGAAGAGAGAGCTCTTCCGTGGTGGGGGTGTACGACATTTGCCGAAGAAGCTCCGCAAGGC	849
Qy	465	LysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValLysPheAspTyrSerCys	484
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Qy	485	GlnGlyValAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeuMetAspIleu	504
Db	910	GAGGAGAGCTCCCGGTATCTTAGACCTGAGACCTGAGACCAAGTACAGACTCATGGACAATCTT	969
Qy	505	ProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLysGlnGlnLysProGlyGlnHis	524
Db	970	CTTCAGCTCTGTTCCCACTGCACCTCCAGACCAAGGCTCTCAAGAGCCGGGGCAGCAC	1022
Qy	525	ThrArgGlnLysSerArgAsnTyrPheArgSerLysSerGlyValArgSerLeuTyrVal	544
Db	1030	ACGGACAGAGGACAGAGAAGAACTACTTCGGAGACAGTCAAGCCGGTCCCTATACGTC	1089
Qy	545	AlaIleCysAsnMetHisGlnPheIleAspGlnGlnLysProAspTyrPheLysLysGlnPhe	564
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Qy	565	ValProPheHisProProPheLeuArgTyrArgGlyProValLeuGlnLysPheAspSer	584
Db	1150	GTTCCCTTCATCTCTCTCCACTGCGGCTACGGAGACCAAGTCTTGGAGAAATTGATTTCG	1209
Qy	585	GlyLysValLeuAsnAspValMetCysLysProGlyProGlnSerAspPheCysLeuLys	604
Db	1210	GGCCTGGATTTAATGATGTCATGTCACAAACAGGAGCTGAGAGTGACTTTCGCTTAAG	1269
Qy	605	ValGlnAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHisGlyLysGlnHis	624
Db	1270	GTAGAGCGGCTGTTCTTGGGCGAACCGGACCGACTCCAGCAGCAGAGTCAAGCAT	1329
Qy	625	GlyGlyLysAspGlnAspGlyGlyAlaArgProAlaLeuAspGlySerAlaAlaLeuGln	644
Db	1330	GGGGGCTTGACCAAGACGGAGAGGCGCGGCTGCTTGACGGTAGCGCCCGCTTGCAA	1389
Qy	645	ProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArgAspSerGlyLys	664
Db	1390	CCCTGCTGCAACGGTGAAGAGCGGAGGCGCTCGGACATGCGCGGGAACTCAGGATC	1449
Qy	665	TyrAspSerSerValProSerSerGlyLeuSerLeuProLeuMetGlnGlyLysSerThr	684
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Qy	685	AspGlnThrGlnThrSerSerLeuThrGlnLysValSerSerSerSerGlyLysGlyGln	704
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Qy	705	GlnGlnProProAlaLeuProSerLysLeuLeuSerSerGlySerCysLysValAspLeu	724
Db	1570	GAGGAACCTCGCGCTCTCTCTCCAGAGCTCTCTCTTGGGTCAGCAAGCAATCTT	1629
Qy	725	GlyCysArgSerTyrThrAspGlnLeuHisAlaValAlaPro	738
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DEFINITION	Pan troglodytes HCM3241 gene, VIRUAL TRANSCRIPT, partial sequence.		
ACCESSION	AY408490		
VERSION	AY408490.1	GI:39764461	GSS.
KEYWORDS	Pan troglodytes (chimpanzee)		
SOURCE			

	ORGANISM	Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE AUTHORS	(Dases 1 to 1677) Clarke,A.G., Gnanowsky,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civiello,D.R., Lu,F., Murphy,B., Perriere,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	
TITLE	Science 302 (5652), 1960-1963 (2003)	
JOURNAL PUBMED REFERENCE	14671302	
AUTHORS	2 (bases 1 to 1677) Clarke,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civiello,D.R., Lu,F., Murphy,B., Perrière,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adam,M.D. and Cargill,M.	
TITLE JOURNAL COMMENT	Direct Submission Submitted (16-Nov-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.	
FEATURES SOURCE	Location/Qualifiers 1..1677 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" <1...>1677 gene /locus_tag="HGM3241"	
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	Query Match: 72.4% Mismatches: 12	
	DB: Indels: 37	
	Gaps: 2	
US-10-616-788-2 (1-738) x AY408490 (1-1677)		
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Db	1 ATGAATTCCTCAACCTTCCGTGAATAGAAATTGGAAAGCATTTATTCCTTAAGCGTGTC 60	
OY	165 ProPhePrSeSerileLysAsnGluSerAnTYrHisProPhePheArgThyAGA 184	
Db	61 CCTTTTCCTTCATTTAAAATAAGAACATTTGCCACCCTTTCTTTAAGACCGCAGTC 120	
OY	185 CyasPLeuLeuGlnIProaspAsnLeuAlaCyLSySPropheTPLySProAgasn 204	
Db	121 -----TGAAGCTCGGAC 135	
OY	205 LeuaSnllEsSerGlnHisGlySeraspMetGlnValSerPheapRHlgaIarProHisasn 224	
Db	136 CTGAACATCAGCAGCGNNMGCTCGGACAATGCAGGTGCTTCCTGCACATGCACCGCACAC 195	
OY	225 PhcgLIpPhaArpPhepheTytleuhIsTyrllysLeuluSHlsGLUGLYPProPheLysArg 244	
Db	196 TTGGGCTCCGTTTTCTTCAATCTTCACTTCAAGCTCCAAGCAAGAAAGACTTTCMAAGCA 255	
OY	245 LyeThtCyalyseGlnGluGlnThrThrglutThrserCybleuleGlnAsnValSer 264	
Db	256 AAGACCTGTAAAGAG----- 270	
OY	265 ProGlyAsPTyrIleIGluLeuValaspApThraentTrhra-glysvaImechis 284	
Db	271 -----CTGGTAGATGACATTACACAAACAAGAAAGTGATATCAT 309	
OY	285 TyrAlaleuLyProvalHisSerProTrpmalagIProlleaGyalamerAlallethr 304	
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 DB 370 GTCCTGCTGAGTCAATCGCATTCGCGACCTCTTCACTGATGTCGCCAAGAG 429
 QY 325 GlnGlnGlnuAniIleTyrSerHisLeuAspGlnGlnSerSerGlnSerSerThrTyrThr 344
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 DB 550 AAGAGATGCGCAGATCAATGAATGTCGACAGTTCCTTCCATCTTCCCGAGACTTC 609
 QY 385 CysGlnCysGlnValAlaLeuAspLeuTyrGlnAspPheSerLeuCysArgGlnGln 404
 DB 610 TGTGCTGTGAGTGTGCTCTGACCTGTGGAGAGACTTCACTCTGTAGAGAGGCGAG 669
 QY 405 ArgGlnTyrValIleGlnLysIleHisGlnSerGlnPheIleValValCysSerLys 424
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 QY 425 GlnMetLysTyrPheValAspLysValAsnTyrLysGlnLysGlnValArgLysSer 444
 DB 730 GGATATAGATCTTGTGTGACAAATGACTTAAACAAACAGAGCGTGGCCAGGCTCG 789
 QY 445 GlnLysGlnGlnuPheLeuValAlaValSerAlaIleAlaGlnLysLeuArgGlnAla 464
 DB 790 GGGAGAGAGAGCTCTTCTGTGGAGCTGAGCTTCCAGCAATCCGAAAGCTCCGCGAGCC 849
 QY 465 LysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSerCys 484
 DB 850 AAGCAGAGTTCGTCGCGGCGCGNNNNNTTATGCGCGTCACTTATGATATTCCTGC 909
 QY 485 GlnGlnLysAspValProGlnIleLeuAspLeuSerThrLysTyrArgLeuMetAsnLeu 504
 DB 910 GAGGAGAGCTCCCGGTATCTTACAGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCTT 969
 QY 505 ProGlnLeuCysSerHisLeuHisAspArgAspHisGlnGlnGlnGlnGlnGlnGlnGln 524
 DB 970 CCCAGCTCTGTTCCACTGCTGCTCCGAGACCAAGGCTCCAGGAGCGGCGAGCAC 1029
 QY 525 ThrArgGlnLysSerArgArgAsnTyrPheArgSerLysSerGlnArgSerLeuTyrVal 544
 DB 1030 ACGGAGACGCGGACGAGAAAGAACTACTTCCGAGCAAGTCAAGCGCGCTCCATACGTC 1089
 QY 545 AlaIleCysAsnMetHisGlnPheIleAspGlnGlnProAspTyrPheGlnLysGlnPhe 564
 DB 1090 GCCATTGTCACATGACACAGTTTATGACAGAGAGCCCACTGTTGCAAAAGCAGTTTC 1149
 QY 565 ValProPheHisProProLeuArgTyrArgGlnProAlaLeuGlnLysPheAspSer 584
 DB 1150 GTTCCCTTCATCTCTCCACTGCTGCTGAGAGCACTTGTGAGAAATTTGATTCG 1209
 QY 585 GlnLysValLeuAsnAspValMetCysLysProGlnLysAspPheCysLeuLys 604
 DB 1210 GCGTGTGTTTAAATATATGATCATGTGAAACAGGCGCTGAGTACTTCTGCTTAAG 1269
 QY 605 ValGlnLysProValLeuGlnValArgGlnProAlaAspSerGlnHisGlnSerGlnHis 624
 DB 1270 GTAGAGCGCGCTCTTCTGTGGGCAACCGGACAGCCCACTCCAGCAGAGTCAAGCAT 1329
 QY 625 GlnGlnLysAspGlnAspGlnValArgProAlaLeuAspGlnLysAlaLeuGln 644
 DB 1330 GGGGCGCTGACCAAGACGCGAGGCGCGCTGCTTACGATGACGCGCGCTGCAA 1389
 QY 645 ProLeuLeuHisThrValLysAlaGlnLysProSerAspMetProArgAspSerGlnLys 664
 DB 1390 CCGCTGTGACACGCGGAAAGCGGAGCGCTCCGAGCACTGCGCGGAGCTCAGGATC 1449

QY 665 TyrAspSerValProSerSerGlnLeuSerLeuMetGlnLysSerThr 684
 DB 1450 TATGACTCTGCTGTGCTTCATCCAGCTATCTTCCACTATGAGAGACTTCTGAGC 1509
 QY 685 AspGlnThrGlnHisSerSerLeuThrGlnSerValSerSerSerSerGlnGln 704
 DB 1510 GACCAAGACAAAGCTTCCCTGAGAGAGAGCTGCTCTCTTCCAGGCGGTGAG 1569
 QY 705 GlnGlnProProAlaLeuProSerLysLeuLeuSerSerGlnCysValAspLeu 724
 DB 1570 GAGGAACCTCTGCGCTTCTTCCAGCTCTCTTCTGTGGGTCAAGCAAGCATTT 1629
 QY 725 GlnCysArgSerTyrThrAspGlnLeuHisAlaValAlaPro 738
 DB 1630 GTTTCGCGACTCATATATTAATCTCCAGCGGTGCGCTT 1671
 RESULT 4
 AY408491 1674 bp DNA linear GSS 12-DEC-2003
 LOCUS
 DEFINITION Mus musculus HCM3241 gene, VIRUTAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY408491
 VERSION AY408491.1 GI:39764462
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 1 (bases 1 to 1674)
 TITLE
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1674)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source 1..1674
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>1674
 /locus_tag="HCM3241"
 ORIGIN
 gene
 Alignment Scores:
 Pred. No.: 2,1e-231 Length: 1674
 Score: 2355.00 Matches: 457
 Percent Similarity: 81.9% Conservatve: 32
 Best Local Similarity: 76.5% Mismatches: 64
 Query Match: 59.7% Indels: 44
 DB: 10 Gaps: 6
 US-10-616-788-2 (1-738) x AY408491 (1-1674)
 QY 145 MetGlnSerGlnProPheLeuAsnMetLysPheGlnThrAspTyrPheValVal 164
 DB 1 ATGAGATTCAGCTTCTTCAATGAAATTTGACACGATTAATTTTAAAGATTTC 60
 QY 165 ProPheProSerLysLeuAsnGlnSerAsnTyrHisProPhePheArgThrArgAla 184


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Db      61 CTTTTCCCTTCATTAAAAAGCAATTAACATCCCTTCTTTCAGAACACGGGTC 120
Qy      185 CyasarpheuleuenginProaarpheuleulaCyulsProphetrlyProaargan 204
Db      121 -----TGAAGCTCGAAC 135
Qy      205 LeuanilIeserginHvlglySerAapMerGlnValSerPheAapH1a1aProH1aAyn 224
Db      136 CTGAATATCAGCAGCATGGTTCTGACATGACAGCTGCTTCGACCATGCCCCGACAGAC 195
Qy      225 PheGlyPheAargPhePheTyrluH1aTyrluValuH1aH1aGlyProPheAarg 244
Db      196 TTGGCTTCCTGGCTTCATGTTCTCTATAGCTCAAGCAGAAAGCCCTTCAGCGCG 255
Qy      245 LydThrcCyelsynglnuglnInThrGluThrThrsrCyulsleuenglnaenValSer 264
Db      256 AAGACCTGACAGGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 282
Qy      265 ProGlyAapTyrlIeGlyLeuValAapAapThraanthThraarglyValMetH1a 284
Db      283 -----NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 309
Qy      285 TyrlAlaLeuLyProValH1aSerProTrpAlaGlyProIlleargAlaMetAlaIleThr 304
Db      310 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 369
Qy      305 ValProleuValIleSerAlaPheAlaThrleuPheThraValMetCyarglyValys 324
Db      370 GTGGCTTCGTGTGATCATCTGCGCTGCAACCTGTCTACTGTGATGTCAAGAAAG 429
Qy      325 GlnGlnGluAanIleTyrlSerH1aLeuAapGlnGlnuSerSerGlnuSerSerThryThr 344
Db      430 CAACAAGAAATATATATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 489
Qy      345 AlaAlaLeuProaargGlnuAargLeuAargProaargProlyValPheLeuCytyrSerSer 364
Db      490 GCGGCTCTCCCGAGAGACAGGCTCCGGCTCCAGCCCAAGGCTTCCTCTCTCAAT 549
Qy      365 LyAapGlyGlnaenH1aMetAenValValGlnCyapheAlaTyrlPheLeuGlnaapPhe 384
Db      550 AAGAGATGGCCAGATTCATGAACGTGTCCAGTTCCTATTCCTGCAAGATTTC 609
Qy      385 CyeglyCyeglyValAlaLeuAapLeuTrpGlnuAapPheSerLeuCyAargGlnGln 404
Db      610 TGGGCTGTGAGGTGGCTCTGAGCTTGTGGAAATTCACGCTTCGACAGAGGGGAG 669
Qy      405 AargGlnTrpValIleGlnuH1aH1aGlnuSerGlnPheIleValValCySerLyA 424
Db      670 AGAAGATGGCCATTCAGAGATTCAGAGTCCAGATTTCATTCATTCATTCATTC 729
Qy      425 GlnMetLyTyrlPheValAapLyAapTyrlPheIleIleGlyGlyValGlyAargGlySer 444
Db      730 GGCATGAAGTACTTGTGATGAAGAAACCTTCAGACACAAAGAGGACCCGGGGAG 789
Qy      445 GlnLyGlnuGlnuPheLeuValAlaValSerAlaIleAgluLyAargGlnAla 464
Db      790 GCCCAAGGCGAGTTCCTCTGCTGGCCGCTGGCAGCATTCTGAGAGCTCCGTCAGGCC 849
Qy      465 LyeglnSerSerSerAlaAlaLeuSerLyAapPheIleAlaValTyrlPheAapTyrlSerCyA 484
Db      850 AAGCAGAGCTCATCTGCGCAGCTGCGCAAGTTCATCCCGCTCATCTTCGATTATTCCTGT 909
Qy      485 GlnGlnLyAapValProGlyIleLeuAapLeuSerThryTyrlAargLeuMetAapAanLeu 504
Db      910 GAAGGGGATATACCTTCGACCTGAGCTGAGCCTGAGCAGCAAGTACAGCTCAAGACCACTT 969
Qy      505 ProGlnuCySerH1aLeuH1aSerAargAapH1aGlyLeuGlnuPro---GlnGln 523
Db      970 CTGAGGTCTGTGCTGCTGCTGCTCACTCA-----GAGAGCAGAGAGGTGCTGGGTCAAG 1020
Qy      524 H1aThraargGlnGlnuSerAargAapTyrlPheAargSerLyAargSerGlyAargSerLeuTy 543
Db      1021 CACCCAGGCGCAGCAGCAGCAAGAACTACTTCGAGAGCAAAATCGGGCCCTCTCTAT 1080

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Qy      544 ValAlaIleCyAapMetH1aGlnPheIleAapGlnGlnuProaapTrpPheGlnuLyGln 563
Db      1081 GTTGCATTTGCAACATGACACAGTTATTCATGAGGAGACCTGACGTGTTGAGAGAGCAG 1140
Qy      564 PheValProPheH1aProProleuAargTyrlAargGlnuProValuGlnuLyAapPheAap 583
Db      1141 TTATATACCTTCAACATGCCCCCTGTGCGCTACAGAGACCAAGTCTCTGAGAAATTTGAC 1200
Qy      584 SerGlyLeuValLeuAapAapValMetCyulsProGlyProGlnuSerAapPheCyuls 603
Db      1201 TCGAGCTGTGTTTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy      604 LyValAlaIleProValIleuGlnuAlaThrglyProAlaAapSerGlnH1a-----Gln 621
Db      1261 AAGTCAGAGCTTGTATCTTGGGCGCGCTGGCGCAGCCGATTCATTATTCATCTGGAG 1320
Qy      622 SerGlnH1aGlyLyLeuAapGlnAapGlyGlnuAargProAlaLeuAapGlySerAla 641
Db      1321 AGTCAGACATGATGAGCTGGACCAAGACATGAGGCGCCGCTCTGTATGATGTCCTCT 1380
Qy      642 AlaLeuGlnProleuLeuH1aThraValIleGlySerProSerAapMetProaargAap 661
Db      1381 GCTTCGACAGCCCTGTTCACAGCAGGAAAGCTGCGACGCTCCCTCAGAGATGCCACGGAGC 1440
Qy      662 SerGlyIleTyrlAapSerSerValProSerSerGlnuLeuSerLeuProleuMetGlnGly 681
Db      1441 TCGAGCATATATATCTTCTGATCCCTCATCAGAGCTCTCTGCTGTGATGAGGGA 1500
Qy      682 LeuSerThraAapGlnThrglyThrsrSerLeuThrglySerValSerSerSerSerGly 701
Db      1501 CTCTCCCGAGATCAGATGAAGAAACATCTTCTGACCGAGAGTATCTTCTCTCTGAGC 1560
Qy      702 LeuGlyGlnGlnuProProAlaLeuProSerLyAapLeuSerSerGlySerCyuls 721
Db      1561 CTAGGAGAGAGAGACCCCTTACCTCCCTTCAGAGCTTTTGCTGAGGTGTCAGCA 1620
Qy      722 AlaAapLeuGlyCyAapSerSerThraAapGlnuLeuH1aAlaValAlaPro 738
Db      1621 ---GAAACATGTTGCCAGACCACTGACAGAACTGCAAGCCCTTCTCT 1668

RESULT 5
CJ025168      908 bp      mRNA      linear      EST 22-OCT-2004
LOCUS      CJ025168
DEFINITION      scrofa cDNA full-length enriched swine cDNA library, adult trachea Sus
ACCESSION      CJ025168
VERSION      CJ025168.1
KEYWORDS      GI:54535376
SOURCE      Sus scrofa (pig)
ORGANISM      Sus scrofa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
      Sus.
REFERENCE      1 (bases 1 to 908)
AUTHORS      Uenishi,H., Enoch,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
      Okumura,N., Hamada,M., and Awata,T.
TITLES      PEDS (Pig EST Data Explorer): construction of a database for ESTs
      derived from porcine full-length cDNA libraries
JOURNAL      Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED      14681463
COMMENT      Contact: Hirohide Uenishi
      Animal Genome Laboratory, Genome Research Department
      National Institute of Agrobiological Sciences
      2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
      Tel: +81-29-838-8627
      Fax: +81-29-838-8627
      Email: huenishi@affrc.go.jp
      EST project with full-length enriched cDNA libraries carried out in
      Animal Genome Research Program (Japan) by National Institute of
      Agrobiological Sciences and STRF-Institute
      Single pass sequencing of clones derived from oligo-capped cDNA
      library

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Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319 low quality bases were trimmed based on the quality values.

FEATURES

source

Location/Qualifiers

1. 908
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="TCH01B080037"
/tissue_type="trachea"
/dev_stage="adult"
/clone_11b="full-length enriched swine cDNA library, adult trachea"

ORIGIN

Alignment Scores:

Pred. No.:	8.14e-146	Length:	908
Score:	1522.00	Matches:	280
Percent Similarity:	95.6%	Conservative:	5
Best Local Similarity:	94.0%	Mismatches:	13
Query Match:	38.6%	Indels:	0
DB:	7	Gaps:	0

US-10-616-788-2 (1-738) x CJ025168 (1-908)

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QY      1 MetAlaProTTrpLeuGlnLeuCySerValPhePheThrValAlaAlaCysLeuAangly 20
DB      11 ATGGCCCGGCGTGGCGAGCTCTCTCTCTCTTTCACCGCTCAACGCTCCCAACGGC 70
QY      21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyValGalaTrpGlyValAspThrCysGly 40
DB      71 TCCCAATTGGCCCTGGCCGAGGTGGCTCCAGCAAGCTCGGGCGGCGCACCTTGGCC 130
QY      41 TPARGlyValGlyProAlaSerArgAsnSerGlyLeuTyranilLeuThrpheLyTy 60
DB      131 TGGAGGGAGAGTGGCGCGGCGCAGCAAGACAGTGGCTGCAACAATCACTTCAGATAT 190
QY      61 AspAsnGlyThrThrTyrlLeuAsnProValGlyValHisValIleAlaAspAlaGlnAsn 80
DB      191 GACAACTGCACCACTTACTTGGTCTCTGGGAGAGCATGTGATCGCCGACGCAAGAT 250
QY      81 IleThrIleSerGlnTyrlAlaCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
DB      251 ATACCACTACGTAGTACGCTCTCCACAGCAAGTGCACATCTCTCTGCTCCCA 310
QY      101 GlyAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGlnGlnLeuGlySer 120
DB      311 GGGGCGCTGGGAGTCAATTCCTTAAAGATTTCCGGTATATCTGAGAGCTGAAGTCA 370
QY      121 GlyGlyArgGlnCysGlnGlnLeuIleLeuLyAspProLyGlnLeuAsnSerSerPhe 140
DB      371 GAAGGAAGACAGTGCACAACTGATTTCTGAGAGACCCGAGACGCTCAACAGTACTTC 430
QY      141 LyAspArgThrGlyMetGlnSerGlnProPheLeuAsnMetLyPheGlnThrAspTyrlPhe 160
DB      431 AAAAGAGCTGGAATGGAATCTCAGCTTCTTAATTAATGAAATTAAGATTAATCTT 490
QY      161 ValIleValValProPheProSerIleLyAsnGlnSerAsnTyrlHisProPhePhe 180
DB      491 GTCAAGATTTCTCTTTCTCTTCAATTAAGAAAGAAAGCAATTAATCACTTCTTT 550
QY      181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysValyProPheTrp 200
DB      551 AGAAGCCGCGACCTGTGCTCTTATTAAGCCGAGCAACCTGCGCTGTAACCTTCTGG 610
QY      201 LyAspArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
DB      611 AAGCTCTGGAACTCAACATCAACCAACAGCTCAAGACATGCAAGGTCTTCTGACAC 670
QY      221 AlaProHisAsnPheGlyPheArgPhePheTyrlLeuHisTyrlValyLeuLyHisGlyGly 240
DB      671 GCGCCACATACCTTGGCTTCGGTTCTTTTATCTTCACTCAAGAGCTCAAGACAGAAAGA 730

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QY      241 ProPheLyAspArgThrCysLyGlnGlnGlnInThrThrGlnThrSerCysLeuLeu 260
DB      731 CTCTTAAGAGAAAGCTTGCAGACAGCAAAATACAGAGACAGCTCTCTT 790
QY      261 GlnAsnValSerProGlyAspTyrlIleGluLeuValAspAspThrAsnThrArg 280
DB      791 CAATATGATCTCTCTGGGATTAATTAATTAATGAGCTGTGAGACACATTAACAACA 850
QY      281 LyAspValMetHisTyrlAlaLeuLyProValHisSerProTrpAlaGlyProIle 298
DB      851 AAGATGATCATTAATGCTTANNAAACATGATTCCTCCATGGGCTGGGCCATA 904

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RESULT 6

DN282586/c 856 bp mRNA linear EST 02-MAR-2005
LOCUS 1182679 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
DEFINITION DN282586
ACCESSION DN282586.1 GI:60451196
VERSION EST.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 856)
Smith,T.P.L., Roberts,A.J., Echterkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contract: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLR015 Row: B Column: 19
Seq primer: TAGAGGACAGTTCGAGG.
Location/Qualifiers

FEATURES

source

1. 856
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_11b="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN

Alignment Scores:

Pred. No.:	1.27e-141	Length:	856
Score:	1481.00	Matches:	272
Percent Similarity:	97.9%	Conservative:	6
Best Local Similarity:	95.8%	Mismatches:	5
Query Match:	37.5%	Indels:	0
DB:	8	Gaps:	0

US-10-616-788-2 (1-738) x DN282586 (1-856)

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QY      40 GlyTPARGlyValGlyProAlaSerArgAsnSerGlyLeuTyranilLeuThrpheLy 59
DB      854 GCGTGGAGGGAGTGGGCGTGGCCAGCAAGACAGGCGCTGACATCACTTCAAA 795
QY      60 TyAspAsnGlyThrThrTyrlLeuAsnProValGlyValHisValIleAlaAspAlaGln 79
DB      794 TATGACAACTGCACCACTTACTTGAATCCAGTGGGAGAACACATGATCGCTGACGCCAG 735
QY      80 AenIleThrIleSerGlnTyrlAlaCysHisAspGlnValAlaValThrIleLeuTrpSer 99

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Db      734 AACATCACCATGCTGATGCTGCTGCACGACCAAGTGTGCTGACCATTTCTTGGTCC 675
Qy      100 ProGlyAlaLeuGlyYlIeGluPheLeuYleGlyPheArgValIleLeuGluGluLeuYs 119
Db      674 CCGGGGGCCCTCGGCATCGAATTCCTTAAAGATTCCTGAGTCTATCGAGGAGCTCGAAG 615
Qy      120 SerGluGlyArgGlnCysGlnGlnLeuIleLeuYsAspProYsgInLeuAsnSerSer 139
Db      614 TCAGAGGAGCAGACAGTCCCAACACTGATTTCTAAAGAACCCGAGACGCTCAACAGTAGC 555
Qy      140 PheYsArgThrGlyMetGlnSerGlnProPheLeuAsnMetYsPheGluThrAspYr 159
Db      554 TTCAAAAGAGCTGGAGGATGGAATCTCAACCTTTCTGGAATATGAATTTGAAACGATTAAC 495
Qy      160 PheValYsValValProPheProSerIleYleYsAsnGlnSerYrYrIleProPhePhe 179
Db      494 TTTGTAAAGATCGCTCTTTCTTCCATTAATAAATGAATTAATCAACCTTTCTTC 435
Qy      180 PheArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysYsProPhe 199
Db      434 TTCAGAACCCGACAGCTGTGACTGCTATTTGACGCCGACAACTGGCTTTGAACCTTTC 375
Qy      200 TrpYsProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAsp 219
Db      374 TGGAGGCTCGAAGACCTCAACATCATCAGACAGGTTCCGACATGACAGTGTCTTTGAC 315
Qy      220 HisAlaProHisAsnPheGlyPheArgPhePheYrLeuHisGlyYsLeuYsHisGlu 239
Db      314 CATGCGCCCAACCTTTGGCTTCCTGCTTCTCATCTTCAATTAACAGCTTAAGCATGA 255
Qy      240 GlyProPheYsArgYsThrCysYsGlnGlnGlnThrGlnGluThrThrSerCysLeu 259
Db      254 GAGACCTTCAAGGAGAAAGACCTGTAAACAGAGCAAAATACAGATTAACAGCTGCTT 195
Qy      260 LeuGlnAsnValSerProGlyAspYrIleIleGluLeuValAspAspThrAsnThrThr 279
Db      194 CTTCAAAATGTGCTCTCTGGGGAATTAATATGAGTGTGATGACATTAATACAGACA 135
Qy      280 ArgYsValMetHisGlyYrAlaLeuYsProValHisSerProTrpAlaGlyProIleArg 239
Db      134 AGAAAAGTATGATTAATGCTTAAACAGATGATTCCTCGGGGCGCCCATCAGA 75
Qy      300 AlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrVal 319
Db      74 GCTGTGGCCATCTGTCGCAATGGTGTGATTCGACATTCGCGAGCTCTTCAACGGTG 15
Qy      320 MetCysArgYs 323
Db      14 ATGTGCGCGCAA 3

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RESULT 7      851 bp      mRNA      linear      EST 02-MAR-2005
LOCUS      DN283973
DEFINITION  118415 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  DN283973
VERSION     DN283973.1 GI:60452583
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 851)
            Smith,T.P.L., Roberts,A.J., Echeverkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
            A second set of bovine ESTs from pooled-tissue normalized libraries
            Unpublished (2003)
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425 c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLR015 Row: B Column: 19
Seq primer: GTAAATACGACTACTAATGGG.
Location/Qualifiers
1..851
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cisue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN
Alignment Scores:
Pred. No.:      1,72e-140      Length:      851
Score:          1470.00      Matches:      270
Percent Similarity: 97.5%      Conservative: 6
Best Local Similarity: 95.4%      Mismatches: 7
Query Match:      37.2%      Indels:      0
DB:               8      Gaps:      0

US-10-616-788-2 (1-738) x DN283973 (1-851)
Qy      40 GlyTrpArgYsValGlyProAlaSerArgAsnSerGlyLeuYrAsnIleThrPheYs 59
Db      3 GCGTGAAGGGAGTGGGCGTGGCCAGCAAAACAGGGGCTGTACATCACTTCCACA 62
Qy      60 TyrAspAsnCysThrThrYrLeuAsnProValGlyYsHisValIleAlaAspAlaGln 79
Db      63 TATGACAACTGCACCACTTAATCAATCAAGTGGGAGACACATGATCGCTGACGCCAG 122
Qy      80 AsnIleThrIleSerGlnYrAlaCysHisAspGlnValIleValThrIleLeuTrpSer 99
Db      123 AACATCACCATGCTGATGCTGCTGCACGACCAAGTGGCTGTCACTTCTTGGTCC 182
Qy      100 ProGlyAlaLeuGlyYlIeGluPheLeuYsGlyPheArgValIleLeuGluGluLeuYs 119
Db      183 CCGGGGGCCCTCGGCATCGAATTCCTTAAAGATTCCTGAGTCTATCGAGGAGCTCGAAG 242
Qy      120 SerGluGlyArgGlnCysGlnGlnLeuIleLeuYsAspProYsgInLeuAsnSerSer 139
Db      243 TCAGAGGAGCAGACAGTCCCAACACTGATTCRAAAGAACCCGAGACGCTCAACGTAGC 302
Qy      140 PheYsArgThrGlyMetGlnSerGlnProPheLeuAsnMetYsPheGluThrAspYr 159
Db      303 TTCAAAAGAGCTGGAGGATGGAATTCACCTTTCTGGAATGAATTTGAACAGATTAAC 362
Qy      160 PheValYsValValProPheProSerIleYleYsAsnGlnSerYrYrIleProPhePhe 179
Db      363 TTTGTAAAGATGCTCTCTTCTTCCATTAATAAATGAAGCAATTAACACCTTTCTTC 422
Qy      180 PheArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysYsProPhe 199
Db      423 TTCAGAACCCGACAGTGTGACTGCTATTAAGCCGAGCAACACTGGCTGTAAACCTTTC 482
Qy      200 TrpYsProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAsp 219
Db      483 TGGAGGCTCGAAGACCTCAACATCACTGACAGCGGTTGGACATGACGATGCTTTTGAC 542
Qy      220 HisAlaProHisAsnPheGlyPheArgPhePheYrLeuHisGlyYsLeuYsHisGlu 239
Db      543 CATGCGCCCAACCTTTGGCTTCCTTCTTCAATTAATCAACAGCTTAAGCATGA 602
Qy      240 GlyProPheYsArgYsThrCysYsGlnGlnGlnThrGlnGluThrThrSerCysLeu 259
Db      603 GAGACCTTCAAGGAGAAAGACCTGTAAACAGAGCAAAATACAGATTAACAGCTGCTCTT 662

```

Oy		260	LeuginaenValIserProGI.YAspPyriIetIegIuleValIAspAspThrThr 279
Dd		663	CTTCAAAATGTCCTCCCGGGATTATAATTAAGCTGCATGAACGTAAATACACA 722
Oy		280	ArglyVaIMethIstYtAlaleuIadBroVAIHIsSerProtIPalagIProIIearg 299
Dd		723	AGAAAAGATGATCATATATGCCCTTAANAACAGTGCAATTCGCCGTGGGCCATCAGA 782
Oy		300	AlamecIAallethrrValProleuValIallIeserAlapheAathleuPheThrVal 319
Dd		783	GCTGGGCGATCACACTGGCCATTTGGCTGTCATTCGCGATTCGACGCTCTTCA CGGTG 842
Oy		320	MecCyarg 322
Dd		843	ATGTGCCG 851
RESULT 8			
BPI54750			
LOCUS			
DEFINITION		724 bp	mRNA linear EST 30-DEC-2003
ACCESSION	BPI54750		full-length enriched swine CDNA library, adult ovary Sus
VERSION	BPI54750		scrofa cDNA clone OVRM10115H10 5', mRNA sequence.
KEYWORDS	BPI54750.1	GI:40404223	
SOURCE	EST.		
ORGANISM	Sus scrofa (pig)		
REFERENCE			
AUTHORS	1 (bases 1 to 724) Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasing,N. and Awata,T. PNBE (Big EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries Nucleic Acids Res. 32 (1), D484-D488 (2004) 14681463		
JOURNAL			
PUBMED			
COMMENT			
CONTACT:	Hirohide Uenishi		
National Genome Laboratory, Genome Research Department			
National Institute of Agrobiological Sciences			
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan			
Tel.: +81-29-838-8627			
Fax: +81-29-838-8627			
Email: huenishi@affrc.go.jp			
EST project with full-length enriched cDNA libraries carried out in			
Animal Genome Research Program (Japan) by National Institute of			
Agrobiological Sciences and STAF-Institute			
Single pass sequencing of clones derived from oligo-capped cDNA			
library			
Vector sequences were eliminated by RepeatMasker version 2002/07/13			
and crossmatch version 0.990319			
Low quality bases were trimmed based on the quality values.			
Location/Qualifiers			
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/organism="Sus scrofa"			
/mol_type="mRNA"			
/db_xref="taxon:9823"			
/clone="OVRM10115H10"			
/tissue_type="ovary"			
/dev_stage="adult"			
/clone_idb="full-length enriched swine CDNA library, adult			
ovary"			
ORIGIN			
Alignment Scores:			
Pred. NO.:	5.73e-111	Length:	724
Score:	1183.00	Matches:	217
Percent Similarity:	96.8%	Conservative:	5
Best Local Similarity:	94.8%	Mismatches:	7
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0
OS-10-616-788-2 (1-738) x BPI54750 (1-724)			

OY	1	MetLAProTLPLeuGlnLeuCYSerValPhePheThrValAspAlaCYLeuasnGly	20
Db	38	ATGGCCCCGGTGTGGAGCTGTGTTCTGTTCTTCAACCGTCCGCTCAACGCG	97
OY	21	SerGlnLeuAlaValAlaGlyGlySerGlyValArgAlaTrpGlyValAspThrCYsGly	40
Db	98	TCGCATTGGCGCGTGGCGCGAGTGGCTCCAGAGAGCTGGGGGGCGGACACCTGGGCG	157
OY	41	TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTrpAsnIleThrPheLeuTy	60
Db	158	TGGAGGGAGAGGGGGCGCGCCAGACAAACGTGGCTGCACCAATCACTTCACAGAT	217
OY	61	AspAsnCYerThrTrpTrpLeuAsnProValGlyLeuShValIleAlaAspAlaGlnAsn	80
Db	218	GACACATCGACACACTTACTTGAATGCTGTGGGGAAAGCATGTGAATGCGCGAGCCACGAT	277
OY	81	IleThrIleSerGlnTrpAlaCYAsnIleAspGlnValAlaValIleLeuTrpSerPro	100
Db	278	ATCACCAATCACTAGTACGTACGCTGCCACGACCAATGGCAGTCAACATTCTGTGTC	337
OY	101	GlyAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGlnLeuLeuSer	120
Db	338	GGGGCCCTCGGCATCGAATTCCTAAAGAAATTCGGGTAATATCGAGAGACTGAATG	397
OY	121	GluGlyArgGlnCYsGlnGlnLeuIleLeuLeuAspProGlyGlnLeuAsnSerSer	140
Db	398	GAAAGAAAGACAGTGCACCAACTGATATCTGAAGAACCCGAAAGCACTCAACAGTAG	457
OY	141	LeuArgThrGlyMetGluSerGlnProPheLeuAsnMetLeuSerPheGluThrAspTrp	160
Db	458	AAAAGAGCTGAAAGGAATCTCAGCCCTTCTCTGAATATGAAATTTGAAACAGATTACT	517
OY	161	ValIysValValProPheProSerIleLeuAsnGluSerAsnTrpIleProPhePhe	180
Db	518	GTCAGATGTGCCCTTTCTTCTTCATTAAACGAAAGCAATTATCAACCTTTCTCTT	577
OY	181	ArgThrArgAlaCYAspLeuLeuLeuGlnProAspAsnLeuAlaCYLeuProPheTrp	200
Db	578	AGAACCGGACACTGTGACCTGCTATTACAGCGGACAACTGGCGCTGTAAACCTTCGG	637
OY	201	LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis	220
Db	638	AAGCCTGGGAACCTCAACATCAACCAACATGCTCAGACAGCAGCAGCAGTCTTGA	697
OY	221	AlaProHisAsnPheGlyPheArgPhe	229
Db	698	GCGCCACATCACTTCGGGCTTCGGTTTC	724

[illegible]

Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES

source

1..679
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVR010067A07"
/issue_type="ovary"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
ovary"

ORIGIN

Alignment Scores:

Pred. No.:	6,32e-102	Length:	679
Score:	1095.00	Matches:	202
Percent Similarity:	96.8%	Conservative:	7
Best Local Similarity:	93.5%	Mismatches:	7
Query Match:	27.7%	Indels:	0
DB:	5	Gaps:	0

US-10-616-788-2 (1-738) x BW965550 (1-679)

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QY 1 MetAlaProTrrPLeuGlnLeuCySeSerValPhePheThrValAlaAlaCylLeuAlaGly 20
DB 32 ATGAGCCCGGCTGCGAGCTGCTGCTGCTCTTCAACGCTTCACGCTTCACGAGGC 91
QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyValArgAlaTrpGlyValAspThrCysGly 40
DB 92 TCGCAATGGCCGCGCGGAGGTGGCTCCAGCAGACTCGGGCGGCGACCTCGCGC 151
QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyraAsnIleThrPheLeuTyr 60
DB 152 TGGAGGGGAGATGGGGCGGCGGAGCAACAGTGGCTGCACAAACATCATCTTCAGATAT 211
QY 61 AspAsnCyseThrThrTyLeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAsn 80
DB 212 GACAACCTGCACCACTTACTTGAGTCTCTGGGAGAGCATGTGATCGCCGACCAAGAT 271
QY 81 IleThrIleSerGlnTyraCyseHisAspGlnValAlaValThrIleLeuTrpSerPro 100
DB 272 ATCCACCATCAGTCAAGTACGCTGCACAGCAACAGTGCAGTCCATCTCTGCTCCCA 331
QY 101 GlyAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGlnGluLeuLeuSer 120
DB 332 GGGGCGCTGGGAGTCAATTCCTTAAGAGATTCGGGTAAATATCGAGAGAGCTGAATCA 391
QY 121 GluGlyArgGlnCyseGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
DB 392 GAAGGAGAGACAGTGCACCAACATGATTCGAAGAGCCGGAAGCAGCTCAACAGTACCTTC 451
QY 141 LysArgThrGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 160
DB 452 AAAAGAGCTGAATGAGATCTCAGCTTCCTGTAATGAAATTTGAAACAGATTAATTT 511
QY 161 ValLysValValProPheProSerIleLysAsnGlnLysSerAsnTyraHisProPhePhe 180
DB 512 GTCAAGATTTGCTCTTTCTTCATTAAGAAAGCAATATATCACTCTTCTTCTTT 571
QY 181 ArgThrArgAlaCyseAspLeuLeuGlnProAspAsnLeuAlaCyseLysProPheTyr 200
DB 572 AGAAGCCGCACTGTGACTGTATATACAGCCGAGCAACCCGCGCTTAACCTTCTG 631

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QY 201 LysProArgAsnLeuAlaAsnIleSerGlnIleGlySerAspMetGlnVal 216
DB 632 AGCCCTGGAGACCCCTCATCATCAACCAACATGGCTGAGATGCACTGCACTG 679

RESULT 10
BU221978
LOCUS
DEFINITION
603105617F1 CSBQCHN04 Gallus gallus cDNA clone CHEST44a6 5', mRNA
sequence.
ACCESSION
BU221978
VERSION
BU221978.1 GI:25410688
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
Boardman, P. E., Sanz-Bzquez, J., Overton, I. M., Burt, D. W., Bosch, E.,
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES

source

1..692
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="CHEST44a6"
/issue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CSBQCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research
(1996) 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.:	8.91e-101	Length:	692
Score:	1084.00 <td>Matches:</td> <td>190</td>	Matches:	190
Percent Similarity:	95.2% <td>Conservative:</td> <td>26</td>	Conservative:	26
Best Local Similarity:	83.7% <td>Mismatches:</td> <td>11</td>	Mismatches:	11
Query Match:	27.5% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	5	Gaps:	0

US-10-616-788-2 (1-738) x BU221978 (1-692)

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QY 97 LeuTrpSerProGlyAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGln 116
DB 10 GTTGGACAGCAAAATGCCATTTGGATTAATACCTTAAGAGATTCGCGCTTAATCTTGA 69
QY 117 GluLeuLysSerGlnGlyArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 136

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Db 70 GAGTAAATCAGAGGAGCAATGTCAGAGATGTTTAAAGATCCAAAGCACTC 129
 Qy 137 AasnSerPheLeuValGlnMetGlnSerGlnProPheLeuAenMetLysPheGlu 156
 Db 130 AGCCCAAGTTTAAAGACAGAAATCCAAATCCCTTTGCAAAATCGAAGTTTGA 189
 Qy 157 ThrAspPhePheValLysValProPheProSerLelLysAenGlnSerAspThrHis 176
 Db 190 ACAGATTACTTGTCAAGATTGTCCTTTCTTCATTAATAATGAAGTAATATCAC 249
 Qy 177 ProPhePhePheArgLysGlnAAspPheLeuGlnProAenAenLeuAAspCys 196
 Db 250 CCAATCTTTTCCGAATCCGCCATGATTAATGCTACAGCCAGAAACCTCATCTGC 309
 Qy 197 LysPhePheTrpLysProArgAenLeuAenLelSerGlnHisGlnSerAspMetGlnVal 216
 Db 310 AAACCTTACGTAAGCAGCAATCTGAATGTTACCGACAGGGTTTAAATATGCAAGTG 369
 Qy 217 SerPheAspHisAlaProHisAenPheGlyPheArgPhePheTrpLeuHisGlyTrpLeu 236
 Db 370 TCTTTGATCATGCTCCCAACTTGTGATTAATGATTAATCTTCTCACTCAAACTG 429
 Qy 237 LysHisGlnGlyProPheLysArgLysPheTrpCysLysGlnGlnGlnThrGluThrThr 256
 Db 430 AAGCATTAAGGCGCATTCAGCAAAAGACCTGCAAAAGCATCAAAACAGATATCA 489
 Qy 257 SerCysLeuLeuGlnAenValSerProGlyAspTrpLelLelGlnLeuValAspAspThr 276
 Db 490 AGTTGATCTTCTGCAATGTAATCTCCAGGGATTAATATCATCGAGCTGCGATGACACT 549
 Qy 277 AsnThrThrProLysValMetHisGlyTrpAlaLeuLysProValHisSerProTrpAlaGly 296
 Db 550 AATACCAACAAAGAAACAAATGCACTATGCACTAAACAGACACTTTCGCTGCGCTGGA 609
 Qy 297 ProLelArgLalMetAlaLelThrValProLeuValValLelSerAlaPheAlaThrLeu 316
 Db 610 CCAATTAAGACTATGCAATTCAGTCCCTTACTGTTCTCATTTCCGATTTGCAACACTT 669
 Qy 317 PheThrValMetCysArgLys 323
 Db 670 TTCACAGTATGTCGCCA 690

RESULT 11
 BU909956 907 bp mRNA linear EST 17-OCT-2002
 LOCUS 10487146 NICHD XGC Emb1 Xenopus laevis cDNA clone
 DEFINITION IMAGE:6635685 5', mRNA sequence.
 ACCESSION BU909956
 VERSION BU909956.1 GI:24091870
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Bacteria: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipidoidea: Pipidae;
 Xenopodinae: Xenopus; Xenopus.
 1 (bases 1 to 907)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@nci.nih.gov
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: NCI-CCGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L1AM14210 row: d column: 21
 High quality sequence stop: 716.
 Location/Qualifiers

source 1..907
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 /clone_lib="NICHD XGC Emb1"
 /notes="Vector: pCMV-SF0RTE; Site 1: NotI; Site 2: SalI;
 cloned unidirectionally. Primer: Oligo dt. Average insert
 size 1.55 kb. Constructed by Life Technologies. Note: This
 is a Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:
 Pred. No.: 6.72e-98 Length: 907
 Score: 1058.00 Matches: 186
 Percent Similarity: 83.6% Conservative: 49
 Best Local Similarity: 66.2% Mismatches: 43
 Query Match: 26.8% Indels: 3
 DB: 5 Gaps: 1

US-10-616-788-2 (1-738) x BU909956 (1-907)

Qy 26 AlaAlaGlyGlySerGly-----ArgAlaTrpGlyValAspThrCysGlyTrpArgGly 43
 Db 63 GCCACGGAGAGTTCGGAGGACACAGAGGAGATTAGCAGTCTGCGCTCCAAAGGA 122
 Qy 44 ValGlyProLysSerArgAsnSerGlyLeuTrpAsnLelThrPheLysTrpAspAsnCys 63
 Db 123 GCGCTGTGCTGACGAGAACTGCGGCTGCGCAAGTCACTTCCGATATGCAACTGC 182
 Qy 64 ThrThrTrpLeuAsnProValGlyValHisValLelAlaAspAlaGlnAenLelThrLel 83
 Db 183 ACTGCTTACATGAACTCCCGGGGAGAACACAGATTGGGATTTGCAACATATCCATC 242
 Qy 84 SerGlnTrpAlaCysHisAspGlnValAlaValThrLelLeuTrpSerProGlyAlaLeu 103
 Db 243 AGCCAAATTCCTGCAACAGCAAGTGGCGTTTCTGTTCTTCTGACGCGCAATGATATC 302
 Qy 104 GlyLelGlnPheLeuLysGlyPheArgValLelLeuGlnGlnLeuLysSerGlnGlyArg 123
 Db 303 GGCATTGAATACTGTAAGGCTTCGCGGTGCTGTGGAAGATTTGAAGTGGAGGGAGG 362
 Qy 124 GlnCysGlnGlnLeuLelLeuLysAspProLysGlnLeuLysSerPheLysArgThr 143
 Db 363 TTCTGTCAGAGATTTGTGAAGATCCCAACAGCTGATGAAACTTCAAAAGAGTT 422
 Qy 144 GlyMetGlnSerGlnProPheLeuAenMetLysPheGluThrAspTrpPheValLysVal 163
 Db 423 GTAATGGAACACAACTATTTGCAACTGAAATTTGAAACAGATTAATTTTGAATAAT 482
 Qy 164 ValProPheProSerLelLysAenGlnSerAspTrpHisProPhePhePheArgTrpArg 183
 Db 483 GTCCATTTCCCTCCCGCAGAAATGAAGTAATTAATCAATCCGTTCTTTCAGAGCCGC 542
 Qy 184 AlaCysAspLeuLeuGlnProAenAenLeuAAspLysProPheTrpLysArg 203
 Db 543 ACCTGGAAGTCGTTGTCAGCCGACAGCTGACCTGACGCGGTAATGGAACCAAAA 602
 Qy 204 AsnLeuAenLelSerGlnHisGlnSerAspMetGlnValSerPheAspHisAlaProHis 223
 Db 603 AAGCTCAACCTCAACCAAGGAGCAATCAACATGACAGTGTCTTTCACACCGCCGAG 662
 Qy 224 AsnPheGlyPheArgPhePheTrpLeuHisGlyTrpLeuLysHisGlnGlyProPheLys 243
 Db 663 AATTTCGCTTAAATCTATTTCCGTCACATCAAACTGAAGACAGAGGCTCTTTAAA 722
 Qy 244 ArgLysThrCysLysGlnGlnGlnThrThrGluThrThrSerCysLeuLeuGlnAenVal 263
 Db 723 CAGAGATATGCGCGAAGGTCGAAACACAGACTTCAACCAAGCTGATCGAAGAGTA 782
 Qy 264 SerProGlyAspTrpLelLelGlnLeuValAspAspThrAsnThrThrArgLysValMet 283

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Db      783  TCCCGGGGAAATCATGATGAGCTGTGAGACGACCAACGAGAGGAGTTCATG 842
Qy      284  HtTtYAlaLeuYpProValHisSerProTTPAla-GlyProILeArgAlaMetAlaI 303
Db      843  CACTACTCGCTGAAACAGTGCAATTCCTCCCTGGCCGGGTCCTCAATAGACCATTCGCCAT 902
Qy      303 e 303
Db      903  T 903

RESULT 12
BX750910 886 bp mRNA linear EST 09-DEC-2003
BX750910 XGC-gastrula Xenopus tropicalis cDNA clone Tga8082k14 3',
DEFINITION
mRNA sequence.
ACCESSION
BX750910 GI:39640978
VERSION
BX750910.1
KEYWORDS
EST.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 886)
Croning, M.D.R., Ashhurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
REFERENCE
Sanger Xenopus tropicalis EST project 2001 (11_2003)
AUTHORS
Unpublished (2003)
JOURNAL
Contact: Croning MDR
COMMENT
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tga8082k14.q1kT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13
gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107, Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
location/Qualifiers
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/clone="Tga8082k14"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_1lb="XGC-gastrula"
/notes="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

FEATURES
source
1. .886
/organism="Xenopus tropicalis"
/mol_type="mRNA"
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/clone="Tga8082k14"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_1lb="XGC-gastrula"
/notes="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN
Alignment Scores:
Pred. No.: 1.86e-94 Length: 886
Score: 1024.50 Matches: 189
Percent Similarity: 78.0% Conservative: 41
Beet Local Similarity: 64.1% Mismatches: 62
Query Match: 25.9% Indels: 3
DB: 5 Gaps: 1

US-10-616-788-2 (1-738) x BX750910 (1-886)
Qy      314  AlAThLeuPheThrValMetCyArgLysGlyGlnGlnGlnGlnLeuIleTyrSerHisLeu 333
Db      886  GCCACTCTATTCCTGTAATGTGCGCCGACAGAGAGCAAAACATTTCACACCTG 827
Qy      334  AspGlnGlnSerSerGlnSerThrTyrThrAlaIleLeuProArgGlnArgLeuArg 353

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Db      826  GAGAGAGAGAGTTCGGAATCTTCTACTTACGAGGAGAGCTGCATGTGAGAAACCGCGT 767
Qy      354  ProArgProLysValPheLeuCyTyrSerSerLysArgGlyGlnAmhiShetAnVal 373
Db      766  CCGCGCGCTTCGAGTTTATTTGTCTACTCTAGTAAGACTGTCAAAAGACATTAAATGTC 707
Qy      374  ValGlnCyPheAlaTyrPheLeuGlnAerPheCyGlyCyGlyuValAlaLeuAerLeu 393
Db      706  ATCCAGTCTTTCCTTCCTATTTCTTCTACAAAGATTTCTGTGGTGTGAGGTTTCGCTGACCTG 647
Qy      394  TTPGluAspPheSerLeuCyArgGlnGlyGlnArgGlyTyrValIleGlnLysIleHis 413
Db      646  TGGAGAAACCTGAAGATCTGCAAGACGCGGACGCGAGATGCTGAAGACAAAGATCCCG 587
Qy      414  GluSerGlnPheIleIleValValCySerSerLysGlyMetLysTyrPheValAspLys 433
Db      586  GATTCCTCCTACATCATCTGCTGCTCAAGGGCTCAAGTACTTGTGTGAGAGGAAG 527
Qy      434  AenTyrLysHisLysGlyGlyArgGlySerGlyLysGlyGluLeuPheLeuValAla 453
Db      526  AAGCGAAGACAAAGGGGGCGCCCCCGAGACGCGGAAGGGGAGATCTTCCTGACGGCC 467
Qy      454  ValSerAlaIleAlaGlnLysLeuArgGlnAlaLysGlnSerSerAla----- 470
Db      466  ATGTCTATGATTTGGGAGAACTGAGACAGCGCGCGGAGTGGGAGGAGAAACCCGAG 407
Qy      471  AlALeuSerLysPheIleAlaValTyrPheAspTyrSerCyGlnGlyLysValProGly 490
Db      406  GAGCTTGGGAAATTCATCCCGCTATTCGATTCTCTTCCTCCGACTCCGACATCCCGGA 347
Qy      491  IleLeuAspLeuSerThrTyrTyrArgLysMetAspAsnLeuProGlnLeuCySerHis 510
Db      346  ATCTTGAGAACACCAAGAAAGTACAACTGATGACACTTCCCAAGCTTACTACTACAC 287
Qy      511  LeuHisSerArgAspHisGlyLeuGlnGlnProGlyGlnHisThrArgGlnLysArg 530
Db      286  CTGTACTCCAAAGAGCTGAGCTGACGACACCGGAGACGATACCCGCAACATCAGCAAG 227
Qy      531  ArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyrValAlaIleCyAsnMetHis 550
Db      226  CCGCACTACTTCCCGCAGCAAGGCGCGCTGCTTCAATCCCACTGCAACATGACGAC 167
Qy      551  GlnPheIleAspGlnLysProAspTyrPheGlnLysGlnPheValProPheHisProPro 570
Db      166  CAGTACACAGACACGAAACCGATTTGTTTCGAAAGACGACACTCCGGCCCATCCCGG 107
Qy      571  ProLeuArgTyrArgGlnProValLeuGlnLysPheAspSerGlyLeuValLeuAsnArg 590
Db      106  ACCCTCCACTACAGAGCCCGTCATGAGAAAGTTGCACTCCGGGTGTGCTGAACGAC 47
Qy      591  ValMetCyLysLysProGlyProGlnSerAspPheCyLysLysVal 605
Db      46  GTAAACGGGAAACAGGTGCGGAACCGACTTTCCTCCGAAATG 2

RESULT 13
BP275741 583 bp mRNA linear EST 16-SEP-2004
BP275741 Sugano cDNA library, Kidney Homo sapiens cDNA clone
DEFINITION
BP275741 mRNA sequence.
ACCESSION
BP275741
VERSION
BP275741.1 GI:52189473
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
REFERENCE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

```

JOURNAL
PUBMED
COMMENT

Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
SOURCE

1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KDN04362"
/tissue type="kidney"
/clone_lib="Sugano CDNA library, kidney"

ORIGIN

Alignment Scores:

Pred. No.:	1.06e-94	Length:	583
Score:	1024.00	Matches:	191
Percent Similarity:	98.5%	Conservative:	0
Best Local Similarity:	98.5%	Mismatches:	3
Query Match:	25.9%	Indels:	0
DB:	3	Gaps:	0

US-10-616-788-2 (1-738) x BP275741 (1-583)

QY 498 TyraArgLeuMetAspAlaLeuProGlnLeuCySerHisLeuHisSerArgAspHisGly 517
2 TACAGACTCATGAGCAATCTTCTCCAGCTCGTTCCACCTGCAGCTCCGAGACACGAGC 61

QY 518 LeuGlnGluProGlyGlnHisThrArgGlnGlySerArgArgAntyrPheHisSerLys 537
62 CTCAGAGAGCGGGGAGACACACGAGGAGGAGAGAGAACTACTTCCGAGAGAG 121

QY 538 SerGlyArgSerLeuTyraValAlaIleCyAspMetHisGlnPheIleAspGlnGluPro 557
122 TCAGGCGGCTCCCTATACGTCGCTTTCGACATGACACAGTTTATGACGAGAGACCC 181

QY 558 AspTyrPheGlnLysGlnPheValProPheHisProProLeuArgTyraArgLysPro 577
182 GACTGGTTGAAAGAGAGCTTCTGTTCCCTTCATCTCTCCACGCGCTACCGGAGACCA 241

QY 578 ValLeuGlnLysPheAspSerGlyLeuValLeuAspValMetCylGlyProGlyPro 597
242 GTCTTGAGAAATTTGATTCGGGCTTGTATTAAATGATGCAATGTCAAACGAGGCT 301

QY 598 GluSerAspPheCysLeuLysValGluAlaProValLeuGlnLysAlaThrGlyProAlaAsp 617
302 GAGAGTACCTTCTGCTTAAGAGTACGAGGCTGTCTTGGGGCAACCGAGCAGCCGAC 361

QY 618 SerGlnHisGlnSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeu 637
362 TCCAGACAGAGAGTACGATCGAGGCTGAGACCAACGAGGAGGCGCCGCTGCTT 421

QY 638 AspGlySerAlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAsp 657
422 GACGGTACGCGCGCCGCAACCCCTCTGACACGCTGAAAGCGGACGCGCTCCGAC 481

QY 658 MetProArgAspSerGlyIleTyraAspSerSerValProSerSerGlnLeuSerLeuPro 677
482 ATCCCGGGAGCTCAGGCACTTAAGACTCGCTGTGTGCTTCATNCGAGCTGTCTTCCA 541

QY 678 LeuMetGlnLysLeuSerThrAspGlnThrGlnLysSerSer 691
542 CTATGGAAGAGACTCTGAGAGGACACAGCAAGAACTTTCC 583

RESULT 14
BU479802 717 bp mRNA linear EST 30-NOV-2002
LOCUS 603843254.F1 CSBQRBN22 Gallus gallus CDNA clone CHEST828k13 5', mRNA
DEFINITION
Sequence
ACCESSION BU479802

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

BU479802.1 GI:25973379
EST.
Gallus gallus (chicken)
Gallus gallus
Archaeopteryx; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 717)
Boardman, P.E., Sanz-Exquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, M.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
SOURCE

1. 717
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST828k13"
/sex="Male and female"
/tissue type="Chondrocytes isolated from growth plate cartilage"
/dev stage="adult"
/lab host="DH108"
/clone_lib="CSBQRBN22"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI. This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand and synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a library modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., ENAS (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.:	1.67e-94	Length:	717
Score:	1023.50	Matches:	193
Percent Similarity:	91.4%	Conservative:	20
Best Local Similarity:	82.8%	Mismatches:	18
Query Match:	25.9%	Indels:	2
DB:	5	Gaps:	1

US-10-616-788-2 (1-738) x BU479802 (1-717)

QY 266 GlyAspTyrIleIleGluLeuValAspAspThrAsnThrThrArgLysValMetHisTyr 265
3 GGGGATTATATCATCAGCTGCTGATGACATTAATCAACAAAGAAACAAATGCACTAT 62

QY 286 AlaLeuLysProValHisSerProTyrAlaGlyProIleArgAlaMetAlaIleThrVal 305
63 GCATTAACACGATACATCTCCGTGGCTGAGCAACAATAAGACTATGCAATTAACATC 122

QY 306 ProLeuValAlaIleSerAlaPheAlaThrLeuPheThrValMetCysArgLysLysGln 325
123 CTTTGGTTGTCAATTCGGCATTTGCAACCTTTTCAAGTATGATGCGCAAAAGACAG 182

QY 326 GlnGluAsnIleTyraHisLeuAspGlnGluSerSerGlnSerSerThrTyraAla 345

```

Db      183  CAAGAGATATATATATCCATCTAGACGAGAGAGCTCAGATCTTCAGCTTATGTGCA 242
Qy      346  AAlenProArguAgluAgluArgProArgProArgValAheleuCySerSerSerLy 365
Db      243  GGTCTCCCTGTGAAAGACTTGGCCCCGGCCAAAGATTCATCTCTATTCAGTAA 302
Qy      366  AArgGlyInaAnhiSweCanValValGInCySerPheValTyPheLeuGInAepPheCy 385
Db      303  GATTGCCAGAAACATTAATGTTATCCAGCTTCCTTATTTTCACGAGCTTCTGT 362
Qy      386  GlyCySerGluValAlaLeuAepLeuTyPgluAepPheSerLeuCyArgGluGlyIna 405
Db      363  GGCTGTGAGGTGGCTGTGATTTGTGGGAAGATCTGAAATTTGTAAAGAAAGTCA 422
Qy      406  GluTrpValIleGluValIleHisGluSerGlnPheIleIleValValCySerSerLy 425
Db      423  GAATGGCTCATTAATAAATAAATGAATGATCTCAGTTATCATTTGTGTCTCCAA 482
Qy      426  MetLeuTyPheValAepLySlyAenTyPheIleSlyGlyGlyArgGlySerGly 445
Db      483  ATGTAATCTCTCTGTGAAAAAAGAAATGGAAACACAGAGAGTAACCAAGACAGGG 542
Qy      446  LysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluValLeuArgGlnAla 465
Db      543  AAAGAGAACTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 602
Qy      465  ArgInSerSerSerAlaAlaLeuSerLyPheIleAlaValTyPheArgTyPheSer 485
Db      603  GCGAATTCATTAAT--GACCTCTGCAAGTTCATTCAGTCTACTTGTATTAATCT 659
Qy      485  uGlyAepValProGlyTyIleLeuAepLeuSerThrLy 497
Db      660  GCGAGACATTCCTGCTTCTGTGATCTGATCTAAGTCAACAA 696

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```

RESULT 15
LOCUS   CV126214
DEFINITION  748 bp mRNA linear EST 02-SEP-2004
ACCESSION 31913856 NIH_MGC_238 Rattus norvegicus cDNA clone
VERSION 1
KEYWORDS  IMAGE:7453313 5', mRNA sequence.
SOURCE    CV126214.1 GI:51860897
ORGANISM  Rattus norvegicus (Norway rat)

```

```

REFERENCE
AUTHORS  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
TITLE     Sciurognathi; Muridae; Muridae; Murinae; Rattus.
JOURNAL   1 (bases 1 to 748)
COMMENT   NIH-MGC http://mgs.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgaaps-remail.nih.gov
          Tissue Procurement: Howard Jacobs
          cDNA Library Preparation: Express Genomics
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LHAM15711 row: P column: 15
          High quality sequence stop: 689.
          Location/Qualifiers
            1..748
              /organism="Rattus norvegicus"
              /mol_type="mRNA"
              /db_xref="taxon:10116"
              /clone="IMAGE:7453313"
              /tissue_type="testis, pooled"

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/lab host="PH10B TONA"
/clone lib="NIH MGC 238"
/notes="Organ: testis; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACATGTTCTAGATCGCAGCGCGCCGCTT-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary
library is normalized (non-normalized by Express Genomics
NIH MGC_237) and was constructed by Express Genomics
(Frederick, MD)"

```

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Alignment Scores:
Pred. No.: 2,56e-94 Length: 748
Score: 1022.00 Matches: 200
Percent Similarity: 85.6% Conservative: 14
Best Local Similarity: 80.0% Mismatches: 24
Query Match: 25.9% Indels: 12
DB: 7 Gaps: 4

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US-10-616-788-2 (1-738) x CV126214 (1-748)

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Qy      398  SerLeuCyArgGluGluGluInaArgGluTrpValIleGluValIleHisGluSerGlnPhe 417
Db      3  AGCCACTGCATAGAGGGCCAGAGAGATGATTCATCAAGATCCATGATCCAGTTTC 62
Qy      418  IleIleValValCySerSerLyMetLyTyPheValAepLySlyAenTyPheValHis 437
Db      63  ATCATATGCTGTGTGTGTCCAAAGGATGAAGTCTTGTGTGAATGAAGATCAAGACAC 122
Qy      438  LysGlyGlyGlyArg--GlySerGlyLySlyGluLeuPheLeuValAlaValSerAla 456
Db      123  AAAGAGGAGCTGTGTGCGGCAAGGAGGAGAGAGCTTCTCTATGTGCGCGGAGGCC 182
Qy      457  IleAlaGluLeuArgGlnAlaValGluSerSerSerAlaAlaLeuSerLyPheIle 476
Db      183  ATTGCTGAGAAAGTCCGTCAGGCCAAGACAGACTATCTCGCGGCACTGAGCAAGTTCA 242
Qy      477  AlaValTyPheArgTyPheSerGluGlyAepValProGlyTyIleLeuAepLeuSerThr 496
Db      243  ACCGTCTACTTGAATTAATCTGTGAAAGGAGATGTCCTGTATCCCTGAGCTGAGCACC 302
Qy      497  LysTyArgLeuMetAepLeuProGlnLeuCySerSerHisLeuHisSerArgPheHis 516
Db      303  AATATCAAGCTCATGAGCAACCTTCTGTGAGCTGTGTCCATCTACACAGAGAAACAG 362
Qy      517  GlyLeuGluGluProGlyInHisThrArgGlnGlySerArgArgAntTyPheArgSer 536
Db      363  -----GAGGAGCTGGGCGACACCCAGACACAGACAGAGAAAGAACTATTCGGAGC 416
Qy      537  LysSerGlyArgSerLeuTyValAlaIleCyAenMetHisGlnPheIleArgGlu 556
Db      417  AAAGCTGGCCGCTCCCTGTATGTGCAATTCACATGACACAGATTTATGAGGAA 476
Qy      557  ProArgTrpPheGluGluPheValProPheHisProProProLeuArgTyArgGlu 576
Db      477  CCGAGCTGTGTGAGAGAGAGTTTACCTTCACCCGCCCTGTGTGCTACCGAGAG 536
Qy      577  ProValLeuGluTyPheAepSerGlyLeuValIleAepAepValMetCySlyProGly 596
Db      537  CCAATCTGAGAGAGTTTATCTCAGGTTGGTTTAAATGATCTCTAAGCAACAGGG 596
Qy      597  ProGluSerAepPheCyLeuTyValAlaProValLeuGlyValAthrGlyProAla 616
Db      597  CCAAGAAAGTCACTTGTGCTGAAAGTTGAGGCTTCTATCTTGGGGCCACTGGGCA 656
Qy      617  AepSerGlnHis-----GluSerGlnHisGlyGlyLeuAepGln----- 629
Db      657  GACTCTTACTCATCTCTGANGATGAGATGAGCGGCTGAGACCAAGCACTGANGCAGCC 716

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Qy 630 -----AspGIYGIuaIAArgProAlaIeu 637
|||
Db 717 CGCTGTGATGTGTGGCTGCNTGCAGCCCTG 746

Search completed: March 1, 2006, 09:18:55
Job time : 7498 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 10:31:11 ; Search time 165 Seconds

(Without alignments)
1868.837 Million cell updates/sec

Title: US-10-616-788-2

Sequence: 1 MAFWOLGCVFTVNAACNG.....SCKADICGRSYDELAAVAP 738

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417629326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3948	100.0	738	3	US-09-809-567-2
2	3948	100.0	738	4	US-10-216-156-2
3	3948	100.0	738	4	US-10-616-788-2
4	3948	100.0	738	5	US-10-842-006-4
5	3918	99.2	739	3	US-09-912-157-8
6	3918	99.2	739	4	US-10-717-282-8
7	3908	99.0	739	5	US-10-842-006-2
8	3908	99.0	739	5	US-10-608-449-2
9	3901	98.8	753	3	US-09-912-157-2
10	3901	98.8	753	3	US-10-717-282-2
11	3891	98.6	753	3	US-09-912-157-5
12	3891	98.6	753	3	US-10-717-282-5
13	3835.5	97.2	738	3	US-09-863-818A-10
14	3835.5	97.2	738	4	US-10-749-144-10
15	3835.5	97.2	738	5	US-10-924-667-10
16	3706	93.9	728	4	US-10-104-047-3399
17	3681.5	93.2	728	3	US-09-874-503-18
18	3681.5	93.2	728	3	US-09-816-744-18
19	3681.5	93.2	728	3	US-09-747-259-18
20	3681.5	93.2	728	3	US-09-908-827-18
21	3681.5	93.2	728	4	US-10-000-157-18
22	3681.5	93.2	728	4	US-10-410-927-18
23	3681.5	93.2	728	4	US-10-410-374-18
24	3681.5	93.2	728	4	US-10-410-552-18
25	3681.5	93.2	728	4	US-10-458-442-18
26	3681.5	93.2	728	4	US-10-408-385-18
27	3382	85.7	739	3	US-09-912-157-12

28	3382	85.7	739	4	US-10-717-282-12	Sequence 12, Appl
29	3164	80.1	595	5	US-10-477-714-16	Sequence 16, Appl
30	3158	80.0	595	4	US-10-608-449-4	Sequence 4, Appl
31	2701.5	68.4	554	4	US-10-943-348-16	Sequence 16, Appl
32	1333	33.8	296	4	US-09-816-788-19	Sequence 19, Appl
33	315	8.0	810	3	US-09-809-567-3	Sequence 3, Appl
34	315	8.0	810	3	US-10-216-156-3	Sequence 3, Appl
35	315	8.0	810	4	US-10-616-788-3	Sequence 3, Appl
36	315	8.0	866	3	US-09-778-971-9	Sequence 9, Appl
37	315	8.0	866	4	US-10-033-522-1	Sequence 1, Appl
38	315	8.0	866	4	US-10-207-655-107	Sequence 107, Appl
39	315	8.0	866	4	US-10-742-161-10	Sequence 10, Appl
40	315	8.0	866	4	US-10-742-372-10	Sequence 10, Appl
41	315	8.0	866	4	US-10-646-308-4	Sequence 4, Appl
42	315	8.0	866	5	US-10-918-084-1	Sequence 1, Appl
43	315	8.0	866	6	US-11-128-403-9	Sequence 9, Appl
44	298	7.5	864	4	US-10-742-161-2	Sequence 2, Appl
45	298	7.5	864	4	US-10-742-372-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1									
US-09-809-567-2									
Sequence 2, Application US/09809567									
Patent No. US20020045213A1									
GENERAL INFORMATION:									
APPLICANT: Jing, Shuguan									
TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof									
FILE REFERENCE: 01017/36916A									
CURRENT APPLICATION NUMBER: US/09/809,567									
CURRENT FILING DATE: 2001-03-15									
PRIOR APPLICATION NUMBER: 09/724,460									
PRIOR FILING DATE: 2000-11-28									
PRIOR APPLICATION NUMBER: 60/189,816									
PRIOR FILING DATE: 2000-03-16									
NUMBER OF SEQ ID NOS: 17									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 2									
LENGTH: 738									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-809-567-2									
Query Match									
Best Local Similarity 100.0%; Score 3948; DB 3; Length 738;									
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MAFWOLGCVFTVNAACNGSOLAAGSGRAGVDTGCMRGVGPASRNSGLNITTFKY	60						
QY	61	DNCTTYLVNKGKIVADAQNTITISYACHDOVAVITLMSPGALGIFLNGFRITBELKS	120						
DB	61	DNCTTYLVNKGKIVADAQNTITISYACHDOVAVITLMSPGALGIFLNGFRITBELKS	120						
QY	121	EGROCOOLILKPKOLNSFKRTGMSQPLNKKFETDFVKKVPPSIKNESNHPFF	180						
DB	121	EGROCOOLILKPKOLNSFKRTGMSQPLNKKFETDFVKKVPPSIKNESNHPFF	180						
QY	181	RTRACDLILQPNLACKPFWKPRNLTISQHGSDMOVSPHAPNFGFRFYLYKXKHG	240						
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QY	241	PPFRKTKCKOETETTSCLQNVSPEDYIIEVDNTNTRKVMHVALKXVSPWAGPIRA	300						
DB	241	PPFRKTKCKOETETTSCLQNVSPEDYIIEVDNTNTRKVMHVALKXVSPWAGPIRA	300						
QY	301	MAITVPLVVISAFATLFTWCRKQOENITSHLDESSSSSTYTAALPRERLPRPKVFL	360						
DB	301	MAITVPLVVISAFATLFTWCRKQOENITSHLDESSSSSTYTAALPRERLPRPKVFL	360						

QY 361 CYSSKQGNHNMVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIIV 420
DB 361 CYSSKQGNHNMVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIIV 420
QY 421 VCSKGMKYPVDKKNYGHKGGSGKGLFLVAVASIAEKLROAKOSSAALSKFIAYVF 480
DB 421 VCSKGMKYPVDKKNYGHKGGSGKGLFLVAVASIAEKLROAKOSSAALSKFIAYVF 480
QY 481 DYCCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
DB 481 DYCCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
QY 541 SLVVAICNNHOFIDEBPDWEKQFVPHPPPLRYREPVLEKFPDGLVNDVMCKPGESD 600
DB 541 SLVVAICNNHOFIDEBPDWEKQFVPHPPPLRYREPVLEKFPDGLVNDVMCKPGESD 600
QY 601 FCILKVEAPVLGATGPADSGHESQHGGLDQGEARPALDSALLOPLHTTVKAGSPSDMPR 660
DB 601 FCILKVEAPVLGATGPADSGHESQHGGLDQGEARPALDSALLOPLHTTVKAGSPSDMPR 660
QY 661 DSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGIGBEEPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGIGBEEPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELAHAVAP 738
DB 721 KADLCGRSYTDELAHAVAP 738

RESULT 2
US-10-216-156-2
; Sequence 2, Application US/10216156
; Publication No. US2003009980A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/10/216,156
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-156-2

Query Match 100.0%; Score 3948; DB 4; Length 738;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWLOLCVFTVNAACLNQSOLAFAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
DB 1 MAPWLOLCVFTVNAACLNQSOLAFAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
QY 61 DNCTTYLNPVGKIVADANITISQYACHDOVAVTILMSGALGIEFLKGRVILBELKS 120
DB 61 DNCTTYLNPVGKIVADANITISQYACHDOVAVTILMSGALGIEFLKGRVILBELKS 120
QY 121 EGRQCOQLILKDBKOLNSPFRKTGMSQPLANKFETDYFVKVVPSPSINKESNYHPFPE 180
DB 121 EGRQCOQLILKDBKOLNSPFRKTGMSQPLANKFETDYFVKVVPSPSINKESNYHPFPE 180
QY 181 KTRACDULLLOPDLACKPFWKPRNLINISQHGSDMVSFDHAPNFGFRFFYLHYKLKHG 240
DB 181 KTRACDULLLOPDLACKPFWKPRNLINISQHGSDMVSFDHAPNFGFRFFYLHYKLKHG 240

QY 241 PFRKRTCKOQETETTSCLQNVSPGDYIIELVDDINTTRKMYALAKPVHWPAPIRA 300
DB 241 PFRKRTCKOQETETTSCLQNVSPGDYIIELVDDINTTRKMYALAKPVHWPAPIRA 300
QY 301 MATTVLVISAPATLFTWCRKQOENYSHLDESSSSSTYTALPREBLRPRKVL 360
DB 301 MATTVLVISAPATLFTWCRKQOENYSHLDESSSSSTYTALPREBLRPRKVL 360
QY 361 CYSSKQGNHNMVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIIV 420
DB 361 CYSSKQGNHNMVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIIV 420
QY 421 VCSKGMKYPVDKKNYGHKGGSGKGLFLVAVASIAEKLROAKOSSAALSKFIAYVF 480
DB 421 VCSKGMKYPVDKKNYGHKGGSGKGLFLVAVASIAEKLROAKOSSAALSKFIAYVF 480
QY 481 DYCCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
DB 481 DYCCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
QY 541 SLVVAICNNHOFIDEBPDWEKQFVPHPPPLRYREPVLEKFPDGLVNDVMCKPGESD 600
DB 541 SLVVAICNNHOFIDEBPDWEKQFVPHPPPLRYREPVLEKFPDGLVNDVMCKPGESD 600
QY 601 FCILKVEAPVLGATGPADSGHESQHGGLDQGEARPALDSALLOPLHTTVKAGSPSDMPR 660
DB 601 FCILKVEAPVLGATGPADSGHESQHGGLDQGEARPALDSALLOPLHTTVKAGSPSDMPR 660
QY 661 DSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGIGBEEPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGIGBEEPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELAHAVAP 738
DB 721 KADLCGRSYTDELAHAVAP 738

RESULT 3
US-10-616-788-2
; Sequence 2, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/39525
; CURRENT APPLICATION NUMBER: US/10/616,788
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-788-2

Query Match 100.0%; Score 3948; DB 4; Length 738;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWLOLCVFTVNAACLNQSOLAFAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
DB 1 MAPWLOLCVFTVNAACLNQSOLAFAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
QY 61 DNCTTYLNPVGKIVADANITISQYACHDOVAVTILMSGALGIEFLKGRVILBELKS 120
DB 61 DNCTTYLNPVGKIVADANITISQYACHDOVAVTILMSGALGIEFLKGRVILBELKS 120

QY 121 EGRQCOOLIKDPKOLNSSFKRTGMSOPFLANKFETDYFVKVPPPSIKNESNYHPFF 180
DB 121 EGRQCOOLIKDPKOLNSSFKRTGMSOPFLANKFETDYFVKVPPPSIKNESNYHPFF 180
QY 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDQVSPDAPNFGFRFYLYKLGHEG 240
DB 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDQVSPDAPNFGFRFYLYKLGHEG 240
QY 241 PFRKCTCKOQTETTSCLLQNVSPGDYIIELVDDNTTRKVMYALKPHSPWAGIRA 300
DB 241 PFRKCTCKOQTETTSCLLQNVSPGDYIIELVDDNTTRKVMYALKPHSPWAGIRA 300
QY 301 MATTVPLVISAATLFTWCRKQOENIYSHDESSSESTYTAALPRRLPRPKVFL 360
DB 301 MATTVPLVISAATLFTWCRKQOENIYSHDESSSESTYTAALPRRLPRPKVFL 360
QY 361 CYSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGQREWIQKIHESQPIIV 420
DB 361 CYSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGQREWIQKIHESQPIIV 420
QY 421 VCSKMKRYFYDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
DB 421 VCSKMKRYFYDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
QY 481 DYSCEGDVPGIILSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
DB 481 DYSCEGDVPGIILSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
QY 541 SLVVAICNMHQPIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVNDVMCKPGBESD 600
DB 541 SLVVAICNMHQPIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVNDVMCKPGBESD 600
QY 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
DB 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
QY 661 DSGIYSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGGLGEBEPALPSKLLSSGSC 720
DB 661 DSGIYSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGGLGEBEPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAAP 738
DB 721 KADLCGRSYTDELHAAP 738

RESULT 4

US-10-842-006-4
Sequence 4, Application US/10842006
Publication No. US2004023104A1
GENERAL INFORMATION:
APPLICANT: Yang, Ruey-Bing
TITLE OF INVENTION: A Novel Human SBF Molecule and Uses
FILE REFERENCE: MP103-071PRM
CURRENT APPLICATION NUMBER: US/10/842,006
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: 60/469522
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 739
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-842-006-4

Query Match 100.0%; Score 3948; DB 5; Length 739;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFWLOLCVFYFTVNAACLSQALVAAGSGRAMGVDTGMRGVGPARSRNSGLYNTFFKY 60
DB 1 MAFWLOLCVFYFTVNAACLSQALVAAGSGGRAMGVDTGMRGVGPARSRNSGLYNTFFKY 60

QY 61 DNCTTYLNPVKGKVIADAQNTTISOYACHDQVAVTILMSGALGIEFLKGRVILEELKS 120
DB 61 DNCTTYLNPVKGKVIADAQNTTISOYACHDQVAVTILMSGALGIEFLKGRVILEELKS 120
QY 121 EGRQCOOLIKDPKOLNSSFKRTGMSOPFLANKFETDYFVKVPPPSIKNESNYHPFF 180
DB 121 EGRQCOOLIKDPKOLNSSFKRTGMSOPFLANKFETDYFVKVPPPSIKNESNYHPFF 180
QY 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDQVSPDAPNFGFRFYLYKLGHEG 240
DB 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDQVSPDAPNFGFRFYLYKLGHEG 240
QY 241 PFRKCTCKOQTETTSCLLQNVSPGDYIIELVDDNTTRKVMYALKPHSPWAGIRA 300
DB 241 PFRKCTCKOQTETTSCLLQNVSPGDYIIELVDDNTTRKVMYALKPHSPWAGIRA 300
QY 301 MATTVPLVISAATLFTWCRKQOENIYSHDESSSESTYTAALPRRLPRPKVFL 360
DB 301 MATTVPLVISAATLFTWCRKQOENIYSHDESSSESTYTAALPRRLPRPKVFL 360
QY 361 CYSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGQREWIQKIHESQPIIV 420
DB 361 CYSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGQREWIQKIHESQPIIV 420
QY 421 VCSKMKRYFYDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
DB 421 VCSKMKRYFYDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
QY 481 DYSCEGDVPGIILSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
DB 481 DYSCEGDVPGIILSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
QY 541 SLVVAICNMHQPIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVNDVMCKPGBESD 600
DB 541 SLVVAICNMHQPIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVNDVMCKPGBESD 600
QY 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
DB 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
QY 661 DSGIYSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGGLGEBEPALPSKLLSSGSC 720
DB 661 DSGIYSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGGLGEBEPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAAP 738
DB 721 KADLCGRSYTDELHAAP 738

RESULT 5

US-09-912-157-8
Sequence 8, Application US/09912157
Patent No. US20020165348A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Kuestner, Rolf E.
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 739
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-157-8

Query Match 99.2%; Score 3918; DB 3; Length 739;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MAMPWLOLCGVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITPKY 60
DB 1 MAMPWLOLCGVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITPKY 60
QY 61 DICTTYLANPVGKVIADANQNTTISQYACHDQVAVTILMSPGALGIEFLKGFVILEELKS 120
DB 61 DICTTYLANPVGKVIADANQNTTISQYACHDQVAVTILMSPGALGIEFLKGFVILEELKS 120
QY 121 EGRQCOQLILKDKPKOLNSFKRTGMSQPLNMKEETDYFVYVPPPSIKNSNHPFF 180
DB 121 EGRQCOQLILKDKPKOLNSFKRTGMSQPLNMKEETDYFVYVPPPSIKNSNHPFF 180
QY 181 RTACDILLQPDNLACKPMPKPRNLNISQHSQDMQVSPDHAHPNFGFRFFYLHYKLKHG 240
DB 181 RTACDILLQPDNLACKPMPKPRNLNISQHSQDMQVSPDHAHPNFGFRFFYLHYKLKHG 240
QY 241 PFRKRTCKEQOTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
DB 241 PFRKRTCKEQOTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
QY 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTAALPRERLRPRKPVFL 360
DB 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTAALPRERLRPRKPVFL 360
QY 361 CYSKQGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
DB 361 CYSKQGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
QY 421 VCSKGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
DB 421 VCSKGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
QY 481 DVSCEBDVGIILDLSTKYRLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYPFSKSGR 540
DB 481 DVSCEBDVGIILDLSTKYRLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYPFSKSGR 540
QY 541 SLVVAICNMHQFTIDEBPDMFEKQFVPHPPPLRYREPVLEKFDPSGLVNDVWCKPESD 600
DB 541 SLVVAICNMHQFTIDEBPDMFEKQFVPHPPPLRYREPVLEKFDPSGLVNDVWCKPESD 600
QY 601 FCUKVEAPVLAGATGPADSGHESQHGLDQDGEARPALDGSAALOPLHTVKAQSPSDMPR 660
DB 601 FCUKVEAPVLAGATGPADSGHESQHGLDQDGEARPALDGSAALOPLHTVKAQSPSDMPR 660
QY 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAAVAP 738
DB 721 KADLCGRSYTDELHAAVAP 738

RESULT 6
US-10-717-282-8
; Sequence 8, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PaacSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-717-282-8
Query Match 99.2%; Score 3918; DB 4; Length 739;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAMPWLOLCGVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITPKY 60
DB 1 MAMPWLOLCGVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITPKY 60
QY 61 DICTTYLANPVGKVIADANQNTTISQYACHDQVAVTILMSPGALGIEFLKGFVILEELKS 120
DB 61 DICTTYLANPVGKVIADANQNTTISQYACHDQVAVTILMSPGALGIEFLKGFVILEELKS 120
QY 121 EGRQCOQLILKDKPKOLNSFKRTGMSQPLNMKEETDYFVYVPPPSIKNSNHPFF 180
DB 121 EGRQCOQLILKDKPKOLNSFKRTGMSQPLNMKEETDYFVYVPPPSIKNSNHPFF 180
QY 181 RTACDILLQPDNLACKPMPKPRNLNISQHSQDMQVSPDHAHPNFGFRFFYLHYKLKHG 240
DB 181 RTACDILLQPDNLACKPMPKPRNLNISQHSQDMQVSPDHAHPNFGFRFFYLHYKLKHG 240
QY 241 PFRKRTCKEQOTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
DB 241 PFRKRTCKEQOTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
QY 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTAALPRERLRPRKPVFL 360
DB 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTAALPRERLRPRKPVFL 360
QY 361 CYSKQGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
DB 361 CYSKQGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
QY 421 VCSKGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
DB 421 VCSKGMKRYFVDKKNYKKGSGSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFLAVYF 480
QY 481 DVSCEBDVGIILDLSTKYRLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYPFSKSGR 540
DB 481 DVSCEBDVGIILDLSTKYRLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYPFSKSGR 540
QY 541 SLVVAICNMHQFTIDEBPDMFEKQFVPHPPPLRYREPVLEKFDPSGLVNDVWCKPESD 600
DB 541 SLVVAICNMHQFTIDEBPDMFEKQFVPHPPPLRYREPVLEKFDPSGLVNDVWCKPESD 600
QY 601 FCUKVEAPVLAGATGPADSGHESQHGLDQDGEARPALDGSAALOPLHTVKAQSPSDMPR 660
DB 601 FCUKVEAPVLAGATGPADSGHESQHGLDQDGEARPALDGSAALOPLHTVKAQSPSDMPR 660
QY 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAAVAP 738
DB 721 KADLCGRSYTDELHAAVAP 738

RESULT 7
US-10-842-006-2
; Sequence 2, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; APPLICANT: Therefor
; TITLE OF INVENTION: A Novel Human SRF Molecule and Uses
; FILE REFERENCE: MP103-07191PM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08

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NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PaSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 739
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-842-006-2

Query Match 99.0%; Score 3908; DB 5; Length 739;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAWMLQCSVFYFNACLSQSLAAGSGGRAGVDTCCMRGVPASRNSGLNITPKY 60
 DB 1 MAWMLQCSVFYFNACLSQSLAAGSGGRAGVDTCCMRGVPASRNSGLNITPKY 60
 QY 61 DNTCTYANPVGKVIADQNIITISQYACHQVAVTILMSGALGIEFLKGFVILELKS 120
 DB 61 DNTCTYANPVGKVIADQNIITISQYACHQVAVTILMSGALGIEFLKGFVILELKS 120
 QY 121 EGRQCOQLIKDPKOLNSFKRTGMSQPLNKKFETDYVKKVPPPSINBSNYHPPF 180
 DB 121 EGRQCOQLIKDPKOLNSFKRTGMSQPLNKKFETDYVKKVPPPSINBSNYHPPF 180
 QY 181 RTACDILLQPDNLACPFKPRNLNISOHSDMOVSFDHAPHNFGFRFYLYKLGHEG 240
 DB 181 RTACDILLQPDNLACPFKPRNLNISOHSDMOVSFDHAPHNFGFRFYLYKLGHEG 240
 QY 241 PPRKCTCKOQTETTSCLQONSPGDIYIELVDNTTRKVMHYALKPVHSPWAGPIRA 300
 DB 241 PPRKCTCKOQTETTSCLQONSPGDIYIELVDNTTRKVMHYALKPVHSPWAGPIRA 300
 QY 301 MATVPLVISAFAITLFTWCRKKQENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
 DB 301 MATVPLVISAFAITLFTWCRKKQENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
 QY 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDESLCREGOREWVIOKIHESQPIIV 420
 DB 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDESLCREGOREWVIOKIHESQPIIV 420
 QY 421 VCSKGMKTFYDKKQYKKGGRSGKGEFLVAVSAIAEKLRAKQSSSALSFIAVVF 480
 DB 421 VCSKGMKTFYDKKQYKKGGRSGKGEFLVAVSAIAEKLRAKQSSSALSFIAVVF 480
 QY 481 DYCCEGVPGLDLSTKYRLMDNLPOLCSHLHSDHGLQEPGQHTROGSRNRYFRSKGR 540
 DB 481 DYCCEGVPGLDLSTKYRLMDNLPOLCSHLHSDHGLQEPGQHTROGSRNRYFRSKGR 540
 QY 541 SLVVAICNMHQFLIDEBPDWFEKQFVPHPPPLRYREBVLKFPDGLVANDVMCKPGESE 600
 DB 541 SLVVAICNMHQFLIDEBPDWFEKQFVPHPPPLRYREBVLKFPDGLVANDVMCKPGESE 600
 QY 601 FCLEKVEAPVIGAGPADSOHSHQHGIDQGEARPALDGAALQPLHTYKASPSMPR 660
 DB 601 FCLEKVEAPVIGAGPADSOHSHQHGIDQGEARPALDGAALQPLHTYKASPSMPR 660
 QY 661 DSGIYSSVSSSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLLSSGSC 720
 DB 661 DSGIYSSVSSSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLLSSGSC 720
 QY 721 KADLCRSYTDLHAAP 738
 DB 721 KADLCRSYTDLHAAP 738

RESULT 8
 US-10-608-449-2
 Sequence 2, Application US/10608449
 Publication No. US20040265834A1
 GENERAL INFORMATION:
 APPLICANT: Tsinghua University
 TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
 FILE REFERENCE: 12003269C-US

CURRENT APPLICATION NUMBER: US/10/608,449
 CURRENT FILING DATE: 2003-06-30
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 739
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-608-449-2

Query Match 99.0%; Score 3908; DB 5; Length 739;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAWMLQCSVFYFNACLSQSLAAGSGGRAGVDTCCMRGVPASRNSGLNITPKY 60
 DB 1 MAWMLQCSVFYFNACLSQSLAAGSGGRAGVDTCCMRGVPASRNSGLNITPKY 60
 QY 61 DNTCTYANPVGKVIADQNIITISQYACHQVAVTILMSGALGIEFLKGFVILELKS 120
 DB 61 DNTCTYANPVGKVIADQNIITISQYACHQVAVTILMSGALGIEFLKGFVILELKS 120
 QY 121 EGRQCOQLIKDPKOLNSFKRTGMSQPLNKKFETDYVKKVPPPSINBSNYHPPF 180
 DB 121 EGRQCOQLIKDPKOLNSFKRTGMSQPLNKKFETDYVKKVPPPSINBSNYHPPF 180
 QY 181 RTACDILLQPDNLACPFKPRNLNISOHSDMOVSFDHAPHNFGFRFYLYKLGHEG 240
 DB 181 RTACDILLQPDNLACPFKPRNLNISOHSDMOVSFDHAPHNFGFRFYLYKLGHEG 240
 QY 241 PPRKCTCKOQTETTSCLQONSPGDIYIELVDNTTRKVMHYALKPVHSPWAGPIRA 300
 DB 241 PPRKCTCKOQTETTSCLQONSPGDIYIELVDNTTRKVMHYALKPVHSPWAGPIRA 300
 QY 301 MATVPLVISAFAITLFTWCRKKQENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
 DB 301 MATVPLVISAFAITLFTWCRKKQENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
 QY 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDESLCREGOREWVIOKIHESQPIIV 420
 DB 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDESLCREGOREWVIOKIHESQPIIV 420
 QY 421 VCSKGMKTFYDKKQYKKGGRSGKGEFLVAVSAIAEKLRAKQSSSALSFIAVVF 480
 DB 421 VCSKGMKTFYDKKQYKKGGRSGKGEFLVAVSAIAEKLRAKQSSSALSFIAVVF 480
 QY 481 DYCCEGVPGLDLSTKYRLMDNLPOLCSHLHSDHGLQEPGQHTROGSRNRYFRSKGR 540
 DB 481 DYCCEGVPGLDLSTKYRLMDNLPOLCSHLHSDHGLQEPGQHTROGSRNRYFRSKGR 540
 QY 541 SLVVAICNMHQFLIDEBPDWFEKQFVPHPPPLRYREBVLKFPDGLVANDVMCKPGESE 600
 DB 541 SLVVAICNMHQFLIDEBPDWFEKQFVPHPPPLRYREBVLKFPDGLVANDVMCKPGESE 600
 QY 601 FCLEKVEAPVIGAGPADSOHSHQHGIDQGEARPALDGAALQPLHTYKASPSMPR 660
 DB 601 FCLEKVEAPVIGAGPADSOHSHQHGIDQGEARPALDGAALQPLHTYKASPSMPR 660
 QY 661 DSGIYSSVSSSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLLSSGSC 720
 DB 661 DSGIYSSVSSSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLLSSGSC 720
 QY 721 KADLCRSYTDLHAAP 738
 DB 721 KADLCRSYTDLHAAP 738

RESULT 9
 US-09-912-157-2
 Sequence 2, Application US/09912157
 Patent No. US20020165348A1
 GENERAL INFORMATION:
 APPLICANT: Preenell, Scott R.

; APPLICANT: Kuestner, Rolf E.
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Human Cytokine Receptor
 ; FILE REFERENCE: 00-49
 ; CURRENT APPLICATION NUMBER: US/09/912.157
 ; CURRENT FILING DATE: 2001-07-23
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FaastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 753
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-912-157-2

Query Match 98.8%; Score 3901; DB 3; Length 753;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWQLCSVFPTVNACLNGSOLA VAAAGSGRAGVDTGMR-----GVGP 46
 DB 1 MAPWQLCSVFPTVNACLNGSOLA VAAAGSGRAGVDTGMRKKAARPLCVANGVGP 60
 QY 47 ASNSGLNITFRYNDCTTYLNPVGKRVADADONTTISQYACHDQYAVTILMSPGALGIE 106
 DB 61 ASNSGLNITFRYNDCTTYLNPVGKRVADADONTTISQYACHDQYAVTILMSPGALGIE 120
 QY 107 FLKGFVILIELSEGRQCOQLILKDPKOLNSFKRTGMSOPFLMKKETDYPFVAVPF 166
 DB 121 FLKGFVILIELSEGRQCOQLILKDPKOLNSFKRTGMSOPFLMKKETDYPFVAVPF 180
 QY 167 PSIKESNHYHPPFRTTRACDLLLPDNLACKPFWKPRNLNISOHSDMVSPDHAHPNFG 226
 DB 181 PSIKESNHYHPPFRTTRACDLLLPDNLACKPFWKPRNLNISOHSDMVSPDHAHPNFG 240
 QY 227 PRFFLYHYLKHGPPKRTCKOBTETTSCLONVSGDYIIELVDTNTTRKMYHA 286
 DB 241 PRFFLYHYLKHGPPKRTCKOBTETTSCLONVSGDYIIELVDTNTTRKMYHA 300
 QY 287 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTA 346
 DB 301 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTA 360
 QY 347 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLDPCGCEVALDLMEDFSLCREGORE 406
 DB 361 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLDPCGCEVALDLMEDFSLCREGORE 420
 QY 407 WYIQTIESQFIIVVCSKGMKTFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAQ 466
 DB 421 WYIQTIESQFIIVVCSKGMKTFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAQ 480
 QY 467 SSSAALSKFIAYFYDSCGSDVPGILDLSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 526
 DB 481 SSSAALSKFIAYFYDSCGSDVPGILDLSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 540
 QY 527 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPPMFEKQFVPFHPPLRYRPEVLEKDSGL 586
 DB 541 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPPMFEKQFVPFHPPLRYRPEVLEKDSGL 600
 QY 587 VLANDVWCKGPPESDFCLKYEAAPVLGATGPADSOHESOHGGLDODGEARPALDGSALQPL 646
 DB 601 VLANDVWCKGPPESDFCLKYEAAPVLGATGPADSOHESOHGGLDODGEARPALDGSALQPL 660
 QY 647 LHTVYAGSPDMPRDSGIYDSSVPSSELPLMEGLSTQOTETSLTESVSSSGLGEEB 706
 DB 661 LHTVYAGSPDMPRDSGIYDSSVPSSELPLMEGLSTQOTETSLTESVSSSGLGEEB 720
 QY 707 PPALPSKLLSSGSKADLCGRSYTDELHNAVAP 738
 DB 721 PPALPSKLLSSGSKADLCGRSYTDELHNAVAP 752

RESULT 10
 US-10-717-282-2

; Sequence 2, Application US/10717282
 ; Publication No. US20040077052A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Kuestner, Rolf E.
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Human Cytokine Receptor
 ; FILE REFERENCE: 00-49
 ; CURRENT APPLICATION NUMBER: US/10/717,282
 ; CURRENT FILING DATE: 2003-11-19
 ; PRIOR APPLICATION NUMBER: US/09/912,157
 ; PRIOR FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FaastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 753
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-717-282-2

Query Match 98.8%; Score 3901; DB 4; Length 753;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWQLCSVFPTVNACLNGSOLA VAAAGSGRAGVDTGMR-----GVGP 46
 DB 1 MAPWQLCSVFPTVNACLNGSOLA VAAAGSGRAGVDTGMRKKAARPLCVANGVGP 60
 QY 47 ASNSGLNITFRYNDCTTYLNPVGKRVADADONTTISQYACHDQYAVTILMSPGALGIE 106
 DB 61 ASNSGLNITFRYNDCTTYLNPVGKRVADADONTTISQYACHDQYAVTILMSPGALGIE 120
 QY 107 FLKGFVILIELSEGRQCOQLILKDPKOLNSFKRTGMSOPFLMKKETDYPFVAVPF 166
 DB 121 FLKGFVILIELSEGRQCOQLILKDPKOLNSFKRTGMSOPFLMKKETDYPFVAVPF 180
 QY 167 PSIKESNHYHPPFRTTRACDLLLPDNLACKPFWKPRNLNISOHSDMVSPDHAHPNFG 226
 DB 181 PSIKESNHYHPPFRTTRACDLLLPDNLACKPFWKPRNLNISOHSDMVSPDHAHPNFG 240
 QY 227 PRFFLYHYLKHGPPKRTCKOBTETTSCLONVSGDYIIELVDTNTTRKMYHA 286
 DB 241 PRFFLYHYLKHGPPKRTCKOBTETTSCLONVSGDYIIELVDTNTTRKMYHA 300
 QY 287 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTA 346
 DB 301 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTA 360
 QY 347 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLDPCGCEVALDLMEDFSLCREGORE 406
 DB 361 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLDPCGCEVALDLMEDFSLCREGORE 420
 QY 407 WYIQTIESQFIIVVCSKGMKTFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAQ 466
 DB 421 WYIQTIESQFIIVVCSKGMKTFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAQ 480
 QY 467 SSSAALSKFIAYFYDSCGSDVPGILDLSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 526
 DB 481 SSSAALSKFIAYFYDSCGSDVPGILDLSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 540
 QY 527 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPPMFEKQFVPFHPPLRYRPEVLEKDSGL 586
 DB 541 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPPMFEKQFVPFHPPLRYRPEVLEKDSGL 600
 QY 587 VLANDVWCKGPPESDFCLKYEAAPVLGATGPADSOHESOHGGLDODGEARPALDGSALQPL 646
 DB 601 VLANDVWCKGPPESDFCLKYEAAPVLGATGPADSOHESOHGGLDODGEARPALDGSALQPL 660
 QY 647 LHTVYAGSPDMPRDSGIYDSSVPSSELPLMEGLSTQOTETSLTESVSSSGLGEEB 706
 DB 661 LHTVYAGSPDMPRDSGIYDSSVPSSELPLMEGLSTQOTETSLTESVSSSGLGEEB 720
 QY 707 PPALPSKLLSSGSKADLCGRSYTDELHNAVAP 738

Db 721 PPALPSKTLSSSGCKADLCGRSTYDELHAAVAP 752

|||||

RESULT 11

US-09-912-157-5

Sequence 5, Application US/09912157

Patent No. US20020165348A1

GENERAL INFORMATION:

APPLICANT: Presnell, Scott R.

APPLICANT: Kuestner, Rolf E.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: Human Cytokine Receptor

FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/09/912.157

CURRENT FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 753

TYPE: PRT

ORGANISM: Homo sapiens

US-09-912-157-5

Query Match 98.6%; Score 3891; DB 3; Length 753;

Best Local Similarity 97.3%; Pred. No. 0;

Matches 732; Conservative 1; Mismatches 5; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFTVNACLNGSOLAAGSGRAMGVDTGMR-----GVGP 46

Db 1 MAPWLQCSVFTVNACLNGSOLAAGSGRAMGVDTGMRKKAARPRLCVANGVGP 60

Qy 47 ASNSGLYNTFFKYDCTTYLNPVGHVADAOINITISQYACHDQVAVTILMSPGALGIR 106

Db 61 ASNSGLYNTFFKYDCTTYLNPVGHVADAOINITISQYACHDQVAVTILMSPGALGIR 120

Qy 107 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVP 166

Db 121 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVP 180

Qy 167 PSIKNSNTHPFFFRTRACDLLOPDNLACKPFWKPRNLNISQHSQDMQVSPHAPHNFG 226

Db 181 PSIKNSNTHPFFFRTRACDLLOPDNLACKPFWKPRNLNISQHSQDMQVSPHAPHNFG 240

Qy 227 FRFFYLHYLKHGPPKRTCKOQTETTSCLQNVSPGDYIILVDDTNTTRKVMHYA 286

Db 241 FRFFYLHYLKHGPPKRTCKOQTETTSCLQNVSPGDYIILVDDTNTTRKVMHYA 300

Qy 287 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENIYSHLDESSSSSTYTAA 346

Db 301 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENIYSHLDESSSSSTYTAA 360

Qy 347 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSICREGORE 406

Db 361 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSICREGORE 420

Qy 407 WVIQKHESQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVASIAEKLQAQK 466

Db 421 WVIQKHESQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVASIAEKLQAQK 480

Qy 467 SSSAALSKPIAYFYDYSCGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPQOHR 526

Db 481 SSSAALSKPIAYFYDYSCGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPQOHR 540

Qy 527 QGSRNRYFSSKSGRSLYVAICNMHOFIDBEPWFKEQFVFPHPPLRYRBPVLEKFDGSL 586

Db 541 QGSRNRYFSSKSGRSLYVAICNMHOFIDBEPWFKEQFVFPHPPLRYRBPVLEKFDGSL 600

Qy 587 VLNDVNCCKPESDFCLKVAAPVLTGATGPADSQHESQHGGLDQGEARPALDGSALQPL 646

Db 601 VLNDVNCCKPESDFCLKVAAPVLTGATGPADSQHESQHGGLDQGEARPALDGSALQPL 660

Qy 647 LHTVKAQSPBDMRDGIDYSSVPSSELPLMEGLSTQDTETTSILTESVSSSSGIGEEZ 706

Db 661 LHTVKAQSPBDMRDGIDYSSVPSSELPLMEGLSTQDTETTSILTESVSSSSGIGEEZ 720

|||||

RESULT 12

US-10-717-282-5

Sequence 5, Application US/10717282

Publication No. US2004007052A1

GENERAL INFORMATION:

APPLICANT: Presnell, Scott R.

APPLICANT: Kuestner, Rolf E.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: Human Cytokine Receptor

FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/10/717.282

CURRENT FILING DATE: 2003-11-19

PRIOR APPLICATION NUMBER: US/09/912.157

PRIOR FILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 753

TYPE: PRT

ORGANISM: Homo sapiens

US-10-717-282-5

Query Match 98.6%; Score 3891; DB 4; Length 753;

Best Local Similarity 97.3%; Pred. No. 0;

Matches 732; Conservative 1; Mismatches 5; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFTVNACLNGSOLAAGSGRAMGVDTGMR-----GVGP 46

Db 1 MAPWLQCSVFTVNACLNGSOLAAGSGRAMGVDTGMRKKAARPRLCVANGVGP 60

Qy 47 ASNSGLYNTFFKYDCTTYLNPVGHVADAOINITISQYACHDQVAVTILMSPGALGIR 106

Db 61 ASNSGLYNTFFKYDCTTYLNPVGHVADAOINITISQYACHDQVAVTILMSPGALGIR 120

Qy 107 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVP 166

Db 121 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVP 180

Qy 167 PSIKNSNTHPFFFRTRACDLLOPDNLACKPFWKPRNLNISQHSQDMQVSPHAPHNFG 226

Db 181 PSIKNSNTHPFFFRTRACDLLOPDNLACKPFWKPRNLNISQHSQDMQVSPHAPHNFG 240

Qy 227 FRFFYLHYLKHGPPKRTCKOQTETTSCLQNVSPGDYIILVDDTNTTRKVMHYA 286

Db 241 FRFFYLHYLKHGPPKRTCKOQTETTSCLQNVSPGDYIILVDDTNTTRKVMHYA 300

Qy 287 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENIYSHLDESSSSSTYTAA 346

Db 301 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENIYSHLDESSSSSTYTAA 360

Qy 347 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSICREGORE 406

Db 361 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSICREGORE 420

Qy 407 WVIQKHESQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVASIAEKLQAQK 466

Db 421 WVIQKHESQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVASIAEKLQAQK 480

Qy 467 SSSAALSKPIAYFYDYSCGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPQOHR 526

Db 481 SSSAALSKPIAYFYDYSCGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPQOHR 540

Qy 527 QGSRNRYFSSKSGRSLYVAICNMHOFIDBEPWFKEQFVFPHPPLRYRBPVLEKFDGSL 586

Db 541 QGSRNRYFSSKSGRSLYVAICNMHOFIDBEPWFKEQFVFPHPPLRYRBPVLEKFDGSL 600

QY 587 VLVNDWCKPESDPCFLKVEAPVLTGATGPADSGHESQHGGLDDGGEARPALDSSAALQPL 646
 DB 601 VLVNDWCKPESDPCFLKVEAPVLTGATGPADSGHESQHGGLDDGGEARPALDSSAALQPL 660
 QY 647 LHTVKAQSPDMRDSGIDYSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEER 706
 DB 661 LHTVKAQSPDMRDSGIDYSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEER 720
 QY 707 PPLPESKLLSSGCKADLCGRSTYDELHAAVAP 738
 DB 721 PPLPESKLLSSGCKADLCGRSTYDELHAAVAP 752

RESULT 13
 US-09-863-818A-10
 / Sequence 10, Application US/09863818A
 / Publication No. US20030092881A1
 / GENERAL INFORMATION:
 / APPLICANT: Gorman, Daniel M.
 / TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
 / FILE REFERENCE: DX01170K
 / CURRENT APPLICATION NUMBER: US/09/863,818A
 / PRIOR FILING DATE: 2001-05-23
 / PRIOR APPLICATION NUMBER: US 60/206,862
 / PRIOR FILING DATE: 2000-05-24
 / NUMBER OF SEQ ID NOS: 22
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 10
 / LENGTH: 738
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (18)..(18)
 / OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
 / NAME/KEY: misc_feature
 / LOCATION: (26)..(26)
 / OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
 / NAME/KEY: misc_feature
 / LOCATION: (109)..(109)
 / OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
 / NAME/KEY: misc_feature
 / LOCATION: (120)..(120)
 / OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
 / NAME/KEY: misc_feature
 / LOCATION: (134)..(134)
 / OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
 / NAME/KEY: misc_feature
 / LOCATION: (8)..(8)
 / OTHER INFORMATION: unknown amino
 / NAME/KEY: misc_feature
 / LOCATION: (144)..(144)
 / OTHER INFORMATION: unknown amino
 / NAME/KEY: misc_feature
 / LOCATION: (170)..(170)
 / OTHER INFORMATION: unknown amino
 / NAME/KEY: misc_feature
 / LOCATION: (194)..(194)
 / OTHER INFORMATION: unknown amino
 / NAME/KEY: misc_feature
 / LOCATION: (442)..(442)
 / OTHER INFORMATION: unknown amino
 / NAME/KEY: misc_feature
 / LOCATION: (475)..(475)
 / OTHER INFORMATION: unknown amino
 / NAME/KEY: misc_feature
 / LOCATION: (519)..(519)
 / OTHER INFORMATION: unknown amino
 / US-09-863-818A-10

Query Match 97.2%; Score 3835.5; DB 3; Length 738;
 Best Local Similarity 97.8%; Pred. No. 0;

Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;
 QY 1 MAPWLOLGVFPFTVNACLNGSOLAFAAGSGRAMGVDTGQWGVGPASRNSGLYNTTFKY 60
 DB 1 MAPWLOLGVFPFTVNACLNGSOLAFAAGSGRAMGVDTGQWGVGPASRNSGLYNTTFKY 60
 QY 61 DICTTYLANVGVKAVIADAQNTTISQYACHDOVAVITLWSPGALGIEFLGFRVILELKS 120
 DB 61 DICTTYLANVGVKAVIADAQNTTISQYACHDOVAVITLWSPGALGIEFLGFRVILELKS 120
 QY 121 EGRQCOQLIKDPKQINSFKRTGMSOPPLNKKFETDYFKVVPSPISKNBNHPFF 180
 DB 121 EGRQCOQLIKDPKQINSFKRTGMSOPPLNKKFETDYFKVVPSPISKNBNHPFF 179
 QY 181 RTKACDILLQPNLACKPFWKPRNLTISQHSQDMOVSFPHAPNRFPRFYLYLKHG 240
 DB 181 RTKACDILLQPNLACKPFWKPRNLTISQHSQDMOVSFPHAPNRFPRFYLYLKHG 239
 QY 241 PFKRTCKQEQETTESCLQNVSPDYIIEIVDNTTRKVMHYALKEVHSPMAGPIRA 300
 DB 241 PFKRTCKQEQETTESCLQNVSPDYIIEIVDNTTRKVMHYALKEVHSPMAGPIRA 299
 QY 301 MATVPLVVISAPAILFTWCRKQOENIYSHLDESSSTYTAALPRELRPRPKVL 360
 DB 301 MATVPLVVISAPAILFTWCRKQOENIYSHLDESSSTYTAALPRELRPRPKVL 359
 QY 361 CYSSKQGNHNVVOCFAFLDPCGCEVALDMEBPSLCRSGQREWVLOKHESQFTIV 420
 DB 361 CYSSKQGNHNVVOCFAFLDPCGCEVALDMEBPSLCRSGQREWVLOKHESQFTIV 419
 QY 421 VCSKGMKVFVDKKNYGHKGRSGSGKGLFLVAVSAIAEKLQAQSSAALSKPIAVYF 480
 DB 421 VCSKGMKVFVDKKNYGHKGRSGSGKGLFLVAVSAIAEKLQAQSSAALSKPIAVYF 479
 QY 481 DYSCEGDVPIILDSTKYFLMDNLPOLCSHLHSRDHGLPEQOHTQSGRRNYFRSKGR 540
 DB 481 DYSCEGDVPIILDSTKYFLMDNLPOLCSHLHSRDHGLPEQOHTQSGRRNYFRSKGR 539
 QY 541 SLVYALCMNHQRIIDEPDMEKQFVFPHPPLRYRBPVLEKDSGLVNDWCKPESD 600
 DB 541 SLVYALCMNHQRIIDEPDMEKQFVFPHPPLRYRBPVLEKDSGLVNDWCKPESD 599
 QY 601 FCLKVEAPVLTGATGPADSGHESQHGGLDDGGEARPALDSSAALQPLLHTVKAQSPDMR 660
 DB 601 FCLKVEAPVLTGATGPADSGHESQHGGLDDGGEARPALDSSAALQPLLHTVKAQSPDMR 659
 QY 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEERPALPSKLLSSGSC 720
 DB 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEERPALPSKLLSSGSC 719
 QY 721 KADLCGRSTYDELHAAVAP 738
 DB 721 KADLCGRSTYDELHAAVAP 737

RESULT 14
 US-10-749-144-10
 / Sequence 10, Application US/10749144
 / Publication No. US20040197306A1
 / GENERAL INFORMATION:
 / APPLICANT: Gorman, Daniel M.
 / TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
 / FILE REFERENCE: DX01170K1
 / CURRENT APPLICATION NUMBER: US/10/749,144
 / PRIOR FILING DATE: 2003-12-29
 / PRIOR APPLICATION NUMBER: US 60/206,862
 / PRIOR FILING DATE: 2000-05-24
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 10
 / LENGTH: 738
 / TYPE: PRT
 / ORGANISM: Homo sapiens

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FEATURE:
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
FEATURE:
NAME/KEY: misc feature
LOCATION: (26)..(26)
OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
FEATURE:
NAME/KEY: misc feature
LOCATION: (109)..(109)
OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
FEATURE:
NAME/KEY: misc feature
LOCATION: (120)..(120)
OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (134)..(134)
OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
US-10-749-144-10

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Query Match          97.2%; Score 3835.5; DB 4; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

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QY 1 MAEWLQCSVFTYVNAALNGSQLAAVANGSGRAWGVDTCCRGVGPASRNSGLYNTTFKY 60
DB 1 MAEWLQCSVFTYVNAALNGSQLAAVANGSGRAWGVDTCCRGVGPASRNSGLYNTTFKY 60
QY 61 DNTCTYINPVGKVIADAQNTTISOVACHOVANTILMSGALIEFLKPRVLEELKS 120
DB 61 DNTCTYINPVGKVIADAQNTTISOVACHOVANTILMSGALIEFLKPRVLEELKS 120
QY 121 EGRQCOQLIKDPRKQNSSFKRTGMSQPLANKFETDYFKVVPFSIKNESYHPPFP 180
DB 121 EGRQCOQLIKDPRKQNSSFKRTGMSQPLANKFETDYFKVVPFSIKNESYHPPFP 180
QY 181 RTBACDILLOPDLNACPKPKNLNTISOHSDQVSPDHAHNFGFRFYLYHKLHEG 240
DB 181 RTBACDILLOPDLNACPKPKNLNTISOHSDQVSPDHAHNFGFRFYLYHKLHEG 240
QY 241 PPRKCTCKOQTETTSCLLONSRQYIIEVDVTTTKRMVYALAKPHSPAGIRA 300
DB 241 PPRKCTCKOQTETTSCLLONSRQYIIEVDVTTTKRMVYALAKPHSPAGIRA 300
QY 301 MATVPLVVSAPATLFTVMCRKQKQENIYSHLDESSSSTYPAALPRELRPRPVFL 360
DB 301 MATVPLVVSAPATLFTVMCRKQKQENIYSHLDESSSSTYPAALPRELRPRPVFL 360
QY 361 CYSSKQGNMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQPIV 420
DB 361 CYSSKQGNMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQPIV 420
QY 421 VCSKGMKTFYDKKRYKRGSGSGKQELFLVAVSAIAEKLRAKQKSSAALSTFIAYVF 480
DB 421 VCSKGMKTFYDKKRYKRGSGSGKQELFLVAVSAIAEKLRAKQKSSAALSTFIAYVF 480
QY 481 DYCCEGDPVGLDSTKYRLMDNLPOCSHLHSRHDHLOEPGQHTRGSSRNYRYSRSGR 540
DB 481 DYCCEGDPVGLDSTKYRLMDNLPOCSHLHSRHDHLOEPGQHTRGSSRNYRYSRSGR 540
QY 541 SLVVAICNMHQFIDEBDFWEKQFVPPHPPRLRYREPLLEKFPDGLVANDVMCKPGBSD 600
DB 541 SLVVAICNMHQFIDEBDFWEKQFVPPHPPRLRYREPLLEKFPDGLVANDVMCKPGBSD 600
QY 601 FCLKVEAPVLDGAPADSOHSHQGLDQGEARPAIDGSAALQPLAHYKAGSPSPMPR 660
DB 601 FCLKVEAPVLDGAPADSOHSHQGLDQGEARPAIDGSAALQPLAHYKAGSPSPMPR 660
QY 661 DSGIYDSSVSSSLPLMEGLSTDOTETSLTSSVSSSGGLGEEPPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVSSSLPLMEGLSTDOTETSLTSSVSSSGGLGEEPPPALPSKLLSSGSC 720

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QY 721 KADLCRSTYDEHNAVAP 738
DB 720 KADLCRSTYDEHNAVAP 737

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RESULT 15

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US-10-924-667-10
Sequence 10, Application US/10924667
Publication No. US20050009145A1
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND
METHODS
FILE REFERENCES: DX01170K
CURRENT APPLICATION NUMBER: US/10/924,667
CURRENT FILING DATE: 2004-08-23
PRIOR APPLICATION NUMBER: US/09/863,818
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,862
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 738
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or
Leu.
FEATURE:
NAME/KEY: misc feature
LOCATION: (26)..(26)
OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or
Met.
FEATURE:
NAME/KEY: misc feature
LOCATION: (109)..(109)
OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or
Cys.
FEATURE:
NAME/KEY: misc feature
LOCATION: (120)..(120)
OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or
Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (134)..(134)
OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (144)..(144)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc feature
LOCATION: (145)..(145)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc feature
LOCATION: (170)..(170)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc feature
LOCATION: (194)..(194)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc feature
LOCATION: (442)..(442)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc feature

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; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-10-924-667-10
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Query Match 97.2%; Score 3835.5; DB 5; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

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QY 1 MAPWLQCSVFVFNACINSQLAVAAGSGRAMGVDTCCMGVGPASRNSGLYNITFKY 60
DB 1 MAPWLQCSVFVFNACINSQLAVAAGSGRAMGVDTCCMGVGPASRNSGLYNITFKY 60
QY 61 DNCTTYLNPVGKVIADANQNTTISQYACHDQVAVTILMSPALGIEFLKGFVILEELKS 120
DB 61 DNCTTYLNPVGKVIADANQNTTISQYACHDQVAVTILMSPALGIEFLKGFVILEELKS 120
QY 121 EGRQCOQLIKDKPKQLNSSFRTGMSQPLNKKFETDYFVKVVPSPSICNBSNTHPPFP 180
DB 121 EGRQCOQLIKDKPKQLNSSFRTGMSQPLNKKFETDYFVKVVPSPSICNBSNTHPPFP 180
QY 121 EGRQCOQLIKDKPKQLNSSFRTGMSQPLNKKFETDYFVKVVPSPSICNBSNTHPPFP 179
DB 121 EGRQCOQLIKDKPKQLNSSFRTGMSQPLNKKFETDYFVKVVPSPSICNBSNTHPPFP 179
QY 181 RTACDLLOPDNLACKPFKPRNLNISQHSQDMQVSFDHAPNPFGRFPYLYKLKHEG 240
DB 181 RTACDLLOPDNLACKPFKPRNLNISQHSQDMQVSFDHAPNPFGRFPYLYKLKHEG 240
QY 241 PFRKCTCKOBTETTSCLLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPWAGPIRA 300
DB 241 PFRKCTCKOBTETTSCLLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPWAGPIRA 300
QY 240 PFRKCTCKOBTETTSCLLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPWAGPIRA 299
DB 240 PFRKCTCKOBTETTSCLLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPWAGPIRA 299
QY 301 MATTVPLVVISAPATLFTWCRKKQENITSHLDESSSESTYTAALPRRLRPRPKVFL 360
DB 301 MATTVPLVVISAPATLFTWCRKKQENITSHLDESSSESTYTAALPRRLRPRPKVFL 360
QY 300 VAITVPLVVISAPATLFTWCRKKQENITSHLDESSSESTYTAALPRRLRPRPKVFL 359
DB 300 VAITVPLVVISAPATLFTWCRKKQENITSHLDESSSESTYTAALPRRLRPRPKVFL 359
QY 361 CYSKKGQNMNVVOCFAVFLQDFCGCEVALDLMEPSLCREGOREWVIOKIHESQPIIV 420
DB 361 CYSKKGQNMNVVOCFAVFLQDFCGCEVALDLMEPSLCREGOREWVIOKIHESQPIIV 420
QY 360 CYSKKGQNMNVVOCFAVFLQDFCGCEVALDLMEPSLCREGOREWVIOKIHESQPIIV 419
DB 360 CYSKKGQNMNVVOCFAVFLQDFCGCEVALDLMEPSLCREGOREWVIOKIHESQPIIV 419
QY 421 VCSKGMKYPVDKKNYKHGGGSGSGKGEFLVAVSAIAEKLROAKOSSNALSKEFLAVVF 480
DB 421 VCSKGMKYPVDKKNYKHGGGSGSGKGEFLVAVSAIAEKLROAKOSSNALSKEFLAVVF 480
QY 420 VCSKGMKYPVDKKNYKHGGGSGSGKGEFLVAVSAIAEKLROAKOSSNALSKEFLAVVF 479
DB 420 VCSKGMKYPVDKKNYKHGGGSGSGKGEFLVAVSAIAEKLROAKOSSNALSKEFLAVVF 479
QY 481 DYSCEBDVPGIILSTKYRLMDNLPCSLHSHRDHGLQEPGQHTROGSRNRYFRSKSGR 540
DB 481 DYSCEBDVPGIILSTKYRLMDNLPCSLHSHRDHGLQEPGQHTROGSRNRYFRSKSGR 540
QY 480 DYSCEBDVPGIILSTKYRLMDNLPCSLHSHRDHGLQEPGQHTROGSRNRYFRSKSGR 539
DB 480 DYSCEBDVPGIILSTKYRLMDNLPCSLHSHRDHGLQEPGQHTROGSRNRYFRSKSGR 539
QY 541 SLTYVALCNMHQFIDEBDPMEFKQFVPPHPPRLRYREPVLEKFPDGLVANDVCKPGPESD 600
DB 541 SLTYVALCNMHQFIDEBDPMEFKQFVPPHPPRLRYREPVLEKFPDGLVANDVCKPGPESD 600
QY 540 SLTYVALCNMHQFIDEBDPMEFKQFVPPHPPRLRYREPVLEKFPDGLVANDVCKPGPESD 599
DB 540 SLTYVALCNMHQFIDEBDPMEFKQFVPPHPPRLRYREPVLEKFPDGLVANDVCKPGPESD 599
QY 601 FCLKVEAPVLGATGPADSQHSQHGLDQGEARPALDGSALQPLLHTVYKAGSPSDMPR 660
DB 601 FCLKVEAPVLGATGPADSQHSQHGLDQGEARPALDGSALQPLLHTVYKAGSPSDMPR 660
QY 600 FCLKVEAPVLGATGPADSQHSQHGLDQGEARPALDGSALQPLLHTVYKAGSPSDMPR 659
DB 600 FCLKVEAPVLGATGPADSQHSQHGLDQGEARPALDGSALQPLLHTVYKAGSPSDMPR 659
QY 661 DSGIYSSVSSSLSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLSSGSC 720
DB 661 DSGIYSSVSSSLSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLSSGSC 720
QY 660 DSGIYSSVSSSLSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLSSGSC 719
DB 660 DSGIYSSVSSSLSLPLMEGLSTDQETSSLTESVSSSGLGEBEPALPSKLSSGSC 719
QY 721 KADLGCRSYTDELHAAVAP 738
DB 721 KADLGCRSYTDELHAAVAP 738
QY 720 KADLGCRSYTDELHAAVAP 737
DB 720 KADLGCRSYTDELHAAVAP 737
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Search completed: March 1, 2006, 10:34:42
Job time : 169 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:32:17 ; Search time 21 Seconds

(Without alignments)
701.013 Million cell updates/sec

Title: US-10-616-788-2

Sequence: 1 MAFWQLGCVFTVNAACNG.....SKADLCGRSYDELAHAP 738

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 133702 seqs, 19947517 residues

Total number of hits satisfying chosen parameters: 133702

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA New:

- 1: /cgn2_6/ptoddata/1/pubpaa/us08_NEW_PUB pep:*
- 2: /cgn2_6/ptoddata/1/pubpaa/us06_NEW_PUB pep:*
- 3: /cgn2_6/ptoddata/1/pubpaa/us07_NEW_PUB pep:*
- 4: /cgn2_6/ptoddata/1/pubpaa/PCR_NEW_PUB pep:*
- 5: /cgn2_6/ptoddata/1/pubpaa/us09_NEW_PUB pep:*
- 6: /cgn2_6/ptoddata/1/pubpaa/us10_NEW_PUB pep:*
- 7: /cgn2_6/ptoddata/1/pubpaa/us11_NEW_PUB pep:*
- 8: /cgn2_6/ptoddata/1/pubpaa/us60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3706	93.9	728	US-11-072-512-3399	Sequence 3399, Ap
2	134.5	3.4	385	US-09-978-360A-438	Sequence 438, App
3	134.5	3.4	502	US-10-063-703-158	Sequence 158, App
4	134.5	3.4	502	US-11-102-240-158	Sequence 158, App
5	112.5	2.8	730	US-10-821-234-1019	Sequence 1019, Ap
6	103.5	2.6	988	US-10-510-524-1	Sequence 1, Appli
7	99.5	2.5	1273	US-11-181-330-8	Sequence 8, Appli
8	98.5	2.5	998	US-11-203-251A-88	Sequence 88, Appl
9	98.5	2.5	2343	US-10-330-773-904	Sequence 904, Appl
10	98	2.5	984	US-11-113-424-60	Sequence 60, Appl
11	97	2.5	2880	US-11-115-639-31	Sequence 31, Appl
12	97	2.5	2880	US-11-115-639-32	Sequence 32, Appl
13	97	2.5	2880	US-11-115-639-33	Sequence 33, Appl
14	95	2.4	984	US-11-203-251A-85	Sequence 85, Appl
15	95	2.4	2098	US-10-055-877-253	Sequence 253, App
16	94	2.4	903	US-11-072-512-2951	Sequence 2951, Ap
17	92	2.3	1130	US-11-086-482-1	Sequence 1, Appli
18	92	2.3	1130	US-11-192-341-23	Sequence 23, Appl
19	91.5	2.3	347	US-11-118-122-2	Sequence 2, Appli
20	91.5	2.3	575	US-11-150-533-5	Sequence 5, Appli
21	91.5	2.3	688	US-11-150-533-10	Sequence 10, Appl
22	91.5	2.3	705	US-10-063-703-162	Sequence 162, App
23	91.5	2.3	705	US-11-102-240-162	Sequence 162, App
24	91.5	2.3	705	US-11-150-533-11	Sequence 11, Appl
25	91.5	2.3	791	US-11-072-512-3296	Sequence 3296, Ap

26	91	2.3	2326	US-11-126-313-37	Sequence 37, Appl
27	91	2.3	2811	US-10-877-346-27	Sequence 27, Appl
28	91	2.3	5405	US-11-108-172-1116	Sequence 1116, Ap
29	90.5	2.3	901	US-11-072-512-2920	Sequence 2920, Ap
30	90.5	2.3	1055	US-11-169-041-155	Sequence 155, App
31	90.5	2.3	1055	US-11-072-175-139	Sequence 139, App
32	90.5	2.3	1055	US-11-203-251A-86	Sequence 86, Appl
33	90.5	2.3	2314	US-11-097-728-2	Sequence 2, Appli
34	90.5	2.3	2353	US-11-097-728-6	Sequence 6, Appli
35	90.5	2.3	2641	US-10-877-346-63	Sequence 63, Appl
36	90	2.3	987	US-10-770-726-61	Sequence 61, Appl
37	90	2.3	987	US-11-203-251A-87	Sequence 87, Appl
38	89.5	2.3	509	US-11-072-512-2072	Sequence 2072, Ap
39	89.5	2.3	1346	US-11-060-005-2	Sequence 2, Appli
40	89	2.3	625	US-10-131-826A-70	Sequence 70, Appl
41	89	2.3	625	US-10-973-115B-70	Sequence 70, Appl
42	89	2.3	979	US-10-636-320-6	Sequence 6, Appli
43	88.5	2.2	871	US-10-933-025-3	Sequence 3, Appli
44	88.5	2.2	8746	US-11-098-686-10232	Sequence 10232, A
45	87.5	2.2	867	US-10-131-826A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-11-072-512-3399
; Sequence 3399, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YUKI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKI, ICHIRO
; APPLICANT: SEKI, NOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCES: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3399
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3399

Query Match 93.9%; Score 3706; DB 7; Length 728;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 694; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 41 MRCVGPASRNSGLNYITFKYDNCCTTYLNPVGKRVADAQNTTISQYACHDOVAVTLLMSP 100
Db 30 MCVGVPASRNSGLNYITFKYDNCCTTYLNPVGKRVADAQNTTISQYACHDOVAVTLLMSP 89
Qy 101 GAGTIFLKGFRVILELSEGRQCOQLIKPKQKLNSEFKRGMSQPLMKPFETDYR 160

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Db 90 GAGIEFLKGFVYLELEKSEGRQCOQLILKDPKQLSSFKRTGMEQPLINKMKEFTDYF 149
Qy 161 VKVPPPSINSESNYHFFFRTRACDILLQPDNLACPFKPNLNTSQSGSMQVSFDH 220
Db 150 VKVPPPSINSESNYHFFFRTRACDILLQPDNLACPFKPNLNTSQSGSMQVSFDH 209
Qy 221 APNFGFRPYLYKLKHEGPFKRTCKQRTETTSCLQONVSPGDYIELVDNTTTR 280
Db 210 APNFGFRPYLYKLKHEGPFKRTCKQRTETTSCLQONVSPGDYIELVDNTTTR 269
Qy 281 KVMHYALKPVHSPWAGPIRAMAITVPLVISAPATLFTVNCRRKQOENIYSHLDESSSES 340
Db 270 KVMHYALKPVHSPWAGPIRAMAITVPLVISAPATLFTVNCRRKQOENIYSHLDESSSES 329
Qy 341 STYTAALPRERLPRPRVFLCYSSKQGNMNVVQCAVFLQPCGCEVALDLMEBPSLC 400
Db 330 STYTAALPRERLPRPRVFLCYSSKQGNMNVVQCAVFLQPCGCEVALDLMEBPSLC 389
Qy 401 REGQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGSGKGLFLVAVSAIAEK 460
Db 390 REGQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGSGKGLFLVAVSAIAEK 449
Qy 461 LRQAKSSSAALSKEFLAVYFDYSCGDPVPGILDLSTRYRLMDNLPOLCSHLHSRDHGLQ 520
Db 450 LRQAKSSSAALSKEFLAVYFDYSCGDPVPGILDLSTRYRLMDNLPOLCSHLHSRDHGLQ 509
Qy 521 PGQHTQGSRRNFRSSGSLVYALICNMHQFIIDEEDWFEKQFVPHPPPLYREYVLE 580
Db 510 PGQHTQGSRRNFRSSGSLVYALICNMHQFIIDEEDWFEKQFVPHPPPLYREYVLE 569
Qy 581 KPFGSLVNDVMCKPESDFCLKEAPVIGATGPADSOHESOHGGGLDQGEARPALDGS 640
Db 570 KPFGSLVNDVMCKPESDFCLKEAPVIGATGPADSOHESOHGGGLDQGEARPALDGS 629
Qy 641 AALQPLHTYKAGSPSDMPDSGIIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSS 700
Db 630 AALQPLHTYKAGSPSDMPDSGIIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSS 689
Qy 701 GLGEEPPALPSKLLSSGSKADLGCRSYDELHNAVAP 738
Db 690 GLGEEPPALPSKLLSSGSKADLGCRSYDELHNAVAP 727

RESULT 2
US-09-978-360A-438
; Sequence 438, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclet, Aymeric
; APPLICANT: Bouguetel, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56, US4, CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
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; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent .pm
; SEQ ID NO 438
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -184...-1
US-09-978-360A-438

Query Match 3.4%, Score 134.5, DB 5, Length 385;
Best Local Similarity 20.1%; Pred. No. 0.00024;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;

Qy 204 NUNISGHSDMQVSF-----DHAPNFGFRPYLYLYKLKHEGPFKRTCK----- 247
Db 26 NANMEDGSMGVSNTSPGCLDH-----IMKYK-----KKCVAGSLMDPN 66
Qy 248 -----KQOTTR---TTSCLQONVSPGDYIELVDNTTTRKVMHYALKPVHSPWAGPIR 299
Db 67 TRACKNEBTEVNFPTTTL-----GNRYMALIQHSTI-----IGSQVEEPHOKQT 114
Qy 300 AMAITVPLVISAPATL-----FTVNCRRKQOENIYSHLDESSSES 341
Db 115 RASVIVPVGDSBGATVQLTYPFPTGSDICRHKKGVVLC---PQGVPPPLDNNKSKG 171
Qy 342 TYTAAL-----PRELR-----PRKPYFLCYSSKQGNMNV 372
Db 172 GWPLLLLSLVATWYLVAGIYLMRHERIKTSTTLPLPIKVLVYPSBEICFH-- 229
Qy 373 VVQCFAYFLDPCGCEVALDLMEBPSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDK 432
Db 230 TICYFTFELQNHCRSEVILEKQKKIAMEGVQMLATQKAAADKVVPLSLDVAVSVC 289
Qy 433 KNYKHKGGSGKGLFLVAVSAIAEKLRQAKSSSAALSKEFLAVYFDYSCGDPVPGIL 492
Db 290 TCGSEKSPSENSQ--DLFPLAFNLFCSDLR-----SQHLHKYVVYVFRBIDTKDYNAL 343
Qy 493 DLSTKRYLMDNLPOLCSHL 511
Db 344 SVCPKTHLMKDATAPCAEL 362

RESULT 3
US-10-063-703-158
; Sequence 158, Application US/10063703
; Publication No. US20060008901A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gueney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,703
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION removed - See Palm or file wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 158
; LENGTH: 502
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TYPE: PRT
ORGANISM: Homo Sapien
US-10-63-703-158

Query Match 3.4%; Score 134.5; DB 6; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.00036;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;

QY 204 NUNISQSGDMQVSF-----DHAPHNFGFRFLYHKLHGEFPKRTKTC----- 247
DB 143 NANNNEGSPMSVNFSPGCLD-----IMKYK-----KCCVKAAGSLMDPN 183
QY 248 -----KOEOTTE---TTSCLQNVSPGDYIELVDNTTRKVMHAKLVHSPMAGPIR 299
DB 184 ITACKKNEEVEVNFITTP-----GNRYMALIOHSTI-----IGSQVFEPHOKQT 231
QY 300 AMATVPLVVISAFATL-----FTVMCRKKQENIYSHLDESESS 341
DB 232 RASVIVFVTDGSGATVQLTPYPPTGSDCIRHKGVVLC---PQGVPPPLDNNKSPG 288
QY 342 TYTAAAL-----PRERLR-----PRPKVFLCYSSKDGQNNHN 372
DB 289 GWPLPLLSLVATWVAVGILYMMRHERIKTFSFTTLLPPIKVLVVPSEICFHN-- 346
QY 373 VVOCFAVFLDPGCGEVALDLMEDFSLCRGQREWVIOKIHESQFIIVVCSKMKYVDK 432
DB 347 TICFTEFLQNHCRSEVILEKMKQKIAEMGPVOMLATQKKAADKVFLSLNDVNSVCDG 406
QY 433 KNYKHGGGSGSGKGLFLVAVSAIAEKLQAKOSSAALSKFIAYFEDYCSGDPVGL 492
DB 407 TCGKSGSPSPENSG-DLPLAFNLFCSDLR-----SQIHLKVVVVFREIDTDVYNAL 460
QY 493 DLSTKRLMDNLPOLCSHL 511
DB 461 SVCPKXHLMDATAFCAEL 479

RESULT 4
US-11-102-240-158
Sequence 158, Application US/11102240
Publication No. US20050260647A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
TITLE OF INVENTION: ESOPHAGEAL TUMOR
FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 158
LENGTH: 502
TYPE: PRT
ORGANISM: Homo Sapien
US-11-102-240-158

Query Match 3.4%; Score 134.5; DB 7; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.00036;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;
QY 204 NUNISQSGDMQVSF-----DHAPHNFGFRFLYHKLHGEFPKRTKTC----- 247

DB 143 NANNNEGSPMSVNFSPGCLD-----IMKYK-----KCCVKAAGSLMDPN 183
QY 248 -----KOEOTTE---TTSCLQNVSPGDYIELVDNTTRKVMHAKLVHSPMAGPIR 299
DB 184 ITACKKNEEVEVNFITTP-----GNRYMALIOHSTI-----IGSQVFEPHOKQT 231
QY 300 AMATVPLVVISAFATL-----FTVMCRKKQENIYSHLDESESS 341
DB 232 RASVIVFVTDGSGATVQLTPYPPTGSDCIRHKGVVLC---PQGVPPPLDNNKSPG 288
QY 342 TYTAAAL-----PRERLR-----PRPKVFLCYSSKDGQNNHN 372
DB 289 GWPLPLLSLVATWVAVGILYMMRHERIKTFSFTTLLPPIKVLVVPSEICFHN-- 346
QY 373 VVOCFAVFLDPGCGEVALDLMEDFSLCRGQREWVIOKIHESQFIIVVCSKMKYVDK 432
DB 347 TICFTEFLQNHCRSEVILEKMKQKIAEMGPVOMLATQKKAADKVFLSLNDVNSVCDG 406
QY 433 KNYKHGGGSGSGKGLFLVAVSAIAEKLQAKOSSAALSKFIAYFEDYCSGDPVGL 492
DB 407 TCGKSGSPSPENSG-DLPLAFNLFCSDLR-----SQIHLKVVVVFREIDTDVYNAL 460
QY 493 DLSTKRLMDNLPOLCSHL 511
DB 461 SVCPKXHLMDATAFCAEL 479

RESULT 5
US-10-821-234-1019
Sequence 1019, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Seache-Crafin, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes version 1.0
SEQ ID NO 1019
LENGTH: 730
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1019

Query Match 2.8%; Score 112.5; DB 6; Length 730;
Best Local Similarity 19.7%; Pred. No. 0.066;
Matches 144; Conservative 80; Mismatches 261; Indels 247; Gaps 33;

QY 153 MKETDYPKVVVPPSITKNSNHPFRFRACDLLOP----- 192
DB 88 LKTEBDY-----IYPSV-----HEVLGRGEPPLILPQFGVWEGTNEHTISIPETE 137
QY 193 -----NLACKP-----FMKPRMLNISQSGDMQVSFDHAPHNFGFRFLYHKLH 235
DB 138 PLOSPPTKYLGNPAPARIYRKHFLGKEHN-----YSLDTA-----LGHVFSIKYD 186
QY 236 L-----KHGEPFKRTKQKOBOTETTSCLQNVSPGDYIELVDNTTRKVMHAKLVH 291
DB 187 VIDQEHRLRLATKCRTHADVIRISCLTEFPVAVQMAKLVCDVAVDR-----FYPVL 240
QY 292 SPWAGPIRAMATVPLVVISAFATLFTVMCRKKQENIYSHLDESESSSTYTAALP 348
DB 241 YPVAAS---RLIVFEDHVISNNKFGVIOKLGQTSSEB---LFTSNEBAPAFVFLR 292
QY 349 RERLRPRPKVFLCYSSKDGQNNHNWVQCFAYFLDPGCGEVALDLMEDFSLCR--- 401
DB 293 -----FLGQKTK-----LQDFKGRGGLDVYHGGQGTESVVCNFR 327

QY 402 -----EGOREMVIQKIHESQFIIVVCSKMKYFVDK-----KNYK 436
DB 328 NKEIMFHVSTKLEPYTEBGDAQOLQKRIHNDIVAV-----VFQDENTPVPVPMIASNFL 381
QY 437 H-----KGGGSGSGKGLFLVAVSAIAE-----KLQAKOSSAALSKEFLA 477
DB 382 HAVVVAOAEAGG---PDGPLYKVSVTARDVDFPGPPLPDPAVFRKQPFQEFILFTGLIN 438
QY 478 VYFDYGC-EGDVYGLDLSKTKRLMDNLPOLCSHLSRD-HGLQEPQGHTRQSSRRVYF- 534
DB 439 A--EYACYKAEKPAKLEERTALLETLYEEL-HHSQSMWGLGDEDKNENSGGGGFF 495
QY 535 -----RSKSGRSL-----YVAICMHOPIDEBPDMFE-----KQVFPHPPLR 573
DB 496 ESFRKVRVRSQMDAMGLSNKKPNVSTSHSGSFANNPDLAAGAISLIVGKSTRK 555
QY 574 YREPVLEKFDGVLVNDWCKPGEPSDFCLKVEAPVLGATGPADSOHESGHGLDQGEA 633
DB 556 KSGPFGSRSSAIGIENI-----QEVQKRSPSPAGQKTP-DSGHVSGEPKSE----- 602
QY 634 RPLDGSALQPLHTYKAGSPSDMPRDSGIYSSVSSELS-----LPLMEGLSTDQTE 688
DB 603 ---NSSTGSPSPMTTKNAETPAQAEALXDFSRSSASSPASVYEEETEGVDEDTG 658
QY 689 TSS-----LTSVSSSSG-----LGESEBPALPSKL 714
DB 659 LBSVSSSGTPHKRDSFTYSTWLEDVSSTTSGSSPGRSPRHPDAGLGDLPACPEIKQL 718
QY 715 LSSGSCKADIGC 726
DB 719 EASEQHMPQLGC 730

RESULT 6
US-10-510-524-1
; Sequence 1, Application US/10510524
; Publication No. US20050260209A1
; GENERAL INFORMATION:
; APPLICANT: BOYD, ROBERT S
; APPLICANT: FLETCHER, GRAHAM C
; APPLICANT: HUDSON, LYNDEY J
; APPLICANT: PATEL, SONAL
; APPLICANT: TERRETT, JONATHAN A
; TITLE OF INVENTION: AN EPHRIN-B RECEPTOR PROTEIN INVOLVED IN CARCINOMA
; FILE REFERENCE: 2543-1-037PCT/US
; CURRENT APPLICATION NUMBER: US/10/510,524
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0208089.3
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-524-1

Query Match 2.6%; Score 103.5; DB 6; Length 998;
Best Local Similarity 18.8%; Pred. No. 0.71;
Matches 148; Conservative 119; Mismatches 293; Indels 229; Gaps 39;

QY 42 RGVGPSRNSGLNIFPKYN-----CTTYLNPVGHVADQNITISQYACHQVAVT 95
DB 309 RTTSPASASICTGNNPFRADSDSADSACTVPSB-PGCVISNV-----NETSLI 356
QY 96 ILWS-GALGIEFLKGRVILLEELKSEG-----RQCQQLIKPKQLNSFKETGMESQP 149
DB 357 LEWSEPRDLGVRDGLVNYVCKCKHAGSASACRCDNDVEFPRQGLSEPRVHTS--- 413
QY 150 FLNMKEETDVFVAVPPPSIKNSNVHPPFFRTACDLLQPDNLACKCPWKPRNINISQ 209
DB 414 --HLAHTRYTPEVQAVNVGSGSKPLPRRYAAVNTTNGAAPSEV-----PTLRHSS 464

QY 210 HSGDMOVSPDHAHPNFGPFFLYLHYKLKHEGPF-KKTKCKOQOTETTSTCLIONVP-GD 267
DB 465 SSSSLTSLNAPPERPFG---VLIDYMKY---PEKSEBGLASTVTSQMSVOLDGLRPPDR 518
QY 268 YIIELVDDNTTRTKVMHYA-LKPVH---SPWAGPIRAMAITVPLVISAFTL----- 316
DB 519 YVVQV-----RARTVAGQYGRPAPEFTTSBRSGAQOLQOLPLIVGSAATGLVAVVA 573
QY 317 ---FTYMKCKKQOENIYSHLDESSSSSTYTALPRELRAPRPKPLCTSSSDGQNNMV 373
DB 574 VVVIATVCLRKQPH-----GSDSEYTEKL-QQYLAPEMKYVIDPFTYEDPN--EA 620
QY 374 VOCFAVFLDPC-GCEVALDLMEDFSLCREGOREWVIQKIHESQFIIVVCSKMKYFVDK 432
DB 621 VREFAEIIVSCVKIIEVYGAGEFGEVCR----- 649
QY 433 KNYKHGGGSGSGKGLFLVAVSAI---AEKLQAKOSSAALSKEFLAVFDYSCGDV 488
DB 650 -----GRLKQPGRRVVF-VAIKTLKVGYTERQRDRDIFSEASIMQGF-----DH 691
QY 489 PGILDS---TKR-----LMDNLPOLCSHLSRDHGLQEPQHT----- 525
DB 692 PNITRLEGVVTXSRPYMILTEFMENC-ALDSFLRLND-----GQFTVIQLVGMRLGIAA 744
QY 526 --ROGSRMY-FRSKSGRLVY---AIC-----NMHOPIDEBPDMPEKQFVFPHP- 570
DB 745 GMYLSBNMYVYRDLAARHILVNSNLVCKVSDPGLSRFLIEDPS-----DPTYSLSLG 798
QY 571 --PLRYEP--VLEKFD-----GLVNDWCKPGEPSDFCLKVEAPVLGATGPADS 618
DB 799 KIPIRWTADEALAYRKFTSASDVMSYGIWMHEVMS-----YGERPYMD 842
QY 619 QHESQHGILDQGEARPALDGSALQPLHTYKAGSPSDMPRDSGIYDS----- 667
DB 843 SNQDVINAVEODYRLPPPDCEPTALHQLMLDCWVRDNRNLPKFSQIVNTLIDLKIRNAASL 902
QY 668 ---SVPSSELSPLMEGLSTDQETSSLTSEVSSSSGSGLESEBPALPSKLSSGSKADL 724
DB 903 KYIASQSGMSQPLDRYTPDYTTPTTVGDMDALK-MGRYK-----BSFVAGRASFDL 956
QY 725 GCRSYTDEL 733
DB 957 VAQMTAEDL 965

RESULT 7
US-11-181-330-8
; Sequence 8, Application US/11181330
; Publication No. US20060035283A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S MEDICAL CENTER CORPORATION
; TITLE OF INVENTION: NEUROPROTECTIVE THERAPEUTICS AND ASSAYS FOR IDENTIFYING
; FILE REFERENCE: CMA-3.25
; CURRENT APPLICATION NUMBER: US/11/181,330
; PRIOR FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: PCT/US04/01209
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/440,679
; PRIOR FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 1273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-181-330-8

Query Match 2.5%; Score 99.5; DB 7; Length 1273;
Best Local Similarity 18.5%; Pred. No. 2.4;
Matches 143; Conservative 92; Mismatches 214; Indels 323; Gaps 36;


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QY 112 RVILIELSEKGGCCOOL-ILKD-----PKOLNSPFRGTGME-----SQPLNKKPFTDYFVK 162
DB 243 QVPSHLEBAEAYEQOHLILNNPFLRLPRAASAKKPPITHDVSIFLINS--ETITFLH 300
QY 163 VWPSPISXNENYHPFFRTRACDLLOPNLACKPWPCKRNINISQ-----HGSDMQVS 217
DB 301 QIFVQGLKARISWPTVLADLPDILP-----MNTIYGEFRNHQYSQI- 346
QY 218 FDHAPNFGFRFLYAKLKHGEPFKKTKQEQOTTETTSCLLQNSVPGDYII--ELVD 274
DB 347 LAMCKORNDPKLKHKEAKPD-----C-BERTLETFLTYPMFOIP-RYIILHMLLA 397
QY 275 DT---NTRKVMHYALKPVHSPWAGPIRAMAIVPLVISAPATLPVWCKKQOENIYS 331
DB 398 HTHHEVERNSLDYA-----KSKLELSR 421
QY 332 HLDSESSSTYTAALPRERLPRPKVFLCYSSKQGNHNVQCPAYFLQDPGCEVAL 391
DB 422 IMDEVSETEINIKNLAIERM-----IIE-----GCEILL 451
QY 392 DLWEDF-----SLRCQOREWVIOKHESQPIIVCSKGM 426
DB 452 DTQCFRQOGLILOVPMSEKGIKTRGLSLKKEGEGROCFLEPSK-----LITCRGS 506
QY 427 --KYPVDKKNY-----KHKGG-----RSGKGEFLVA 453
DB 507 GGLHLTKNGVISLIDCTLLEBPSTEEAKSGQDIDHLPKIGVPEKOSPFTVILVA 566
QY 454 VSAIAELRQAKOSSAALSKFIAYPDYSCGDPVILDLSTKYRLMDNLPOLCSHLHS 513
DB 567 SS-----ROKKAAMTSDISQVD--NIRCNGLMNAFENSKV-----TYPMI----- 608
QY 514 RDHGOEPGHTQGSRRNYFRSKGSLVYALCNMHQFIDEBEPEKQVPEPPEPLR 573
DB 609 -----KRTREGTREAE--SRSDASLY-----CDVDVIRSKTMNSCKVQIR 649
QY 574 YR--EPVLEK-----PDSGLVLDVMCKPGEPSDCLKVEAPVL 610
DB 650 YASVERLERLTLRFLSIDFLNTFLHSYRFTTAYVLDKL-----ITTYKPI- 699
QY 611 GATGPADSQHSQHGLDQGEARPA-----LDGSALQPLHTVAKGSPSPDRDS 662
DB 700 -----SALPARWLSLELFPASGONKLLY-----GEPKSPRAT 734
QY 663 GIVDSVPSS-----ELSLPLMEG-----LST 684
DB 735 RKFSPPPLSITKTSPPRRKLSINIPITGKALDLALSCNSNGYTSWYASMSPSK 794
QY 685 DQETSSLTSSVSSSGGLGEE-----EPPLPSTLLSSGCKADLGRSTTD 731
DB 795 ATLDTSKLYVSSSFTNKKIPDEGDTTPKPDPSALSKSS-----EVSMBESD 843

RESULT 8
US-11-203-251A-88
; Sequence 88; Application US/11203251A
; Publication No. US20060039904A1
; GENERAL INFORMATION:
; APPLICANT: MedImmune Inc.
; TITLE OF INVENTION: EPH RECEPTOR P-2 VARIANTS WITH ENHANCED ANTIBODY DEPENDENT
; FILE REFERENCE: A6702US
; CURRENT APPLICATION NUMBER: US/11/203, 251A
; PRIOR FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: 60/601, 634
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: 60/608, 852
; PRIOR FILING DATE: 2004-09-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 998
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-11-203-251A-88
Query Match 2.5%; Score 98.5; DB 7; Length 998;
Best Local Similarity 18.6%; Pred. No. 2;
Matches 147; Conservative 121; Mismatches 292; Indels 229; Gaps 39;

QY 42 RGVPASRNSGLNIFKDN-----CTTYLNVPKGVADANONITISQYACHDQAVT 95
DB 309 RTTSPASICTCHNNYFRADSDASACTVPSR-PGAVISNV-----NETSLI 356
QY 96 ILMS-PCALGIEFLKGFVILIELKSEG-----ROCOQLIKDPKOLNSFKRTGMSQP 149
DB 357 LKMSPRDLGGRDILNVI CKKHGAGASACSRODDNVEFPRQGLERRVHS--- 413
QY 150 FLMKFETDYFVKVWPSPISXNENYHPFFRTRACDLLOPNLACKPWPCKRNINISQ 209
DB 414 --HLAHTRYTFEVOAVNGVSGSKPLPPRYAANITTNQAPSEV-----PTLRHSS 464
QY 210 HGSDMQVSPHAPNFGFRFLYAKLKHGEP-KRKTQEQOTTETTSCLLQNSVPGDY 267
DB 465 SGSSLTLSWAPPRPENG---VILDYEMKY--FEKSEGLASTVTSQWNSVQLGLRPDAR 518
QY 268 YIIELVDDTWTTRKWHYA--LKPVH-----SPWAGPIRAMAIVPLVISAPATL- 316
DB 519 YVVQV-----PANTVAGYGYSRPAPETTSERSGAQLOEQLPLVGSATAGLVFVA 573
QY 317 ---FTWCKRQOENIYSHLDESSSTYTAALPRERLPRPKVFLCYSSKQGNHNV 373
DB 574 VVVIATVCLRKQH-----GSDSEYTEKL-QOYIAPGMKVYIDPTEYEDPN--EA 620
QY 374 VOCFAYFLDQFC-GCEVALDWMEDFSLCREGQREWVIOKHESQPIIVCSKMKRYVDK 432
DB 621 VREFAKRIDVSCYKIEVIGAGEFGEVCR----- 649
QY 433 KNYKHGGKSGKGEFLVAVSAI--AEKLRQAKOSSAALSKFIAYPDYSCGDPV 488
DB 650 -----GRUKQPRREVP-VAITTLKVGYTEKORRDLFLSASIMGP-----DH 691
QY 489 PGILDS--TKYR-----LMDNLPOLCSHLSDHGLQEPGQHT----- 525
DB 692 PNIRLEGVYTKSRPMLILFERFENC-ALDSFLRLND-----GQFVIOGLVGLRGLIA 744
QY 526 --RQSGRRNY-FRSGKSLYV--AIC-----NMHOFIDEBEPEKQVPEPPEPLR 570
DB 745 GMYCLEMNYVHRDLARNILVNSNLVCKVSDGLRFLIEDDPS-----DPTYSILG 798
QY 571 --PLRYREP--VLEKPS-----GIYLDVMCKPGEPSDCLKVEAPVLGATPADS 618
DB 799 KIRIRWTAPALAYRKFTSASDVMSYGIWMEVMS-----YBRRPYMDM 842
QY 619 QHESQGLDQGEARPALDGSALQPLHTTVAKGSPSPDRSGIYDS----- 667
DB 843 SNQDVINAYEQDRLRPPMDCFALHQLMDCVVRBNLRKFSQIVNTLIDKILRNASL 902
QY 668 ---SVPSSELPLMEGLSTQETSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADL 724
DB 903 KYIASAQSGMSQPLDRTVPDYTTFTTVGMDLAIR-MGRYK-----ESFVSGAFASFDL 956
QY 725 GCRSYDEL 733
DB 957 VAOQTAEDL 965

RESULT 9
US-10-330-773-904
; Sequence 904; Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300

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;; CURRENT APPLICATION NUMBER: US/10/330,773
;; CURRENT FILING DATE: 2002-12-27
;; NUMBER OF SEQ ID NOS: 981
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 904
;; LENGTH: 2343
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-330-773-904

Query Match 2.5%; Score 98.5; DB 6; Length 2343;
Best Local Similarity 27.1%; Pred. No. 7.3;
Matches 29; Conservative 18; Mismatches 43; Indels 17; Gaps 4;

QY 606 EAPVLGATGPADQSHQSGHGLDQDGEA---RPALDGSALQPLHTVTKAGSPSDMPDRDS 662
DB 715 EPPAFSGPSPSEFAHNPPLGTSPPAASASPSLEPPTSPQP--RTPKFGASGSEPGK-- 770

QY 663 GIYDSSVPSSELSPLPMEGLSTDQETSTLSYSSVSSGLGSEBPRA 709
DB 771 ---ERRTMSKEISV-----IHTSSEFKSDPEPGSGLEBDEKPPA 807

RESULT 10
US-11-113-424-60
; Sequence 60, Application US/11/113,424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-113-424-60

Query Match 2.5%; Score 98; DB 7; Length 984;
Best Local Similarity 17.7%; Pred. No. 2.2;
Matches 117; Conservative 86; Mismatches 201; Indels 256; Gaps 32;

QY 185 CDLLLPDNLACPFKPKENLNISQHSQMDQVSDHAHNFGRFFYLAKLKHGEPFKR 244
DB 373 CD-----DNE-----FVPRQLGLTECVSISLMAHTPYTFDQAI---NGVSKSPFP 420
QY 245 KTKCKQOTTESTCLQNVSPGDYIIELVDTTTRKVMY---ALKPVSPAPGPIRAM 301
DB 421 QHVSVAITTNQA-----PSYVPIHQVSAITMSITLSLWPOBQPN 461
QY 302 AITVPLVISAFAFLFTVMCKRKQENIYSHLDESESSSTYPAALPRELRAP----- 354

DB 462 GIILDEI-----RYEKEHNEFNSSNARSQNTARI--DGLRGMVYVQ 505
QY 355 -RPKFLCYSKDQGNHNVVOCFAVFLQDFGCGEVALDLMEDFSLCRGOREMVIQKH 413
DB 506 VRAKTVAGYGFSGK-----MCFQTLTDD---DYKSELREQPLIASSAAGV----- 551
QY 414 ESQPII-----VCSGK-----GMKVFDDKKNY----- 436
DB 552 ---FVSVLVAISIVCSRKQAVSKAAYSDKLQHYSTGRGSPGKFIYIDPFYEDPNEAYR 608
QY 437 -----HKGGRSGSKRELVLVVASAI-----AETLRQAKGS 467
DB 609 BFAKEIDVSPVKIEEYVIGAGEEYVYGRKLKPGKREIY-VAIKTLKAGYSEKQRDPJS 667
QY 468 SSAAISKFTAVVFDYSCBGVDFQIILDS---FKYR-----LMDVLPOLCSHHSRDHG 517
DB 668 EASIMQF-----DHEPIITLBGVYTKSRVMTITERMEN-GALDSFLROND-- 713
QY 518 LQEPGQHT-----RQGRNNY-FRSKSGRLVY---AICNMHQF----- 552
DB 714 ---GQFTYIQLVGMRLGIAQMKYLSMNYYHRDLAANNILVNSVLCKVSDPFGLSRYL 769
QY 553 IDEEPPWFEKQVPPHPP-----PLRYREP---VLEKFS-----GLVINDVCKKG 596
DB 770 QDQTSQ-----PRTYSLGCKIPVRWTAPEALAYRKFTSADVWSYGIWMEVWS--- 819
QY 597 PESDPLKTVAPVLGATGPADQSHQSGHGLDQDGEARPALGSAALQPLHTVTKAGSPS 656
DB 820 -----FGRPYWMSNODVINAIEDRPLPPPMQCPALHQMLMDCKQKRN 866
QY 657 DNEPDSGIYD-----SSVPSSELSPLPMEGLSTDQETSTLSYSSV 698
DB 867 SRPRFAELIVNTLDKMRNPASLKTVAITAVVSQ---PLDRSIDPFAFTVDWMLSA 922

RESULT 11
US-11-115-639-31
; Sequence 31, Application US/11/115,639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rothelein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: Macneil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-31

Query Match 2.5%; Score 97; DB 7; Length 2890;
Best Local Similarity 18.6%; Pred. No. 14;
Matches 110; Conservative 68; Mismatches 162; Indels 250; Gaps 26;

QY 45 GPASRNSGLYNT-----FKYDNCCTTYLNPVGKHIADAQNTITSQY----- 86
DB 2304 GTASRSQDEREIVASKEGFRFYNLRTYTNKEGKNIIANRRNASILVVEPKIKAPFDGL 2363
QY 87 ---ACHDOYAVNTI-----LMSPGALGIEPLKGF 111
DB 2364 RIETVYEEVAVSVKQGDQAKFVLRRSDIVKPSLQAGVGCKI EGKVLVLYAAGHKVHKGG 2423
QY 112 RV--ILBE---LKSBRQCOQLLK--DPKQUNSSPKRTGMESOPFLNKK-FETDYFVAV 163

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Db 2424 STADIIQEGMNVNPNRI.PYASELLVKNONDPADQVNAKKGVIKYVYVLEANHLERTTGICK 2483
Qy 164 VPPPSIK-----NESNYHPFFRTACDILL-----QPDNLACKP----- 198
Db 2484 GDMVSEKGLFAYIADONGREAAH---YIAROSEIILIDNSEVSTNSVASKPTTNTFKTI 2540
Qy 199 -FWKPNINLSQHGSDMOVSFDHAPNFGFRFFYLHYKLKHGPPFRKTC----- 247
Db 2541 ATMDPYNTPII-----ADFGKKGFDVVIAGVTY 2569
Qy 248 --KOEQTTEITSCILONVSPGDYIIEVDNTTRKVMHYALKPVHSPMAGPIRAMAITY 305
Db 2570 AEREDENTGITSLVNDYIPSGYKPSLFLR-GANGEMRYFLRPKTS----- 2615
Qy 306 PLVVISAPATLFTWCKRQOENIYSHLDESESSSTYALPR-----ERLPRPKVFL 360
Db 2616 --IAISDSSV-----EQAEVLAKIPKATVKSNDITGCLPRVSELFEARPKRDXVA 2665
Qy 361 CVSSKDGQNMNVVOCFAVFLQDFCGCEVALDLMEDPSLCRQOREMVIQKIHESQFIY 420
Db 2666 ILSEVDG-----IVSFG-----KPIINKKHIIY 2688
Qy 421 VCSKG--MKYFVDK-----KNYKHKGCG-----RSGKGLFLVAVS--- 455
Db 2689 TSKDGRSMDFVVDKQKQIILVHADFEVHAGEAMTDVSISSHDILRISGEKELYKYIVSEVQ 2748
Qy 456 -----AIAEK-----LRQAKOSSAALSKEFIAYFPDYSGEGDV 488
Db 2749 QYRRQGVSIADKHIEIIVSQMLRQVRIIDSGD-SKEFI-----EGDL 2789
```

RESULT 12

```
US-11-115-639-32
; Sequence 32, Application US/11115639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rochelein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-32
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Query Match 2.5%; Score 97; DB 7; Length 2890;

Best Local Similarity 18.6%; Pred. No. 14; Matches 110; Conservative 68; Mismatches 162; Indels 250; Gaps 26;

```
Qy 45 GPASRNSGLYNT-----FKYDNCCTTYLNPVSKHVIADQNTTISQY----- 86
Db 2304 GTRSRQDERELIYASKEGFRFYNLRTYTKESKNIIANRRNASILVVEPKIAPPDGEL 2363
Qy 87 ---ACHDOVAVTI-----LMSFGALGIEFLKGP 111
Db 2364 RIETVVEEVVSVKNGDQAKFVLRSDDIVKSELGAGKIEGKYLLPYASGHVKHKG 2423
Qy 112 RV--IIEE--LKSEGRQCOOLILK--DPKOLNSSFKRTGMSQPLNKK--FETDVFVY 163
Db 2424 STADIIQEGMNVNPNRI.PYASELLVKNONDPADQVNAKKGVIKYVYVLEANHLERTTGICK 2483
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Qy 164 VPPPSIK-----NESNYHPFFRTACDILL-----QPDNLACKP----- 198
Db 2484 GDMVSEKGLFAYIADONGREAAH---YIAROSEIILIDNSEVSTNSVASKPTTNTFKTI 2540
Qy 199 -FWKPNINLSQHGSDMOVSFDHAPNFGFRFFYLHYKLKHGPPFRKTC----- 247
Db 2541 ATMDPYNTPII-----ADFGKKGFDVVIAGVTY 2569
Qy 248 --KOEQTTEITSCILONVSPGDYIIEVDNTTRKVMHYALKPVHSPMAGPIRAMAITY 305
Db 2570 AEREDENTGITSLVNDYIPSGYKPSLFLR-GANGEMRYFLRPKTS----- 2615
Qy 306 PLVVISAPATLFTWCKRQOENIYSHLDESESSSTYALPR-----ERLPRPKVFL 360
Db 2616 --IAISDSSV-----EQAEVLAKIPKATVKSNDITGCLPRVSELFEARPKRDXVA 2665
Qy 361 CVSSKDGQNMNVVOCFAVFLQDFCGCEVALDLMEDPSLCRQOREMVIQKIHESQFIY 420
Db 2666 ILSEVDG-----IVSFG-----KPIINKKHIIY 2688
Qy 421 VCSKG--MKYFVDK-----KNYKHKGCG-----RSGKGLFLVAVS--- 455
Db 2689 TSKDGRSMDFVVDKQKQIILVHADFEVHAGEAMTDVSISSHDILRISGEKELYKYIVSEVQ 2748
Qy 456 -----AIAEK-----LRQAKOSSAALSKEFIAYFPDYSGEGDV 488
Db 2749 QYRRQGVSIADKHIEIIVSQMLRQVRIIDSGD-SKEFI-----EGDL 2789
```

RESULT 13

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US-11-115-639-33
; Sequence 33, Application US/11115639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rochelein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-33
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Query Match 2.5%; Score 97; DB 7; Length 2890;

Best Local Similarity 18.6%; Pred. No. 14; Matches 110; Conservative 68; Mismatches 162; Indels 250; Gaps 26;

```
Qy 45 GPASRNSGLYNT-----FKYDNCCTTYLNPVSKHVIADQNTTISQY----- 86
Db 2304 GTRSRQDERELIYASKEGFRFYNLRTYTKESKNIIANRRNASILVVEPKIAPPDGEL 2363
Qy 87 ---ACHDOVAVTI-----LMSFGALGIEFLKGP 111
Db 2364 RIETVVEEVVSVKNGDQAKFVLRSDDIVKSELGAGKIEGKYLLPYASGHVKHKG 2423
Qy 112 RV--IIEE--LKSEGRQCOOLILK--DPKOLNSSFKRTGMSQPLNKK--FETDVFVY 163
Db 2424 STADIIQEGMNVNPNRI.PYASELLVKNONDPADQVNAKKGVIKYVYVLEANHLERTTGICK 2483
Qy 164 VPPPSIK-----NESNYHPFFRTACDILL-----QPDNLACKP----- 198
Db 2484 GDMVSEKGLFAYIADONGREAAH---YIAROSEIILIDNSEVSTNSVASKPTTNTFKTI 2540
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QY 199 -FWKPNLNISQHGSDMVSFDHAPNFGFRFFYLHKLKHGEPFRKTC- 247
DB 2541 ATMDPNTPII-----ADFGKGVFVDVIAGTV 2669
QY 248 --KQEQTTETSCLLQNSPGDYIIELVDDTNTTKRMHVALKPVNSPMAGPIRAMAIIY 305
DB 2570 AAEKEDNTGITSIVVDYIPSGYKPSLFE-GANGEMRFFLEPKIS- 2615
QY 306 PLVVISAPATLFTVMCRKKQOENIYSHLDESESSSTYTAALPR-----ERLAPRPVFL 360
DB 2616 --IAIDGSSV-----EQAEVLAKIPATYKSRDITGGLRVSLEFPAKRPKEDVA 2665
QY 361 CYSSKQGNHNVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIIV 420
DB 2666 ILSEVDG-----IVSFG-----KPINKEHIIY 2688
QY 421 VCSKG--MKYFDK-----KNYKHKGG-----RSGKGEFLVANS- 455
DB 2689 TSKDGRSMDFYVDKQKQILVHADEPVHAGEAMTDGVISHDILRISQEKELYKXIYSEVQ 2748
QY 456 -----AIABK-----LRQAKQSSALSKEFIANYFPDYSGEDV 488
DB 2749 QYTRQGVSIADKHIEIIVSQMLRQVRIIDSGD-SKFI-----EGDL 2789

RESULT 14

US-11-203-251A-85
; Sequence 85, Application US/11203251A
; Publication No. US200603904A1
; GENERAL INFORMATION:
; APPLICANT: Medimmune Inc.
; TITLE OF INVENTION: EPH RECEPTOR FC VARIANTS WITH ENHANCED ANTIBODY DEPENDENT
; TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY
; FILE REFERENCE: AE702US
; CURRENT APPLICATION NUMBER: US/11/203,251A
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: 60/601,634
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: 60/608,852
; PRIOR FILING DATE: 2004-09-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-203-251A-85

Query Match 2.4%; Score 95; DB 7; Length 984;

Best local Similarity 17.6%; Pred. No. 4.2;
Matches 116; Conservative 87; Mismatches 201; Indels 256; Gaps 32;

QY 185 CDLLQPDNLACKPFWKPNLNISQHGSDMVSFDHAPNFGFRFFYLHKLKHGEPKR 244
DB 373 CD-----DNVE-----FVPRQLGLTECRVSISSIMATPYFDIOAI---NGVSKSPFP 420
QY 245 KTCQKQGTETTSCLQNSPGDYIIELVDDTNTTKRMVY---ALKPVNSPMAGPIRAM 301
DB 421 QHVSNNITNQAA-----DSTVPIHMQVASATKMSITLSLPOPEQPN 461
QY 302 AITVPLVVISAPATLFTVMCRKKQOENIYSHLDESESSSTYTAALPRELRP----- 354
DB 462 GILLDVEI-----RYEKENHEFNSSMARSGTNTARI--DGLRGMVYVVG 505
QY 355 -REKVELCYSSKQGNHNVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIH 413
DB 506 VVARVTAAGKFSGK-----MCFQTLTD---DYKSELREQPLIAGSAAAGVV----- 551
QY 414 ESQFI-----VCSK-----GMYFDKKNYK----- 436
DB 552 ---FVSVLVAISIVCSRKAIVSKAVVSDKLQHYSTGSGSGPMKXIYIDPTYEDPNEAVR 608

QY 437 -----HKGGRSGKGELFLVAVSAI-----AEKLRQAKOS 467
DB 609 EFAKEIDVSVKILEEYIGAGEGEVYKGRLLPKGREIY-VAIKTLKAGYSEKQRDFLS 667
QY 468 SGAALSKFIANYFDVSCBEDVDGIIILDS---TKYR-----LMDLPLQCSLHSDRG 517
DB 668 EASIMQF-----DHEVITRLBEVVTSKSRVMTITTEFEN-GALDSFLROND- 713
QY 518 LQEPGQHT-----RQGRNNY-FRSKGRSLYV---AICNMQF----- 552
DB 714 -----GGFTYIQLVGMRLGIAAGKMYLAEMNYVHRDLAANILVNSLVCKVSPFGLSRYL 769
QY 553 IDBEPDFEKKQVPPHP-----PLRYRP---VLEKFS-----GLVLDNVCCKG 596
DB 770 QDTSQ-----FTYSSLGKIPVRYWPAIAYRKFTSADVWSYGIVMWEVMS--- 819
QY 597 PESDPLKYEARVLTAGTSGADSOHSGHGLDODGAPRALDSALQPLHTVYKAGSPS 656
DB 820 -----FGRPYWDSNDVINALQDYRLPPPMCCPALHQLMDLMDQXDRN 866
QY 657 DMPDQGIYD-----SSVPSSELSPLMEGLSTDQETSLTESVS 698
DB 867 SRPRFAEIVNTDKMTRNPSLKTVAITRAVDSQ-----PLDQSIQDFTAFTTVDWLSA 922

RESULT 15

US-10-055-877-253
; Sequence 253, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DecistoFaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kikuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zehrusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corinne
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Bolog, Perence
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 60/264,478
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/263,351
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 60/272,870
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: 60/275,990
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/275,927
 ; PRIOR FILING DATE: 2001-03-14
 ; Remaining Prior Application data removed - See file Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 512
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 253
 ; LENGTH: 2098
 ; TYPE: PR
 ; ORGANISM: Rattus norvegicus
 ; US-10-055-877-253

Query Match 2.4%; Score 95; DB 6; Length 2098;

Best Local Similarity 21.4%; Pred. No. 13; Matches 101; Conservative 61; Mismatches 189; Indels 122; Gaps 24;

QY 335 EESSESSTYALPRELPRPKVFLCYSSKDGONHNVVQCFAYFLDPCGEVALDLW 394
 DB 1249 EESLDKTSHSV--RRAR-----YVKNPOAFNNYKVCIAEYQDRA-----LV 1290
 QY 395 EDSFLCRGQREWNIOKHESOFIIVCSKMKYFVDKKNYKHKGGGSG-----KGE 448
 DB 1291 GDFMSRDNVED-----PKVCAKEPKEFVEKLEKFPSSGLRNPNIPTLOE 1338
 QY 449 LF-----LVASATAEKLROKQSSAALSKFIAYFPDYSCGDVPGILDSTK----- 497
 DB 1339 LFAKYRVLAIGDEKDRKEDELNSVEDIHFLVL-----QNLIOSTLSLSNSQSNCSOS 1392
 QY 498 ---YRLMDN-----LPQLCSHLHSRDHGLQEPQHTROGSRN-----YFRSKGR 540
 DB 1393 FOIFRLYREPREVLAFAFECQKSLVNRVSHS--QEPKKNRAVPFVPMSTQLSOSTY 1451
 QY 541 SLV-----VAIC-NMHQPID-----EEDWFEKOFPVPHPP-----PLRYR 575
 DB 1452 KLFPTWFPPTVCTESQFYDLRANGILDQPDHSPFMDMSNDPSSDLVAFSLDSPGHC 1511
 QY 576 BPVLEKPDGSLVNDVMCKKCPESDFCL--KYEAPVLCATGPADSGHESQHGLDQGE 632
 DB 1512 VTALALFSLGLLSVDVRI--PEQIVVDSMSWSEYMKSLG-----KDGGLDDDE 1560
 QY 633 ARPALGSALOPLIHTVTKAGSPD---MPRDSGIYDSVPS--SELSPLMEGLSTQ 686
 DB 1561 BEDLDGSGTKRQSVR-VKAKQASHTKYTLMR--GYI--TVPGMVSTRNLNPNDSIVNS 1615
 QY 687 TETSSLTESVSSSGLEEEPPALPFSKLSSGSCADLIGCRSYTD-ELHAAVAP 738
 DB 1616 CQVKFRLNTPATHLGPTGTATPLEELQAGPSCLPASFTSLVDPQLHTRCP 1668

Search completed: March 1, 2006, 10:35:08
 Job time : 24 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:30:22 ; Search time 48 Seconds
(Without alignments)

1271.139 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
Sequence: 1 MAPMTQLGCVFPTVNAALNG.....SCRADGCRSYDELHAAVAP 738

Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5.COMB.pep:*
2: /cgn2_6/prodata/1/aa/6.COMB.pep:*
3: /cgn2_6/prodata/1/aa/H.COMB.pep:*
4: /cgn2_6/prodata/1/aa/PCRS.COMB.pep:*
5: /cgn2_6/prodata/1/aa/R2.COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3706	93.9	728	2	US-10-104-047-3399
2	3681.5	93.2	728	2	US-09-747-259-18
3	3681.5	93.2	728	2	US-09-816-744-18
4	315	8.0	866	1	US-08-620-694A-10
5	315	8.0	866	2	US-09-022-255-10
6	315	8.0	866	2	US-09-022-696-10
7	315	8.0	866	2	US-08-978-773-4
8	315	8.0	866	2	US-09-022-253-10
9	315	8.0	866	2	US-09-022-260-10
10	315	8.0	866	2	US-09-022-259-10
11	315	8.0	866	2	US-09-022-257-10
12	315	8.0	866	2	US-09-549-679-10
13	315	8.0	866	2	US-10-033-522-1
14	315	8.0	866	2	US-09-949-002-403
15	315	8.0	876	2	US-09-949-002-412
16	298	7.5	864	1	US-08-620-694A-2
17	298	7.5	864	2	US-09-022-255-2
18	298	7.5	864	2	US-09-022-696-2
19	298	7.5	864	2	US-08-978-773-2
20	298	7.5	864	2	US-09-022-253-2
21	298	7.5	864	2	US-09-022-260-2
22	298	7.5	864	2	US-09-022-259-2
23	298	7.5	864	2	US-09-022-257-2
24	298	7.5	864	2	US-09-549-679-2
25	134.5	3.4	502	2	US-09-599-3608-106
26	134.5	3.4	502	2	US-09-747-259-12
27	134.5	3.4	502	2	US-09-816-744-12

28	134.5	3.4	504	2	US-09-949-016-11658	Sequence 11658, A
29	117.5	3.0	617	2	US-09-188-930-303	Sequence 303, App
30	117.5	3.0	617	2	US-09-312-283C-303	Sequence 303, App
31	116	2.9	552	2	US-09-949-016-8005	Sequence 8005, Ap
32	110.5	2.8	549	2	US-09-949-016-6384	Sequence 6384, Ap
33	106.5	2.7	489	2	US-09-248-796B-25826	Sequence 25826, A
34	105.5	2.7	595	1	US-08-468-036-3	Sequence 3, App1
35	105.5	2.7	595	1	US-08-376-843-3	Sequence 3, App1
36	105.5	2.7	970	2	US-09-538-092-664	Sequence 664, App
37	105	2.7	993	1	US-08-348-143-1	Sequence 1, App1
38	105	2.7	993	1	US-08-571-785-1	Sequence 1, App1
39	105	2.7	993	2	US-09-192-435-1	Sequence 1, App1
40	105	2.7	993	2	US-09-558-340-1	Sequence 1, App1
41	103.5	2.6	998	1	US-08-449-645A-20	Sequence 20, App1
42	103.5	2.6	998	1	US-08-702-367A-20	Sequence 20, App1
43	103.5	2.6	998	4	PCT-US95-04681-20	Sequence 20, App1
44	101	2.6	838	2	US-09-949-016-9916	Sequence 9916, Ap
45	101	2.6	838	2	US-09-949-016-9917	Sequence 9917, Ap

ALIGNMENTS

RESULT 1									
US-10-104-047-3399									
Sequence 3399, Application US/10104047									
Patent No. 6943241									
GENERAL INFORMATION:									
APPLICANT: HELIX RESEARCH INSTITUTE									
TITLE OF INVENTION: No. 6943241el full length cDNA									
FILE REFERENCE: H1-A0105									
CURRENT APPLICATION NUMBER: US/10/104, 047									
CURRENT FILING DATE: 2002-03-25									
PRIOR APPLICATION NUMBER:									
PRIOR FILING DATE:									
NUMBER OF SEQ ID NOS: 4096									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 3399									
LENGTH: 728									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-104-047-3399									
Query Match									
Best Local Similarity 93.9%; Score 3706; DB 2; Length 728;									
Matches 694; Conservativity 2; Mismatches 2; Indels 0; Gaps 0;									
QY	41	MRGVGASRNSGLYNTFRYDNCCTLYNPVGRVADAOINITISQYACHDQVAVTILMSP	100						
DB	30	WQGVGASRNSGLYNTFRYDNCCTLYNPVGRVADAOINITISQYACHDQVAVTILMSP	89						
QY	101	GALGIEPLKGFVYILELSEBGRCCOOLILKDPKOLNSPFRKTMESOPPLANKFETDYF	160						
DB	90	GALGIEPLKGFVYILELSEBGRCCOOLILKDPKOLNSPFRKTMESOPPLANKFETDYF	149						
QY	161	VKVVPPPSIKNSNTHPPFRTRACDILLIOPDLAKPFRKPNLNIISQHSIMQVSFDH	220						
DB	150	VKVVPPPSIKNSNTHPPFRTRACDILLIOPDLAKPFRKPNLNIISQHSIMQVSFDH	209						
QY	221	APNPFRRFYLHYLKHGSPFRKTKCKOETETTSCLLOVNSPDYIIEVDNTNTR	280						
DB	210	APNPFRRFYLHYLKHGSPFRKTKCKOETETTSCLLOVNSPDYIIEVDNTNTR	269						
QY	281	KVHGVYALKVHSPWAPIRAMATTVLVISAFATLFTVMCRKQOENIYSHLDESSSES	340						
DB	270	KVHGVYALKVHSPWAPIRAMATTVLVISAFATLFTVMCRKQOENIYSHLDESSSES	329						
QY	341	STYTAALPRERLRPRKPVLCYSSKQGNHNVVQCFAYFLDPCGCEVALDMEDFSLC	400						
DB	330	STYTAALPRERLRPRKPVLCYSSKQGNHNVVQCFAYFLDPCGCEVALDMEDFSLC	389						
QY	401	REGQRMVIOKHESQFIIVVCSKGMKVFVDKKNNYHGKGGSGSGGELFLVAVSAIAEK	460						

Db 390 REGQREWVIOKIHESQFIIVVCSKGMKYFVDKINVKHKGGRSGSGKGLFVAVSAIAEK 449
QY 461 LRQAKSSSAALSKFLAVVVDYSCGQVPGILDLSTKYRLMDNLPOICSHLSHRDGLQ 520
Db 450 LRQAKSSSAALSKFLAVVVDYSCGQVPGILDLSTKYRLMDNLPOICSHLSHRDGLQ 509
QY 521 PGQHTQGSRRNFRSKSGSLVVALCMHQFTIDEEPMFEKQFVFPHPPLRYREPVLE 580
Db 510 PGQHTQGSRRNFRSKSGSLVVALCMHQFTIDEEPMFEKQFVFPHPPLRYREPVLE 569
QY 581 KPDSGLVNDVMCKPGPESDFCLKVEAPVIGATGPADSOHSGHGLDQGEARPALDGS 640
Db 570 KPDSGLVNDVMCKPGPESDFCLKVEAPVIGATGPADSOHSGHGLDQGEARPALDGS 629
QY 641 AALQPLHTVKAQSPDMPDSDGIYDSVPSSELPLMEGLSTDQETSLSVESSSS 700
Db 630 AALQPLHTVKAQSPDMPDSDGIYDSVPSSELPLMEGLSTDQETSLSVESSSS 699
QY 701 GLGEEPPALPSKLSSGCKADLGCRRSYTDELHAAVAP 738
Db 690 GLGEEPPALPSKLSSGCKADLGCRRSYTDELHAAVAP 727

RESULT 2
US-09-747-259-18
; Sequence 18, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Flavioff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Vansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747, 259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311, 632
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172, 096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175, 481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213, 087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644, 848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/242, 837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253, 646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 18
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-18

Query Match 93.2%; Score 3681.5; DB 2; Length 728;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 694; Conservative 2; Mismatches 3; Indels 13; Gaps 1;

QY 40 GWRGVGPASRNSGLVNIIFPKYDNCCTYLANPVGKVIADQNTISQYACHDQVAATILMS 99
Db 16 GEOGVGPASRNSGLVNIIFPKYDNCCTYLANPVGKVIADQNTISQYACHDQVAATILMS 75
QY 100 PGALGIEFLKGFRRVILIEBKSEGRQOQILKDPQOLNSFKRTGMEQPLNMKETDY 159
Db 76 PGALGIEFLKGFRRVILIEBKSEGRQOQILKDPQOLNSFKRTGMEQPLNMKETDY 135
QY 160 FYKVVPFSPKIESNHPFFPRTACDILLOPDNLACRFMPKRYNLTISO----- 209
Db 136 FYKVVPFSPKIESNHPFFPRTACDILLOPDNLACRFMPKRYNLTISOHSDMQVSD 195
QY 210 --HGSDMQVSDHAPHNHGFYLYHKLKHEGPFKRTCKQEQTTETTSCLQNVSPG 266
Db 196 HAPKSGDMQVSDHAPHNHGFYLYHKLKHEGPFKRTCKQEQTTETTSCLQNVSPG 255
QY 267 DYIIEVDNTTTRKVMYALKPVHSPWAGPIRAMAIVPLVISAFAITLFTWCRKQO 326
Db 256 DYIIEVDNTTTRKVMYALKPVHSPWAGPIRAMAIVPLVISAFAITLFTWCRKQO 315
QY 327 ENIYSHLDESESSSTYTALPRELRPRPKVFLCYSSSDQGNHNVQCFAYFLDDFCG 386
Db 316 ENIYSHLDESESSSTYTALPRELRPRPKVFLCYSSSDQGNHNVQCFAYFLDDFCG 375
QY 387 CEVALDLMEFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKINVKHKGGRSGSK 446
Db 376 CEVALDLMEFSLCREGQREWVIOKIHESQFIIVVCSKGMKYFVDKINVKHKGGRSGSK 435
QY 447 GELFVAVASIAIEKLRQAKSSSAALSKFLAVVVDYSCGQVPGILDLSTKYRLMDNLPO 506
Db 436 GELFVAVASIAIEKLRQAKSSSAALSKFLAVVVDYSCGQVPGILDLSTKYRLMDNLPO 495
QY 507 LSHLSHRDHGQEBQHTROGSRNFRSKSGSLVVALCMHQFTIDEEPMFEKQFVP 566
Db 496 LSHLSHRDHGQEBQHTROGSRNFRSKSGSLVVALCMHQFTIDEEPMFEKQFVP 555
QY 567 FHPPLRYREPVLEKPDGLVNDVMCKPGPESDFCLKVEAPVIGATGPADSOHSGHGL 626
Db 556 FHPPLRYREPVLEKPDGLVNDVMCKPGPESDFCLKVEAPVIGATGPADSOHSGHGL 615
QY 627 LDQGEARPALDGSAAQPLHTVKAQSPDMPDSDGIYDSVPSSELPLMEGLSTDQ 686
Db 616 LDQGEARPALDGSAAQPLHTVKAQSPDMPDSDGIYDSVPSSELPLMEGLSTDQ 675
QY 687 TETSSLTESVSSSGIGEEPPALPSKLSSGCKADLGCRRSYTDELHAAVAP 738
Db 676 TETSSLTESVSSSGIGEEPPALPSKLSSGCKADLGCRRSYTDELHAAVAP 727

RESULT 3
US-09-816-744-18
; Sequence 18, Application US/09816744
; Patent No. 6579530
; GENERAL INFORMATION:

APPLICANT: Chen, Jian
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Li, Hanzhong
 APPLICANT: Hillan, Kenneth
 APPLICANT: Thomas, Daniel
 APPLICANT: Vanlookeren, Menno
 APPLICANT: Vandlen, Richard
 APPLICANT: Watanabe, Colin
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William
 APPLICANT: Yaneura, Daniel
 TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 FILE REFERENCE: P1381R1C1P2 (US)
 CURRENT APPLICATION NUMBER: US/09/816,744
 PRIOR APPLICATION DATA removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 39
 SEQ ID NO 18
 LENGTH: 728
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-816-744-18

Query Match 93.2%; Score 3681.5; DB 2; Length 728;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 69; Conservative 2; Mismatches 3; Indels 13; Gaps 1;

40 GMRGVPASNSGLNITFRYDNCCTYLNFGKHVIAADQNTITISQYACHDQVAATILMS 99
 16 GEGGVGPASNSGLNITFRYDNCCTYLNFGKHVIAADQNTITISQYACHDQVAATILMS 75
 100 PGALGIEPLKGFVILIELKSEGRQCOQLIKDPOKOLNSFKKTGMSOPLMKKETDY 159
 76 PGALGIEPLKGFVILIELKSEGRQCOQLIKDPOKOLNSFKKTGMSOPLMKKETDY 135
 160 FVAVVPPSIXNSNYHPPFRTACDILLQPNLACKPPMKRNINISQ----- 209
 136 FVAVVPPSIXNSNYHPPFRTACDILLQPNLACKPPMKRNINISQHGSDMOVSPD 135
 210 --HGSDMOVSPDPAHNFGRFPFYLYHKLKEGPPFKTKCKEQTTETTSCLLQNVSPG 266
 196 HAPHGSDMOVSPDPAHNFGRFPFYLYHKLKEGPPFKTKCKEQTTETTSCLLQNVSPG 255
 267 DYIIELVDNTTRKVMHYALKVHSHWAGPIRAMATTVLVVISAATLFTWCRKQ 326
 256 DYIIELVDNTTRKVMHYALKVHSHWAGPIRAMATTVLVVISAATLFTWCRKQ 315
 327 ENYSHLDESSSSSTYTALPREBLRPPKVFACSSKXGQONHNVVOCFAVFLDOPCG 386
 316 ENYSHLDESSSSSTYTALPREBLRPPKVFACSSKXGQONHNVVOCFAVFLDOPCG 375
 387 CEVALDLMEDPSLCRGEQREWVIQKIHESQFIIVVCSKMKYFYVKKXVHGKGGGSGK 446
 376 CEVALDLMEDPSLCRGEQREWVIQKIHESQFIIVVCSKMKYFYVKKXVHGKGGGSGK 435
 447 GEIPLVAVSAIAKLRQAKOSSSALSKFIAYVFDVSCBEDVPGILDSTKRYLMDLPQ 506
 436 GEIPLVAVSAIAKLRQAKOSSSALSKFIAYVFDVSCBEDVPGILDSTKRYLMDLPQ 495
 507 LCGHLSRDLGLDOPGOTRQGSRRNYFRSKGSLVVALCNMHOPIDEBPDMPEKQFVP 566
 496 LCGHLSRDLGLDOPGOTRQGSRRNYFRSKGSLVVALCNMHOPIDEBPDMPEKQFVP 555
 567 FHDPPLRYRBPVLEKEDSGVLVNDVMCKPGPESDFCLKVAAPVIGATGPADSGHESQHG 626
 556 FHDPPLRYRBPVLEKEDSGVLVNDVMCKPGPESDFCLKVAAPVIGATGPADSGHESQHG 615
 627 LDODGERARPLDGSALQPLILHTYKAGSPSDMRDSDGIYDSSVPSSELSPLEGLSTQ 686

Db 616 LDODGERARPLDGSALQPLILHTYKAGSPSDMRDSDGIYDSSVPSSELSPLEGLSTQ 675
 Qy 687 TETSSLTESVSSSGGIEEPPALPSKLLSSGCKADLCGRSTYDELHAAVAP 738
 Db 676 TETSSLTESVSSSGGIEEPPALPSKLLSSGCKADLCGRSTYDELHAAVAP 727

RESULT 4
 US-08-620-694A-10
 Sequence 10, Application US/08620694A
 Patent No. 5869286
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 APPLICANT: Spriggs, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: No. 5869286e1 Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,694A
 FILING DATE: 21 MARCH 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 08/538,765
 FILING DATE: 7 AUGUST 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/410,535
 FILING DATE: 23 MARCH 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-620-694A-10

Query Match 8.0%; Score 315; DB 1; Length 866;
 Best Local Similarity 22.9%; Pred. No. 5,7e-24;
 Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

55 NITFKYDNC--TTYLNPVGRVIAADQNTITISQYACHDQ-----VAATILMS 99
 49 NCTVKNSTCIDSDSIHP-----RNLTPSSPKDQIQLHFAHQOQDLFPVAHIEMT 99
 100 -PGALGIEPLKGFVILIELKSEGRQCOQLIKDPOKOLNSFKKTGMSOPLMKKETDY 158
 100 LQTDASILYBEGMELSLVLDQNTLRLCVR--FEFLSKLHHNRKRRFTTSHEV--VDPDQ 156
 159 YFVKV--VPPSIXNSNYHPPFRTACDILLQPNLACK--PPMKRNT----- 205
 157 YEVTVHLPKPIIDGDPNHSKNPFLVPCBCHARKMVTTCOMSSGSLMDP--NIVETLEAH 215

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QY 206 -----NISQSGDMQVSPDHAPHNFRFFFLYHYLKHGEPFKRTCKOBTETT 256
DB 216 QLRVSTPLWNESTHYQLITSPHMEHNSCFEHHM-HIPAPREBFHQSNTVTLRNK 274
QY 257 SCLQNVSPDYIIEIVDT--NTTRKVMHYALKPHSHWAGPIRAMAIVLVISAF 313
DB 275 GCCRHOVOIQPFSSCLNDCLRHSATVSCPEMDTPEPIDVPLWVWFYITISILVG 334
QY 314 ATLFTVMCRKQOENIYSHLDESSBSTYTAALPRELRPRP---KYFLCYSSKXGON 369
DB 335 SYLLIVICMTWRLAGS---EKYSDTKYTDGLPAADLPPPLKPRKWIYISA-DHPL 390
QY 370 HNNVQCFAYFLQDPGCEVALDLWEDFSLCREGOREWV---IQKHESQFIIVCSKG 425
DB 391 YVDVVLKFAQFLITAGTEVALDLLEBQAISEAGVMTWVGROKQEWESNKIIVLCNRG 450
QY 426 MKYFVDKKNYKKGCG-----RSGKGELFLVAVSAIAEKLROAKSSAALSFLFA 477
DB 451 TR---AKQALLGKAPVRLRCDHGKPVGDLEFTAAMNMLPDKR---PACFGTYV 501
QY 478 VYF-DYSCGVDVPGILDSTKYRLMDNLPOLCSHLSRDLQBPQHTROG--SRNYP 534
DB 502 CFSEVSCDGDVDDLFGAARVPLMDRFEV--YFRIQDLEMFQPGHMRVGLSGDNYL 559
QY 535 RSKSGSLYVAICNMHQFIDEEPWFPE-----KQVYFHPPLRYREPVLEKFDGSL 586
DB 560 RSPGGRQLRAALDRPDWQVRCPDWFECENLYSADQDAPSLDEEV-FEERPLP-GTGI 617
QY 587 VANDVCKGPEBDFCLKEAPVLTGTPADSQHSQH-----624
DB 618 VKRAPLVRE-PGSQACLAID-PLVGBEGGAIVAKLEPHIQPRGAPAPQPLHTLVLAABEG 675
QY 625 -----GGLDDGEARPALDGSALLOPLHTVYKASPSMDRDSIYSSVSELSL 676
DB 676 ALVAAVEPGLADGAAVRLALAGEBACPLSGPGAG-----RNSVLP--LPVDPEDS 726
QY 677 PLMEGLSTDQETSSLTESVSSSGLGEERPALPSKLSGSCAKDLGC 726
DB 727 PL--GSSTPMASPDLLPEDVR-----EHLGMLSLFEGSLSCQAQGGC 768

RESULT 5
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanielow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-255-10

Query Match      8.0%; Score 315; DB 2; Length 866;
Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

QY 55 NITPKYDNC--TTLNPNVGNVIAADQNT-----ISQYACHDQ-----VAATILMS 99
DB 49 NCTVKNSTCLDSDSWHP-----RNLTPSSPKDQIQLFPAHTQOGLPPVAHIEMT 99
QY 100 -FGALGIEFLKGFVILIELKSEGRQCOOLIKDPKOLNSSFKRTGMSQPLNMKFETD 158
DB 100 LQDASILYLBGAEISVLDQANTNERLCVR--FEPLSKLRHHRNRFTTSHV--VDPDG 156
QY 159 YFVKV--VFPSPIKNESNYHPFFFTACDLLLOPDNLACK--PFWKPRNL-----205
DB 157 YEYTVHLLPKPIPDGDPNHQSKNPLVPDCEHARMKVTPFCMSSGSLMDE-NITVETLEAH 215
QY 206 -----NISQSGDMQVSPDHAPHNFRFFFLYHYLKHGEPFKRTCKOBTETT 256
DB 216 QLRVSTPLWNESTHYQLITSPHMEHNSCFEHHM-HIPAPREBFHQSNTVTLRNK 274
QY 257 SCLQNVSPDYIIEIVDT--NTTRKVMHYALKPHSHWAGPIRAMAIVLVISAF 313
DB 275 GCCRHOVOIQPFSSCLNDCLRHSATVSCPEMDTPEPIDVPLWVWFYITISILVG 334
QY 314 ATLFTVMCRKQOENIYSHLDESSBSTYTAALPRELRPRP---KYFLCYSSKXGON 369
DB 335 SYLLIVICMTWRLAGS---EKYSDTKYTDGLPAADLPPPLKPRKWIYISA-DHPL 390
QY 370 HNNVQCFAYFLQDPGCEVALDLWEDFSLCREGOREWV---IQKHESQFIIVCSKG 425
DB 391 YVDVVLKFAQFLITAGTEVALDLLEBQAISEAGVMTWVGROKQEWESNKIIVLCNRG 450
QY 426 MKYFVDKKNYKKGCG-----RSGKGELFLVAVSAIAEKLROAKSSAALSFLFA 477
DB 451 TR---AKQALLGKAPVRLRCDHGKPVGDLEFTAAMNMLPDKR---PACFGTYV 501
QY 478 VYF-DYSCGVDVPGILDSTKYRLMDNLPOLCSHLSRDLQBPQHTROG--SRNYP 534
DB 502 CFSEVSCDGDVDDLFGAARVPLMDRFEV--YFRIQDLEMFQPGHMRVGLSGDNYL 559
QY 535 RSKSGSLYVAICNMHQFIDEEPWFPE-----KQVYFHPPLRYREPVLEKFDGSL 586
DB 560 RSPGGRQLRAALDRPDWQVRCPDWFECENLYSADQDAPSLDEEV-FEERPLP-GTGI 617
QY 587 VANDVCKGPEBDFCLKEAPVLTGTPADSQHSQH-----624
DB 618 VKRAPLVRE-PGSQACLAID-PLVGBEGGAIVAKLEPHIQPRGAPAPQPLHTLVLAABEG 675
QY 625 -----GGLDDGEARPALDGSALLOPLHTVYKASPSMDRDSIYSSVSELSL 676
DB 676 ALVAAVEPGLADGAAVRLALAGEBACPLSGPGAG-----RNSVLP--LPVDPEDS 726
QY 677 PLMEGLSTDQETSSLTESVSSSGLGEERPALPSKLSGSCAKDLGC 726
DB 727 PL--GSSTPMASPDLLPEDVR-----EHLGMLSLFEGSLSCQAQGGC 768

```

RESULT 6

US-09-022-696-10
 ; Sequence 10, Application US/09022696
 ; Patent No. 6072037
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Faniow, William
 ; TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/022,696
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/620,694
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US98/0410,535
 ; FILING DATE: 23 MARCH 1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,695
 ; REFERENCE/DOCKET NUMBER: 2617-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 866 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-022-696-10

Query Match 8.0%; Score 315; DB 2; Length 866;
 Best Local Similarity 22.9%; Pred. No. 5,7e-24;
 Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

QY 55 NIPKYNDC--TYLNPVGVNADANIT-----ISQVACHDQ-----VAVTILMS 99
 DB 49 NCTVKNSTCLDDSWHP-----RNLTPSSPKDLQIQLHRAHTQOGLFPVAAHLEWT 99
 QY 100 -PGALGIEFLKGRVILIELKSEGOCCOLILKDPKQINSFKRTGMSQPLNMKEETD 158
 DB 100 LQTDASILYIEGALSTLQANTNERLCVR--FEFLSKLRHHRMRRTFSHFV--VDPDQ 156
 QY 159 YFAKV--VPPPSIKNESNHPFFRTACDLLLPDNLACK--PFWKPRNL----- 205
 DB 157 YETVYHLLPKPIPDGDHNSKNFLVPDCHARKVTPPCSSGSLMDP--NITVETLEAH 215
 QY 206 -----NISQHSMOVSPDAPNPFRRFYLLYKAKHGPCFKATCKQEQTTETT 236
 DB 216 QLRVSEFTLWNESTHYQILTSFPMENHSCFEHNR--HIPAPRBEFFQRSNVTLLTNLK 274
 QY 257 SCLLQNVSPGDYIIELVDT--NTRKVAHYALKPVHSPWAGIRAMALTVPVVISAF 313
 DB 275 GCCRHQVQIQPFPSSCLNCLRHSAIVSCPEMDTPPPIPDYMLVWYMTTGISILLVG 334

RESULT 7

US-08-978-773-4
 ; Sequence 4, Application US/08978773
 ; Patent No. 6083906
 ; GENERAL INFORMATION:
 ; APPLICANT: Trout, Anthony
 ; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple PowerMacintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,773
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 60/052,525
 ; FILING DATE: 27 NOVEMBER 1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2623-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 866 amino acids
 ; TYPE: amino acid

QY 314 ATLEFWCKRKGQENTYSHDESSSESTYTAALPRELRPP-----KVFLCYSKQGN 369
 DB 335 SVILLIVCMTWRLAGPS---EKYSDDTKYTDGLPAAADLPPILKPKRWIITSA--DHPL 390
 QY 370 HANVQCFAYFLQDFGCEVALDLMEDFSLCREGQEWV-----IOLHESQFIIVCSKG 425
 DB 391 YQVVLKFAQFLTACTETVALDLLEGOAISBAGWTVWRQOEWESNSKIIVLCRSG 450
 QY 426 MKYFVDRKNYKHKGQ-----RSGKGEFLVAVSAIAEKLQAKQSSAALSKEIA 477
 DB 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAAMNMLIPDKR-----PACFGTYVV 501
 QY 478 VVE-DYSCBGDVPGIIDLSTKYRLMDNLPLQCHHNSRDGLQEPQHTQG--SRNRYF 534
 DB 502 CYFSEVSCDGDVDDLFGAARFPLMDRFEV--YFRIQDLEMFQPGMHWVGLSGNYL 559
 QY 535 RSKGSLVYVAICNMQFIDSEPDWFE-----KQVFFHPPLRYRPPVLEKFPDGL 586
 DB 560 RSPGRLRALRLRFRDQVRCDFWFEBCENTYASADQDASLDBEV--FEERPLRP--GTGI 617
 QY 587 VLNDVCKPGPESDFCLKYAPVLAGATGPADQSHEQH----- 624
 DB 618 VKQAPLVRE--PGSQACIAD--FLVGEKGAAVAKLEPHLQPRGQAPAPQLHTLVLAEEG 675
 QY 625 -----GGLDDGGRAPLDSALQPLHTVYKAGSPEDMRDSCGYDSSVPSSEL 676
 DB 676 ALVAAVEPGPLADGAAVRLAEGEGACPLGSPGAG-----RNSVLF--LPVDPEDS 726
 QY 677 PLMEGLSTQDTERSTLSYSSSSSGAGEERPALPSKLLSSGSCCKADLGC 726
 DB 727 PL--GSSTPMASPDLLPBDVR-----EHLGMLSLFEGSLSCQAGGC 768

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-773-4

Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

```

QY 55 NTFKYNDC--TYLNPVGHVADANNT-----ISQVACHQ-----VAVTILWS 99
DB 49 NCTVKNSTGLDSDWHP-----RNLTPSSPKDLOQLHFAHQOGLFPVANHIEWT 99
QY 100 -PGALGIEPLKGFVILBELKSEGRQCOQLIKDPKOLNSFKRTGMSQPLANKFETD 158
DB 100 LQTDASILYLEGABLSVLQNTNERLCVR--PEFLSKLHHNRMRFTFSHFV-VDPDGE 156
QY 159 YFVKV--VPPSITKESNTHPPFRTRACDLLQPDNLACK--PFWKPRNL----- 205
DB 157 YEVTVNHLKPRIPDGPBNHQSKNFLVPDCEHAKMKVTPCMSSGSLMDP-NITVETLEAH 215
QY 206 -----NISGSDMVSFDHAPNNGFRFFYLHYKAKHGSPKRTCKQEQOTETT 256
DB 216 QLRVSTLWNESTHYQILTSFPHMNHSCFEHMH-HIPARPEEFHQNSVNTLTIRNLK 274
QY 257 SCILQNVSPGDYIIEIVDDT--NTTRKVMHYALKPVHSPMAGPIRAMAITVPLVVISAF 313
DB 275 GGCRRHQVOIQPFSSGLNDCLRHSAIVSCPEMDTPEPIEDVMPVWVYFTGISILVIG 334
QY 314 ATLFTVMCRKQOENIYSHLDESSBSSTYTAALPRERLRPP--KVFLCYSSKDGON 369
DB 335 SVILLIVCMTWRLAGSGS--EKYSDDTKYTDGLPADLIPPLKPRKWIIVISA-DHPL 390
QY 370 HNNVVOCPAYFLDPFGCGEVALDLMBDFSLCREGOREWV----IKIHNSQPLIIVCSKG 425
DB 391 YDVVVKLKPQFLITACGTEVALDLLEBOAISAGVMTWGRQKQEWESNSKIIVLCSRG 450
QY 426 MKYFVVDKKNYKHKGG-----RSGSGELFLVAVSAIAEKLQAKOSSAALSKEFTA 477
DB 451 TR----AKNQALLIGRAPVRLRCDHGKPVGDLTFTAMNMILLPPFKR-----PACFGTYV 501
QY 478 VVF-DYSCGDVPGIIDLSTKRYLMONLPOLCSHLHSRDHGLQEOEPQHTQG--SRRTNF 534
DB 502 CYFSEVSCGDVVDLFGCAAPRYPLMDRFEEV--YFRIQIDLEMPQGRMHRVGLSDNYL 559
QY 535 RSGSGSLVVAIGNMHQPIDEEDWPE-----KQFVPHRPLRYRPRVLEKDSGL 586
DB 560 RSGGQQLRALDRFRDMQVRCDFECENTYLSADQDAPSLDEEV-FEERPLLP-GTGI 617
QY 587 VLNDVCKECPESDPCIKYEAIVLGATGPADSOHESQH-----624
DB 618 VKRAPVLR-PSGQACLALD-PLVGEEGCAVAKLEPHLOPQGPAPQPLHTVLAAEAG 675
QY 625 -----GGLDDGARRPALDGSAAILOPLHTVKAQSPDMPRDSGIYDSSVPSSELSL 676
DB 676 ALVAAVEPGLADGAVALRLALAGEACPLDGSAGAG-----RNSVLF--LPVDPDS 726
QY 677 PLMEGISTQGTSTSTESVSSSSGIGREPRALPSEKLSGCKADLGC 726
DB 727 PL--GSSTPMASPDLLPEDVR-----EHLGLMISLFEQSLSCQAQGC 768

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RESULT 8
US-09-022-253-10

Sequence 10, Application US/09022253
Patent No. 6096305

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Farnlow, William

TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

```

/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: Apple Power Macintosh
/ SOFTWARE: Microsoft Word for Apple, Version 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/022,253
/ FILING DATE:
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US/08/620,694
/ FILING DATE: 21-MARCH-1996
/ APPLICATION NUMBER: USN 08/538,765
/ FILING DATE: 7 AUGUST 1995
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: USN 08/410,535
/ FILING DATE: 23 MARCH 1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,695
/ REFERENCE/DOCKET NUMBER: 2617-B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206)
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 866 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-022-253-10

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Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

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QY 55 NTFKYNDC--TYLNPVGHVADANNT-----ISQVACHQ-----VAVTILWS 99
DB 49 NCTVKNSTGLDSDWHP-----RNLTPSSPKDLOQLHFAHQOGLFPVANHIEWT 99
QY 100 -PGALGIEPLKGFVILBELKSEGRQCOQLIKDPKOLNSFKRTGMSQPLANKFETD 158
DB 100 LQTDASILYLEGABLSVLQNTNERLCVR--PEFLSKLHHNRMRFTFSHFV-VDPDGE 156
QY 159 YFVKV--VPPSITKESNTHPPFRTRACDLLQPDNLACK--PFWKPRNL----- 205
DB 157 YEVTVNHLKPRIPDGPBNHQSKNFLVPDCEHAKMKVTPCMSSGSLMDP-NITVETLEAH 215
QY 206 -----NISGSDMVSFDHAPNNGFRFFYLHYKAKHGSPKRTCKQEQOTETT 256
DB 216 QLRVSTLWNESTHYQILTSFPHMNHSCFEHMH-HIPARPEEFHQNSVNTLTIRNLK 274
QY 257 SCILQNVSPGDYIIEIVDDT--NTTRKVMHYALKPVHSPMAGPIRAMAITVPLVVISAF 313
DB 275 GGCRRHQVOIQPFSSGLNDCLRHSAIVSCPEMDTPEPIEDVMPVWVYFTGISILVIG 334
QY 314 ATLFTVMCRKQOENIYSHLDESSBSSTYTAALPRERLRPP--KVFLCYSSKDGON 369
DB 335 SVILLIVCMTWRLAGSGS--EKYSDDTKYTDGLPADLIPPLKPRKWIIVISA-DHPL 390
QY 370 HNNVVOCPAYFLDPFGCGEVALDLMBDFSLCREGOREWV----IKIHNSQPLIIVCSKG 425
DB 391 YDVVVKLKPQFLITACGTEVALDLLEBOAISAGVMTWGRQKQEWESNSKIIVLCSKG 450
QY 426 MKYFVVDKKNYKHKGG-----RSGSGELFLVAVSAIAEKLQAKOSSAALSKEFTA 477

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Db 451 TR----AKQALLGRGAPVRLCDHGKPVGDLFTAAANNMLPDKF-----PACFGTYVV 501
Qy 478 VYF-DYSCGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDLGLOEPQHTROG--SRNRY 534
Db 502 CYFSEVSCGDVVDLFGAARPYLMDRFEEV--YFRIDLEMPQGRMHRVGLSGDNYL 559
Qy 535 RSKSGSLVVAICNMHQFIDEBPWF-----KQVFFHPPLRYRREPLEKFDGSL 586
Db 560 RSPGGRQLAALDRFRDQVRCDFWECENLYSADQDAPSLDEEV-FEELPLP- GTGI 617
Qy 587 VLNDVWCKGPEBSDFCLKVAPVLTGATGPADSQHSQH----- 624
Db 618 VKRAPLVRS-PGSOACIAD-PLVGEEGGAVAKLEPHLQPRGAPAPQPLHTLVLAEBG 675
Qy 625 -----GGLDDGRRPALDGSALQPLHTVKAQSPDMRDSGITDSSVPSSEL 676
Db 676 ALVAAVEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDPEDS 726
Qy 677 PLMEGLSTQDTERSTLSESVSSSGLEBEPALPSKLSGSCAKDLGC 726
Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGMLSLFEGSLSCQAGGC 768

RESULT 9

US-09-022-260-10
Sequence 10, Application US/09022260
Patent No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanelow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-10
Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

Qy 55 NTFKYDNC--TTYANPVGKAVIADAQNT-----ISQYACDQ-----VAATILMS 99
Db 49 NCTVKNSTCIDLSWIHP-----RNLTPSPKDLQIQLFHATQOQDLFPVAHIEWT 99
Qy 100 -PGALIEFLKGRVILIELKSBGRQCOOLIKDPKQLNSSFRTMSEQPLNMKEFD 158
Db 100 LQTDASILYLGAEISVLQLTNTERLCVR--FEELSKLHHHRKMFRTSHFV-VPPDOE 156
Qy 159 YFVKV--VPEPSIKNSNHPFEFFTRACDLLQPDNLACK--PWXKRNLT----- 205
Db 157 YEVTVHLLPKPIPDGDPNHSKNFLVPDEHARMKVTTCMSGSLMDP-NIVETLEAH 215
Qy 206 -----NISQSGDMQVSPDHANFNFPFYLHYLKHGPPKRTCKQEQTTETT 256
Db 216 QLRSFTLWNSTHYQILLTSPFMENHSCFEHMH-HIPAPPEEFHORSNVTLTIRNLK 274
Qy 257 SCLQVNSPDYIIELVDT--NTTRKVMHAKKPVHSPMAGPIAMATVPLVVISAF 313
Db 275 GCCRHQVQIQPFSSCLNDCLRHSAVSCEPMDTPEPIPDYMPLVWYFRTGISILVAG 334
Qy 314 ATLFTWCKRKOQENIYSHDEESSSESTYTAALPRELRPRP---KYFLCYSSKQGN 369
Db 335 SVTLIVCTWKLARGS---EKYSDTKYTGDLPAADILPPLKRYKWIYSA-DHPL 390
Qy 370 HNNVQCFAYFIODFCGCEVALDLMEDFSLCBEGRENV---IQKHESQFIIVCSHG 425
Db 391 YVDVVLKFAQFLITACGTEVALDLLEEQAISEAGVWTVGRQKEWVESNSKIIVLCRG 450
Qy 426 MKYFVDKRYKTKRGK-----RSGKGELELVAVNSIAETLRQAKSSSALSKFLA 477
Db 451 TR----AKQALLGRGAPVRLCDHGKPVGDLFTAAANNMLPDKF-----PACFGTYVV 501
Qy 478 VYF-DYSCGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDLGLOEPQHTROG--SRNRY 534
Db 502 CYFSEVSCGDVVDLFGAARPYLMDRFEEV--YFRIDLEMPQGRMHRVGLSGDNYL 559
Qy 535 RSKSGSLVVAICNMHQFIDEBPWF-----KQVFFHPPLRYRREPLEKFDGSL 586
Db 560 RSPGGRQLAALDRFRDQVRCDFWECENLYSADQDAPSLDEEV-FEELPLP- GTGI 617
Qy 587 VLNDVWCKGPEBSDFCLKVAPVLTGATGPADSQHSQH----- 624
Db 618 VKRAPLVRS-PGSOACIAD-PLVGEEGGAVAKLEPHLQPRGAPAPQPLHTLVLAEBG 675
Qy 625 -----GGLDDGRRPALDGSALQPLHTVKAQSPDMRDSGITDSSVPSSEL 676
Db 676 ALVAAVEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDPEDS 726
Qy 677 PLMEGLSTQDTERSTLSESVSSSGLEBEPALPSKLSGSCAKDLGC 726
Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGMLSLFEGSLSCQAGGC 768

RESULT 10

US-09-022-259-10
Sequence 10, Application US/09022259
Patent No. 6101104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanelow, William
TITLE OF INVENTION: No. 6101104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-259-10
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Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5.7e-24; Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

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55 NITPKYDNC--TLYLNPVKGVIADQNT-----ISQYACHQ-----VAVTILMS 99
49 NCTVKNSTCLDSDWIHP-----RNLTPSSPKDLQIQLHFAHTQOQDLFPVAHIEMT 99
100 -PGALGIEPLKGRVILBELKSGROCOQILKDPKQLNSFKRTGMSQPLMKFETD 158
100 LQTDASILYLEGALSLVQLNTNERLCVR--PEFLSKLRHHRMRPTFSHFV--VDPDGE 156
159 YPKRV--VPPPSIKNESNHPFRFRACDILLQPDNLAK--PFYKRNLT-----205
157 YEVTYHRLPRPIPDGDPNHQSKNPLVDPCEHAKMKVTPPCSSGSLMDP--NITVETLEAH 215
206 -----NISQHSQDMQVSPHAPRNFGRFPFYLYKLKHGPRFKRTCKQEQTETT 256
216 QLRVSTLTWNESHYQILTLSPFMENHSCFEMNH--HIPRREBEFRQSNVTLIRNLK 274
257 SCLQNVSPDYILIELVDLT--NTTRKVMYALKPVHSGAPIRAMATVPLVVISAF 313
275 GCCRHQVQIOPFSSCLNDCLRHSATVSCPEMDTPREDVYMLWYVFTGISILVVG 334
314 ATLPTWCKRQKQENIYSHLDESSSSSTYALPREKLRRP---KVPLCTSSQDGN 359
335 SVILLVCMTRWLAGPQS---EKYSDTKYTKTDGLPAADLLPPLKPKRWIITSA--DHPL 390
370 HMMVOCFAFLQDFGCEVALDLMEDFSLCRREGOREWV---IQKHESQFIIVCSKG 425
391 YUDVYLKFAQFLITACTEVALDLLEQALISEAGWMTVGRQKQENVESKIIIVLCSRG 450
426 MKYFVDKVKNYKHGG-----RSGSGELFLVAVSAIAEKLQAKOSSSAALSKFIA 477
451 TR-----AKQDALLGRGARVRLRCDHGRVGDLLFTAAWMMILPRPKR-----PACFGYVV 501
478 VVF--DYSCEBDVVGILDLSTKYRLMDNLPOLCSHLSHRDGLORPGQHTQG--SRNRY 534
502 CVFSSEVSCDGDVLDLFGAARPRYPLMDRFBEV--YFRLODLEMPQPGMHVGLSELGDNYL 559
535 RSGSGSLVYALICNMHQFIDEBPDMFE-----KQFVFPHPRLRYRPFVLKRTDGL 586
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DB 560 RSPGGRQLAALDRFRDWQVRCDFWECENTLYSADQDAPSIDEXV-FPEPLLP-CTGI 617
QY 587 YLNDWCKRQPSDFLKYEARVYLGATGPADQSHSQH-----624
DB 618 VKRAPLVRE-PSQACLAID-PLVGEEGGAVAKLEPHIQPGQAPAPQPLHTLVLAEBG 675
QY 625 -----GGLQDGEARPALDGSALOPLHTVKGSPSDMPRDSGIYDSSVPSSELSL 676
DB 676 ALVAAVEPPLADGAARVRLALNGEGACPLSPGAG-----RNSVLF---LPVDPDS 726
QY 677 PLMEGLSTDQTESLTVESVSSSGIGEBEPALPSKLLSSGCCRADLGC 726
DB 727 PL--GSSTWMA SPDLLPEDEV-----EHLFGMLSLFQSLSCQAGGSC 768
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RESULT 11
US-09-022-257-10
Sequence 10, Application US/09022257
Patent No. 6197525

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,257

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 866 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-257-10

Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5.7e-24;

Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

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55 NITPKYDNC--TLYLNPVKGVIADQNT-----ISQYACHQ-----VAVTILMS 99
49 NCTVKNSTCLDSDWIHP-----RNLTPSSPKDLQIQLHFAHTQOQDLFPVAHIEMT 99
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QY 100 -PGALGIEFLKGRVILIEELKSEGRQCOQLILKDPKQINSFKRTGMSQPLMKFETD 158
 DB 100 LQTDASILYEGALSTVLQNTNRRLCVR--FEFLSLRHHRRWRTFSHFV--VDDOE 156
 QY 159 YFAKV--VPPSINKSNYHFFPRTACDILLQPNLACK--PFMKPRL----- 205
 DB 157 YEVVHHLKPRIPDGDNDHOSKNFLVPDCEHARKVTTPCMSGSLMDP--NIVETLEAH 215
 QY 206 -----NISQSDMQVSPDAPNPNFGRFYLLHYKLKHEPFRKTKCKQQTETT 256
 DB 216 QLRVSTLWMESTHYQILTSFPMENHSCFENH--HIPAPREEFHORSVTLTLNLK 274
 QY 257 SCLQNVSPDYIIELVDT--NTTRKVMHYALKPVHSPWAGIRAMATVPLVISA 313
 DB 275 GCRHQVQIQPFSSCINDCLRHSAATVSCPEMPTPEPIDYMLWYFITSILLVG 334
 QY 314 ATLFTWCRKQOENIYSHLDESSSSTYTAALPRELRPR--KVLCSYKQGN 369
 DB 335 SVILLIVCMTWRLAGPS--EKYSDTKYTDGLPADLIPPLKPRKWTIYSA--DHPL 390
 QY 370 HANVOCFAFLDFCGCEVALDLMEDFSLCRGOREWV----IQKHESQFTIVVCSKG 425
 DB 391 YDVVLKFAQFLTLACTEVALDLBEQALSEAGVMTWGRQKQEWESNSKIIVLCSRG 450
 QY 426 MKCFVDKQNYKHGGG-----RSGKGEFLVAVSAIAEKLROAKQSSAALSKEIA 477
 DB 451 TR----AKQOALLGRGAPVRLRCDHKGKPVGDLFTAAAMNMLIPDKR-----PACFGTYV 501
 QY 478 VYF-DYSCBGDVPGLDLSKTYRLMDNLPOLCSHLSRDHLOEPOHTRQG--SRNYP 534
 DB 502 CYSEVSCDGDVPLFGAARYPPLMDRFEV--YFRIDLEMPQPGMHVGLSGNYL 559
 QY 535 RSKSGRLVYALCNMHOPIDEBPWF-----KQVFPHPPLRYRREPLEKFDGL 586
 DB 560 RSPGGRQALRALRFRDMQVRCDFWFCENLYSADDDAPSLDBEV--FEELPLP--GTGI 617
 QY 587 VLVDMVCKPESDFCLKVAEPVLTGATGRPADSCHESQH----- 624
 DB 618 VKQAPLVR--PGSQACLAID--PLVGEEGAAVAKLEPHLOPRGQAPAPLHTLVLAEEG 675
 QY 625 -----GGLDDGEARPALDGSALLOPLHTVYKAGSPDMPRDSGIYDSSVPSLSL 676
 DB 676 ALVAAVPEGLADGAVALRLALAGEGACPLIGSPAG-----RNSVLP--LPVDEDS 726
 QY 677 PLMEGLSTQDETSSLTESVSSSGLEEBEPALPSKLLSGSCAKDGLC 726
 DB 727 PL--GSSTPMASPLLPEDVR-----EHLGLMLSLFBQSLSCQAGGC 768

RESULT 12
 US-09-549-679-10
 ; Sequence 10, Application US/09549679
 ; Patent No. 6680057
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; Spriggs, Melanie
 ; Panblow, William
 ; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/549, 679

; FILING DATE: 14-Apr-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/620,694
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: USN 08/410,535
 ; FILING DATE: 23 MARCH 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,695
 ; REFERENCE/DOCKET NUMBER: 2617-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206)
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 866 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 ; US-09-549-679-10
 ;
 ; Query Match 8.0%; Score 315; DB 2; Length 866;
 ; Best Local Similarity 22.9%; Pred. No. 5,7e-24;
 ; Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;
 ;
 ; 55 NITFKYDNC--TTLNPGKGVADANIT-----ISQVACHQD---VAVTLWS 99
 ; DB 49 NCTVKNSTGLDSDMHP-----RNLTPSSPKDLQILHFAHQOGLFPVAHIEMT 99
 ;
 ; QY 100 -PGALGIEFLKGRVILIEELKSEGRQCOQLILKDPKQINSFKRTGMSQPLMKFETD 158
 ; DB 100 LQTDASILYEGALSTVLQNTNRRLCVR--FEFLSLRHHRRWRTFSHFV--VDDOE 156
 ;
 ; QY 159 YFAKV--VPPSINKSNYHFFPRTACDILLQPNLACK--PFMKPRL----- 205
 ; DB 157 YEVVHHLKPRIPDGDNDHOSKNFLVPDCEHARKVTTPCMSGSLMDP--NIVETLEAH 215
 ;
 ; QY 206 -----NISQSDMQVSPDAPNPNFGRFYLLHYKLKHEPFRKTKCKQQTETT 256
 ; DB 216 QLRVSTLWMESTHYQILTSFPMENHSCFENH--HIPAPREEFHORSVTLTLNLK 274
 ;
 ; QY 257 SCLQNVSPDYIIELVDT--NTTRKVMHYALKPVHSPWAGIRAMATVPLVISA 313
 ; DB 275 GCRHQVQIQPFSSCINDCLRHSAATVSCPEMPTPEPIDYMLWYFITSILLVG 334
 ;
 ; QY 314 ATLFTWCRKQOENIYSHLDESSSSTYTAALPRELRPR--KVLCSYKQGN 369
 ; DB 335 SVILLIVCMTWRLAGPS--EKYSDTKYTDGLPADLIPPLKPRKWTIYSA--DHPL 390
 ;
 ; QY 370 HANVOCFAFLDFCGCEVALDLMEDFSLCRGOREWV----IQKHESQFTIVVCSKG 425
 ; DB 391 YDVVLKFAQFLTLACTEVALDLBEQALSEAGVMTWGRQKQEWESNSKIIVLCSRG 450
 ;
 ; QY 426 MKCFVDKQNYKHGGG-----RSGKGEFLVAVSAIAEKLROAKQSSAALSKEIA 477
 ; DB 451 TR----AKQOALLGRGAPVRLRCDHKGKPVGDLFTAAAMNMLIPDKR-----PACFGTYV 501
 ;
 ; QY 478 VYF-DYSCBGDVPGLDLSKTYRLMDNLPOLCSHLSRDHLOEPOHTRQG--SRNYP 534
 ; DB 502 CYSEVSCDGDVPLFGAARYPPLMDRFEV--YFRIDLEMPQPGMHVGLSGNYL 559
 ;
 ; QY 535 RSKSGRLVYALCNMHOPIDEBPWF-----KQVFPHPPLRYRREPLEKFDGL 586
 ; DB 560 RSPGGRQALRALRFRDMQVRCDFWFCENLYSADDDAPSLDBEV--FEELPLP--GTGI 617
 ;
 ; QY 587 VLVDMVCKPESDFCLKVAEPVLTGATGRPADSCHESQH----- 624
 ; DB 618 VKQAPLVR--PGSQACLAID--PLVGEEGAAVAKLEPHLOPRGQAPAPLHTLVLAEEG 675
 ;
 ; QY 625 -----GGLDDGEARPALDGSALLOPLHTVYKAGSPDMPRDSGIYDSSVPSLSL 676

Db 676 ALVAAVEPGLADGAARLALAGEACPLLSGPGAG-----RNSVLF---LPVDPEDS 726
Qy 677 PLMEGLSTDQETSTLSESVSSSGLEEEPPALPSKLLSSGCKADLGC 726
Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGLMLSLFQSLSCQAQGGC 768

RESULT 13
US-10-033-522-1
Sequence 1, Application US/10033522
Patent No. 6793919
GENERAL INFORMATION:
APPLICANT: MOHLER, Kendall M.
TITLE OF INVENTION: Methode for Treating Rheumatoid Arthritis Using IL-17 Antagonists
FILE REFERENCE: 2982-A
CURRENT APPLICATION NUMBER: US/10/033,522
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 60/241,230
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 866
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-522-1

Query Match 8.0%; Score 315; DB 2; Length 866;
Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

Qy 55 NITPKYDNC--TTYLNPVGKVIADAQNT-----ISQYACHDQ-----VAVTILMS 99
Db 49 NCTVKNSTLDDSWIHP-----RNLTSPSPKDLQQLHFAHTQOQDLFPVANIEMWT 99
Qy 100 -PGALGIEFLKGFVILLEELKSEGRQCOQLILDKPKOLNSFKRTGMSQPLNMKEFTD 158
Db 100 LGTDAISILYEGAEISVLQNTNERLCVR--FEPLSKLHNHRMRFTFSHFV--VDPDQE 156
Qy 159 YPKVY--VPPRSIKNESNHPFFRTFRACDILLQDPNLACK---PRMKPRNL----- 205
Db 157 YEVTYHNLKPRIPDGGPNHOSKNFLVPDCENHAKMKTTPCMSSGSLMDF--NITVETLEAH 215
Qy 206 -----NISQSGDMQVSFDHAPNFGFRFFLYLHYKLKHEGPRKRTCKQEOQTETT 256
Db 216 QLRVSTLWNESTHYQILTSFPMENHSCFEMH--HTRPREBEFHQSNVTLTLRLNK 274
Qy 257 SCLLQNVSPGDYILIELVDLT--NTTRKVMYALKPVNSPWAGPIRAMAITYPLVVISAF 313
Db 275 GCGRHQVOIQPFSSCLNDCLRHSAIVSCPEMDTPREPIDVMPLMVYVFTGISILLVG 334
Qy 314 ATLFTWCKRKKQOENIYSHLDESSSESTYTAALPRERLRPP---KYFLCYSSKDGON 369
Db 335 SVILLIVCMTWRLAGBS---EKYSDDTKYTDGLPAADLIPPLKPKKWIIVISA--DHPL 390
Qy 370 HMMVVCQFAYFLDOPGCEVALDLMEPDLCREGOREWY-----IOKIHESQFIIVCSKG 425
Db 391 YDVVNLKFAQFLTLTACSTVALDLLEQALISEAGVMTWGRQKQOENVESKTIIVLCSRG 450
Qy 426 MKYFVVDKKNYKHKGG-----RSGSGELFLVAVSAIAEKLRAQAKOSSAALSKFA 477
Db 451 TR-----AKWALLGRAPVRLRCDHGKPVGDLPFTAMNMMLLPDKR-----PACFGTYV 501
Qy 478 VYF--DYSCEGDVPGIIDLSTKRYLMDNLPOLCSHLSPDHGLOVPGQHTROG--SRRTNF 534
Db 502 CYFSEVSCDGDVLDLFGAARPRYPLMDRFEV--YFRIDLEMFQPGRMHIVGELSGDNYL 559
Qy 535 RSKSGSLIYVAICMHIQFIQDEBPDPRE-----KQFVPHRPLRYREPVLEKPDSDL 586
Db 560 RSPGSGQLRALRLRFRDQVRCPEWFECEYLVSADDDADSLDEEV--FEPLLRP--GTGI 617
Qy 587 VLANDWCKPGESEDPCLIKVAPYLGAATGPADSQHESQH----- 624

Db 618 VKRAPLVRE--PSSQACLAID--PLVGEEGAANAVALKEPRILQPRGQAPARPLHTLVLAERG 675
Qy 625 -----GGLDQDEARPALDGSAAOLPLHTVKGASPSDMPDSGIYDSSPSSELSL 676
Db 676 ALVAAVEPGLADGAARLALAGEACPLLSGPGAG-----RNSVLF---LPVDPEDS 726
Qy 677 PLMEGLSTDQETSTLSESVSSSGLEEEPPALPSKLLSSGCKADLGC 726
Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGLMLSLFQSLSCQAQGGC 768

RESULT 14
US-09-949-002-403
Sequence 403, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VERTER, J. Craig et al.
TITLE OF INVENTION: POLYMOERPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 403
LENGTH: 866
TYPE: PRT
ORGANISM: Human
US-09-949-002-403

Query Match 8.0%; Score 315; DB 2; Length 866;
Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

Qy 55 NITPKYDNC--TTYLNPVGKVIADAQNT-----ISQYACHDQ-----VAVTILMS 99
Db 49 NCTVKNSTLDDSWIHP-----RNLTSPSPKDLQQLHFAHTQOQDLFPVANIEMWT 99
Qy 100 -PGALGIEFLKGFVILLEELKSEGRQCOQLILDKPKOLNSFKRTGMSQPLNMKEFTD 158
Db 100 LGTDAISILYEGAEISVLQNTNERLCVR--FEPLSKLHNHRMRFTFSHFV--VDPDQE 156
Qy 159 YPKVY--VPPRSIKNESNHPFFRTFRACDILLQDPNLACK---PRMKPRNL----- 205
Db 157 YEVTYHNLKPRIPDGGPNHOSKNFLVPDCENHAKMKTTPCMSSGSLMDF--NITVETLEAH 215
Qy 206 -----NISQSGDMQVSFDHAPNFGFRFFLYLHYKLKHEGPRKRTCKQEOQTETT 256
Db 216 QLRVSTLWNESTHYQILTSFPMENHSCFEMH--HTRPREBEFHQSNVTLTLRLNK 274
Qy 257 SCLLQNVSPGDYILIELVDLT--NTTRKVMYALKPVNSPWAGPIRAMAITYPLVVISAF 313
Db 275 GCGRHQVOIQPFSSCLNDCLRHSAIVSCPEMDTPREPIDVMPLMVYVFTGISILLVG 334
Qy 314 ATLFTWCKRKKQOENIYSHLDESSSESTYTAALPRERLRPP---KYFLCYSSKDGON 369
Db 335 SVILLIVCMTWRLAGBS---EKYSDDTKYTDGLPAADLIPPLKPKKWIIVISA--DHPL 390
Qy 370 HMMVVCQFAYFLDOPGCEVALDLMEPDLCREGOREWY-----IOKIHESQFIIVCSKG 425
Db 391 YDVVNLKFAQFLTLTACSTVALDLLEQALISEAGVMTWGRQKQOENVESKTIIVLCSRG 450
Qy 426 MKYFVVDKKNYKHKGG-----RSGSGELFLVAVSAIAEKLRAQAKOSSAALSKFA 477
Db 451 TR-----AKWALLGRAPVRLRCDHGKPVGDLPFTAMNMMLLPDKR-----PACFGTYV 501
Qy 478 VYF--DYSCEGDVPGIIDLSTKRYLMDNLPOLCSHLSPDHGLOVPGQHTROG--SRRTNF 534
Db 502 CYFSEVSCDGDVLDLFGAARPRYPLMDRFEV--YFRIDLEMFQPGRMHIVGELSGDNYL 559


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QY 535 RSKSGSLVYALICNMHOFIDBEPDME-----KQFVFPHPPLRYREPLEKFDGSL 586
DB 560 RSGGRLRALRDLFRMOWRCBPMFECENLYSADDDABSLDBEV-FEPLLP-CTGI 617
QY 587 VLNDVCKPSPESDFCLKVEAPVLTGATGPADSQHSQH----- 624
DB 618 VKAPALVRE-PGQACLAID-PLVGEAGAAVAKLEPHLQPRGQAPAPQPLHTVLAAEG 675
QY 625 -----GGLDDGGRPALDGAALQPLHTVKAGSPDMRDSGITYSSVPSSEL 676
DB 676 ALVAABEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDEDS 726
QY 677 PLMEGLSTQDTERSTLTSVSSSSGLGEBEPALPSKLLSSGCKADLGC 726
DB 727 PL-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

```

RESULT 15

```

US-09-949-002-412
; Sequence 412, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949, 002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 876
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-412

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Query Match 8.0%; Score 315; DB 2; Length 876;
 Best Local Similarity 22.9%; Pred. No. 5.8e-24;
 Matches 176; Conservative 105; Mismatches 341; Indels 148; Gaps 33;

```

QY 55 NITFKYDNC--TYLNVGKGVIAQAQNT-----ISQYACHDQ-----VAVTILMS 99
DB 59 NCTVKNSTCLDDSWHP-----RNLTPSSPKDQLQIHPAHTQCGDLFPVAHLEWT 109
QY 100 -PGALGIBFLKGRVILIELKSGROCOQLILKDPKOLNSSFKRTGMSQPLMKFETD 158
DB 110 LQTDASTLYEGALSVLQJLNTNERLCVR--FEFLSKLRHHHRMRFTFSHFV--VDPDE 166
QY 159 YFVKV--VPPSIKNBSNHPFFRTACDILLQPDNLACK--PFMKPRNL----- 205
DB 167 YETVTHLPRKIPDGDNDHOSKNFLVPCDHAKMKYTPCMSSGSLMDP--NITVETLEAH 225
QY 206 -----NISQGSMDQVSFDHAPNFGFRFFYLHYKLHSGPFKRTCKOQTTEYT 256
DB 226 QLRVSFTLMNESTHYQILTSFPMENHSCFEHMH--HIPAPREFHQRNSVTLTLNLK 284
QY 257 SCLLQNVSPGDYIIEIVDVT--NTTRKVMHYALKPVHSPWAGIRAMATVPLVVISAP 313
DB 285 GCCRHQVQIOPFPSSCLNDCLRHSAIVSCBMDPTVLTADYMLVWYWFITGISILVG 344
QY 314 ATFTVWCRKQOENIYSHLDESSBSSTYALPRERLRP-----KVELCYSSKQGN 369
DB 345 SVILLIYCMTRLAGPS---EKYSDTKYTDGLPADLIPPLKPRKWIITYSA--DHL 400
QY 370 HNAVOCFAVFLDFCCCEVALDLMEDPSLCRSGQREWV---IQKHESQPIIVVCSKG 425
DB 401 YVDVVLKFAQFLPLACCTEVALDLLEQALISEAGVMTVGRKQKQEWESNKKIIVLC SRG 460
QY 426 MKCFVDDKQNTKHKGG-----RSGKGELFLVAVSAIAKLRQAKOSSSAALSKEIA 477

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DB 461 TR-----AKWQALLRGAPVRLRCHGKGVLDLFTAAANNMLLPDFKR-----PACFGTYV 511
QY 478 YF--DISCEBDVGIIDLSYKRYLMDNLQOLCSHLSRDLGLOPQHTQG--SRNRYF 534
DB 512 CYPSEVSCDGDVDDLFGAARPRYPLMDRFEBV--YFRIODLEMFQPMHRVGLSGDNYL 569
QY 535 RSKSGSLVYALICNMHOFIDBEPDME-----KQFVFPHPPLRYREPLEKFDGSL 586
DB 570 RSPGRLRALRDLFRMOWRCBPMFECENLYSADDDABSLDBEV-FEPLLP-CTGI 627
QY 587 VLNDVCKPSPESDFCLKVEAPVLTGATGPADSQHSQH----- 624
DB 628 VKAPALVRE-PGQACLAID-PLVGEAGAAVAKLEPHLQPRGQAPAPQPLHTVLAAEG 685
QY 625 -----GGLDDGGRPALDGAALQPLHTVKAGSPDMRDSGITYSSVPSSEL 676
DB 686 ALVAABEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDEDS 736
QY 677 PLMEGLSTQDTERSTLTSVSSSSGLGEBEPALPSKLLSSGCKADLGC 726
DB 737 PL-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 778

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Search completed: March 1, 2006, 10:32:01
 Job time : 62 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 10:23:47 ; Search time 90 Seconds
(without alignments)
3602.906 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
Sequence: 1 MAPWQLGCVFPTVNAACNG.....SCKADLCGRSYDELAAVAP 738

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3948	100.0	738	4	AAU09904 Human int
2	3948	100.0	738	8	ADU69244 Human SER
3	3944	99.9	738	4	AAU09953 Human int
4	3943	99.9	738	4	AAU09954 Human int
5	3941	99.8	738	4	AAU09951 Human int
6	3941	99.8	738	4	AAU09952 Human int
7	3941	99.8	738	4	AAU09956 Human int
8	3937	99.7	738	4	AAU09957 Human int
9	3937	99.7	738	4	AAU09955 Human int
10	3918	99.2	738	5	ABR07628 Human CYC
11	3908	99.0	738	8	ADU69242 Human SER
12	3908	99.0	738	8	ADU69242 Human SER
13	3901	98.8	738	5	ABR07626 Human CYC
14	3891	98.6	738	5	ABR07627 Human CYC
15	3835.5	97.2	738	5	ABR07627 Human CYC
16	3830.5	97.0	738	5	ABR07627 Human CYC
17	3706	93.9	738	5	AAU11355 Human DNA
18	3687	93.4	738	4	AAU10602 Human int
19	3681.5	93.2	738	4	AAU04958 Human int
20	3681.5	93.2	738	6	ABU09705 Human int
21	3681.5	93.2	738	6	ABU09705 Human int
22	3681.5	93.2	738	6	ADU43241 Human int
23	3681.5	93.2	738	7	ADU49782 Human int
24	3681.5	93.2	738	7	ADA26975 Human PRO

25	3681.5	93.2	728	7	ADB66909 Human PRO
26	3681.5	93.2	728	7	ABW02061 Human IL-
27	3681.5	93.2	728	7	ADG87393 Human PRO
28	3681.5	93.2	728	7	ADL16689 Human PRO
29	3681.5	93.2	728	8	ADL16650 Human PRO
30	3681.5	93.2	728	8	ADL16650 Human PRO
31	3396.5	86.0	738	8	ADW76588 House mou
32	3382	85.7	738	5	ABR07630 Murine cy
33	3164	80.1	595	6	ABR33485 Human REM
34	3158	80.0	595	4	ABU53091 Human tra
35	3158	80.0	595	5	ABP69026 Human pol
36	3158	80.0	595	8	ADW76620 Human int
37	2701.5	68.4	554	5	AAU91330 Human nov
38	2665.5	67.5	594	8	ADW21236 Murine in
39	1594	40.4	531	8	ADU01630 Human int
40	1333	33.8	296	4	AAU10601 5' portio
41	377	9.5	69	8	ADW21237 Murine in
42	315	8.0	866	2	AAW04185 Human int
43	315	8.0	866	2	AAW61272 Human int
44	315	8.0	866	2	AAW92409 Human int
45	315	8.0	866	3	AAV97131 Human int

ALIGNMENTS

RESULT 1
AAU09904
ID AAU09904 standard; protein; 738 AA.
XX
AC AAU09904;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-asthmatic; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukemic; anti-infectivity; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human.
XX
OS Homo sapiens.
XX
PN MO200168859-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-US008678.
XX
PR 16-MAR-2000; 2000US-0189816P.
PR 28-NOV-2000; 2000US-00724460.
XX
PA (AMGE-) AMGEN INC.
XX
PI Jing S;
XX
DR WPI: 2001-611392/70.
DR N-PSDB; AAS15346.
XX
PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT psoriasis and glaucoma.
XX
PS Claim 2; Page 152-154; 158pp; English.
XX
CC The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-asthmatic, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,

osteopathic, vascular, cytostatic, anti-leukemic, anti-fertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human Interleukin 17 (IL-17) receptor like protein described in the method of the invention

Sequence 738 AA;

Query Match 100.0%; Score 3948; DB 4; Length 738;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEWLQCSVFVTNACLSGSLAAVAGSGRAMGVDTGMRGVPASRNSGLYNTFFKX 60
DB 1 MAEWLQCSVFVTNACLSGSLAAVAGSGRAMGVDTGMRGVPASRNSGLYNTFFKX 60
QY 61 DNCCTTLPVGVKVIADQNITTSQIACHDQVAVTILMSGALGIEFLKFRVILELKS 120
DB 61 DNCCTTLPVGVKVIADQNITTSQIACHDQVAVTILMSGALGIEFLKFRVILELKS 120
QY 121 EGRQCOQLIKDKPKOLNSPFRGTGMSOPFLNKKFEDYFVKVPPSINESNYHPFF 180
DB 121 EGRQCOQLIKDKPKOLNSPFRGTGMSOPFLNKKFEDYFVKVPPSINESNYHPFF 180
QY 181 RTFACDLILQPDNLACKPFWKPRNLINISQHSQDMQVSDHAPNPFGRFFLYLKLKHG 240
DB 181 RTFACDLILQPDNLACKPFWKPRNLINISQHSQDMQVSDHAPNPFGRFFLYLKLKHG 240
QY 241 PFRKRTCKOBQTTETTSCLIQNVSPDYIIELVDTNTTRKVMHVALKPVHSPWAGPIRA 300
DB 241 PFRKRTCKOBQTTETTSCLIQNVSPDYIIELVDTNTTRKVMHVALKPVHSPWAGPIRA 300
QY 301 MATTVPLVVISAPATLFTVMCRKQOENIYSHLDESSSESTYTALPRRLAPRKVPL 360
DB 301 MATTVPLVVISAPATLFTVMCRKQOENIYSHLDESSSESTYTALPRRLAPRKVPL 360
QY 361 CYSSKDGONMNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGQEMWVIOKIHESQFITV 420
DB 361 CYSSKDGONMNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGQEMWVIOKIHESQFITV 420
QY 421 VCSKGMKTFYVDKKNYHKGGRSGKGEFLVAVSAIAEKLRAKQOSSSALSKFIAYVF 480
DB 421 VCSKGMKTFYVDKKNYHKGGRSGKGEFLVAVSAIAEKLRAKQOSSSALSKFIAYVF 480
QY 481 DVSCEBDVGGIILSTKRYLMDNLPOLCSHLHSRDHGLQEPGHTQGSRRNFRKSGR 540
DB 481 DVSCEBDVGGIILSTKRYLMDNLPOLCSHLHSRDHGLQEPGHTQGSRRNFRKSGR 540
QY 541 SLTYVALCNMHOIFDEBPDMFEKQFVPHPPPLKRYREPVLEKFPSGVLVNDWCKPPESD 600
DB 541 SLTYVALCNMHOIFDEBPDMFEKQFVPHPPPLKRYREPVLEKFPSGVLVNDWCKPPESD 600
QY 601 FCLKVAAPVLTGATGPADSGHESQHGSLDDGEARPALDGSALQPLLTHTVAKGSPDMR 660
DB 601 FCLKVAAPVLTGATGPADSGHESQHGSLDDGEARPALDGSALQPLLTHTVAKGSPDMR 660

QY 661 DSGIYDSSVPSSELSLPLMEGLSTDPQTETSLTESVSSSGGEBEPALPSKLSSGSC 720
DB 661 DSGIYDSSVPSSELSLPLMEGLSTDPQTETSLTESVSSSGGEBEPALPSKLSSGSC 720
QY 721 KADLCGRSYTDLHAHAP 738
DB 721 KADLCGRSYTDLHAHAP 738

RESULT 2

ID ADU69244 standard; protein; 739 AA.

ADU69244;

10-FEB-2005 (first entry)

Human SEF amino acid variant SEQ ID NO:4.

KW fibroblast growth factor; SEF; similar expression of RGF genes;
KW cytostatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
KW vasotrophic; hypotensive; nephrotropic; gene therapy; diagnosis;
KW prognosis; proliferative disorders; cardiovascular disorders;
KW renal disease; glomerular disease.

OS Homo sapiens.

XX US2004235104-A1.

PD 25-NOV-2004.

PF 07-MAY-2004; 2004US-00842006.

PR 08-MAY-2003; 2003US-0469522P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Yang R;

XX WPI; 2004-821320/81.

DR N-PSDB; ADU69243.

PT New isolated SEF nucleic acid and polypeptide, useful for monitoring,

PT treating, or diagnosing proliferative and/or differentiative disorders,

PT e.g. ovarian cancer, breast cancer, or cardiovascular disorder including

PT arteriosclerosis.

PS Disclosure; SEQ ID NO 4; 46pp; English.

XX

The invention relates to a novel isolated SEF (similar expression of RGF genes) nucleic acid molecule (I). An SEF of the invention has cytostatic, cardiovascular-gen., antiarteriosclerotic, cardiant, vasotrophic, hypotensive, and nephrotropic activity, and may have a use in gene therapy. The SEF nucleic acids and polypeptides can be used for diagnostic assays, prognostic assays, and monitoring clinical trials. They can also be used for treating a subject at risk of or susceptible to a disorder or having a disorder associated with aberrant or unwanted SEF expression or activity. The SEF molecules can also be used for monitoring, treating, or diagnosing proliferative and/or differentiative disorders, e.g. ovarian cancer, breast cancer, colon cancer, prostatic cancer, RGF related disorder, cardiovascular disorder including arteriosclerosis, coronary artery disease, ischemia, reperfusion injury, restenosis, arterial inflammation, hypertension, endothelial disorders, and a kidney disorder, e.g. glomerulonephritis, vascular neuropathy, renal failure, or glomerular disease. The SEF molecules can also be used as markers of disorders or disease states, as markers for precursors of disease states, as markers for predisposition of disease states, as markers of drug activity, or as markers of the pharmacogenomic profile of a subject. The present sequence represents a variant of the SEF amino acid shown in ADU69242.

Sequence 739 AA;

Query Match 100.0%; Score 3948; DB 8; Length 739;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWLDLQGVFFTVNACLNGSQLAAVAGSGGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 DB 1 MAPWLDLQGVFFTVNACLNGSQLAAVAGSGGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 QY 61 DICTYTLNPGKXIVADQNITTSQYACHDQVAVTILMSFGALGIEFLKGFVILELKS 120
 DB 61 DICTYTLNPGKXIVADQNITTSQYACHDQVAVTILMSFGALGIEFLKGFVILELKS 120
 QY 121 EGRQCCOQLIKDQKOLNSSPKRTGMSQPLANKFEPDYRVKVPSPSINGSNYHPFR 180
 DB 121 EGRQCCOQLIKDQKOLNSSPKRTGMSQPLANKFEPDYRVKVPSPSINGSNYHPFR 180
 QY 181 RTRACDLLOPDLACPKFPRNLNISOHSDMOVSFDHAPNFGFRPYLYLHYLKHG 240
 DB 181 RTRACDLLOPDLACPKFPRNLNISOHSDMOVSFDHAPNFGFRPYLYLHYLKHG 240
 QY 241 PFRKRTCKOQTETTSCLQNVSPGYIIELVDTNTTRKVMHYALKPVHSPWAGPTRA 300
 DB 241 PFRKRTCKOQTETTSCLQNVSPGYIIELVDTNTTRKVMHYALKPVHSPWAGPTRA 300
 QY 301 MATTVLVVISAFTFTWCRKKQENYSHLDESSSESTYTAALPRERLPRPKVFL 360
 DB 301 MATTVLVVISAFTFTWCRKKQENYSHLDESSSESTYTAALPRERLPRPKVFL 360
 QY 361 CVSSKQGNHNVVOCFAVFLDPCGCEVALDMEBPSLCREGOREVNIQKHESQFIY 420
 DB 361 CVSSKQGNHNVVOCFAVFLDPCGCEVALDMEBPSLCREGOREVNIQKHESQFIY 420
 QY 421 VCSKGMKYFVDDKXNYKHGGSGRSGKGLPLVAVSAIAEKLQAKOSSNALSKFIAYVF 480
 DB 421 VCSKGMKYFVDDKXNYKHGGSGRSGKGLPLVAVSAIAEKLQAKOSSNALSKFIAYVF 480
 QY 481 DVSCEGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTQGSRRNFRSSGR 540
 DB 481 DVSCEGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTQGSRRNFRSSGR 540
 QY 541 SLVVAICNMHOFIDEEPDEWKOFPVPRPPLRYRBPVLEKPSGLVNDVMCKPGESP 600
 DB 541 SLVVAICNMHOFIDEEPDEWKOFPVPRPPLRYRBPVLEKPSGLVNDVMCKPGESP 600
 QY 601 FCILKVEAPVLTGATPDSQHSQHGGIDQGEARPALDGSALQPLIHTYKASPSDMR 660
 DB 601 FCILKVEAPVLTGATPDSQHSQHGGIDQGEARPALDGSALQPLIHTYKASPSDMR 660
 QY 661 DSGIYDSSVSSSLSLPLMEGLSTDTQETSSLTRESVSSSGLGEDEPPALPSKLSSGSC 720
 DB 661 DSGIYDSSVSSSLSLPLMEGLSTDTQETSSLTRESVSSSGLGEDEPPALPSKLSSGSC 720
 QY 721 KADLGRSYTDELAAVAP 738
 DB 721 KADLGRSYTDELAAVAP 738

RESULT 3
 AAU09953
 ID AAU09953 standard; protein; 738 AA.
 AC AAU09953;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #3.
 XX
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-fertility; ophthalmological;

KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 XX
 XX
 OS Homo sapiens.
 OS Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 353 /label= Ser, Thr, Ala, Cys
 PN
 XX
 PD MO200168859-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US008678.
 XX
 PR 16-MAR-2000; 2000US-0189816P.
 XX
 PR 28-NOV-2000; 2000US-00724460.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Jing S;
 XX
 DR WPI, 2001-611392/70.
 XX
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 XX
 PS Claim 20; Page; 158pp; English.

CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17R may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17R antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human Interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to
 CC information given in claim 20
 CC
 XX
 XX
 SQ Sequence 738 AA;

Query Match 99.9%; Score 3944; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPWLDLQGVFFTVNACLNGSQLAAVAGSGGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 DB 1 MAPWLDLQGVFFTVNACLNGSQLAAVAGSGGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 QY 61 DICTYTLNPGKXIVADQNITTSQYACHDQVAVTILMSFGALGIEFLKGFVILELKS 120

D	b	61	DNCTTYLNPVGRKAVADADONITTSQYACHDQVAVTLMSPGALGIFLNGFRVILEKLS	120
Q	y	121	EGROCOQILKDPOKJNSFKRTGMSQPLMKKPEPTYFVKVPPPSIKNESYHPFF	180
D	b	121	EGROCOQILKDPOKJNSFKRTGMSQPLMKKPEPTYFVKVPPPSIKNESYHPFF	180
Q	y	181	RTACDILLQDPNLCKPFWKRNANI SGHSDMOVSFDHAPNPFGRFFRYLTKHGB	240
D	b	181	RTACDILLQDPNLCKPFWKRNANI SGHSDMOVSFDHAPNPFGRFFRYLTKHGB	240
Q	y	241	PFKRTCKOEBOTETTSSCLQWVSPEDYIIELVDPNTTRKVMHYLKVHSPWAPIRA	300
D	b	241	PFKRTCKOEBOTETTSSCLQWVSPEDYIIELVDPNTTRKVMHYLKVHSPWAPIRA	300
Q	y	301	MAITVPLVVISAFATLFTVMCRKKOQENIYSHLDESSSSTYTAALPRERLPREKVT	360
D	b	301	MAITVPLVVISAFATLFTVMCRKKOQENIYSHLDESSSSTYTAALPRERLPREKVT	360
Q	y	361	CYSSKDQGNHNVVOCFAYFLDPFGCGEVALDLMEDFSICRBOREWVIOKIHESQITV	420
D	b	361	CYSSKDQGNHNVVOCFAYFLDPFGCGEVALDLMEDFSICRBOREWVIOKIHESQITV	420
Q	y	421	VCSKGMKRFVDKKNYKHKGGGSGSKGELFLVAVSAIAKTLROAKOSSAALSKFAVVF	480
D	b	421	VCSKGMKRFVDKKNYKHKGGGSGSGELFLVAVSAIAKTLROAKOSSAALSKFAVVF	480
Q	y	481	DYSCBGDVPGLIDSTKYRLMDNLPOLCSHLNSRDHGLQEPGQHTQGSRRNYPFRSKGR	540
D	b	481	DYSCBGDVPGLIDSTKYRLMDNLPOLCSHLNSRDHGLQEPGQHTQGSRRNYPFRSKGR	540
Q	y	541	SLYVAICMNHQFIDBEPDWFKEQVPTFRPPLRYRBPVLEKDSGLVINDVCKCPESD	600
D	b	541	SLYVAICMNHQFIDBEPDWFKEQVPTFRPPLRYRBPVLEKDSGLVINDVCKCPESD	600
Q	y	601	FCLKVEAPVLGATGADSOHESQHGLDODGEARPALDGSALQPLHTHYKAGSPEDMR	660
D	b	601	FCLKVEAPVLGATGADSOHESQHGLDODGEARPALDGSALQPLHTHYKAGSPEDMR	660
Q	y	661	DSGIYDSSVPSBSLPLMEGLSTQDTERSSLTESVSSSGLGEERPPALPSKTLSSGSC	720
D	b	661	DSGIYDSSVPSBSLPLMEGLSTQDTERSSLTESVSSSGLGEERPPALPSKTLSSGSC	720
Q	y	721	KADJGCRSYTDELNAVAP 738	
D	b	721	KADJGCRSYTDELNAVAP 738	

RESULT 4			
AAU09954	ID	AAU09954	standard; protein; 738 AA.
XX			
XX	AC	AAU09954;	
XX			
DT		14-FEB-2002	(first entry)
XX			
DE		Human Interleukin 17 (hIL-17) receptor like protein substitution #4.	
XX			
KM		Interleukin 17; hIL-17 receptor like protein; immunomodulatory;	
KM		anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;	
KM		hepatic; anabolic; anorectic; anti- Alzheimer's; anti-parkinsonian;	
KM		anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;	
KM		vascular; cyostatic; anti-leukemic; anti-infectivity; ophthalmological;	
KM		hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;	
KM		bone disease; vascular disorder; eye disorder; cancer; human; mutant;	
KM		muten.	
XX			
OS		Homo sapiens.	
OS		Synthetic.	
XX			
XX			
Key		Location/Qualifiers	
Misc-difference		374	
FT		/label= Val, Ile, Met, Leu, Phe, Ala, Nle	

XX WO200168859-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 15-MAR-2001, 2001WO-US008678.
 XX
 XX 16-MAR-2000; 2000US-0189816P.
 XX 28-NOV-2000; 2000US-00724460.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX
 XX Jing S;
 XX
 XX WPI; 2001-611392/70.
 XX
 XX
 XX
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 XX peoriasts and glaucoma.
 XX
 XX Claim 21, Page; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteoprotective, vascular, cytostatic, anti-leukemic, anti-infectivity and ophthalmologic activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin diseases (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 21

Sequence 738 AA;

Query Match 99.9%; Score 3943; DB 4; Length 738;

```

DESeq2 local normalization: 25.28; read: 40; 0;
Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy	1	MAPWQLTSVFPTLVNACLNGSQLAAVAAGSGRANGVDITGMRGYPASRPSGLNITPFKY	60
Db	1	MAEWQLTSVFPTLVNACLNGSQLAAVAAGSGRANGVDITGMRGYPASRPSGLNITPFKY	60
Qy	61	DNCTTYTLNVEGKRVILADAQNIITISQYACHDOVAATILMSPGALIGFLPKGRVILLEELKS	120
Db	61	DNCTTYTLNVEGKRVILADAQNIITISQYACHDOVAATILMSPGALIGFLPKGRVILLEELKS	120
Qy	121	EGROCCOQLILKDPKQLNSSFRRKTGMSQPLNLMKRETDYFVKVVPFPSIKNESYTHPPFF	180
Db	121	EGROCCOQLILKDPKQLNSSFRRKTGMSQPLNLMKRETDYFVKVVPFPSIKNESYTHPPFF	180
Qy	181	RTFACDILLIQPNILACKPEFKPRNLNITIQHSGDMQVSDFAHNNGFRFPLYLHYLKHGEG	240
Db	181	RTFACDILLIQPNILACKPEFKPRNLNITIQHSGDMQVSDFAHNNGFRFPLYLHYLKHGEG	240

```

QY 241 PPRKRTCKOQETETTSCLLQNVSPGDYIIELVDPNTTRKVMHYALKPVHSPWAGPIRA 300
DB 241 PPRKRTCKOQETETTSCLLQNVSPGDYIIELVDPNTTRKVMHYALKPVHSPWAGPIRA 300
QY 301 MATIVPLVVISAPATLFTVMCRKKQENIYSHLDESSSSSTYTAALPRERLPRPKVFL 360
DB 301 MATIVPLVVISAPATLFTVMCRKKQENIYSHLDESSSSSTYTAALPRERLPRPKVFL 360
QY 361 CYSKKGQNNHNVVOCFAVFLQDFCGCEVALDLMEDFSLCRGQREWVIQKIHESQPIIV 420
DB 361 CYSKKGQNNHNVVOCFAVFLQDFCGCEVALDLMEDFSLCRGQREWVIQKIHESQPIIV 420
QY 421 VCSKGMKYPYDKKQYKHKGGKSSGKGEFLVAVSAIAETLRQAKOSSSALSKFTAVYF 480
DB 421 VCSKGMKYPYDKKQYKHKGGKSSGKGEFLVAVSAIAETLRQAKOSSSALSKFTAVYF 480
QY 481 DVSCEGDVFGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQTRQGSRRNYFRSKSGR 540
DB 481 DVSCEGDVFGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQTRQGSRRNYFRSKSGR 540
QY 541 SLTVVALCNMHQFIDEBPDMFEKQFVPPHPPPLRYRBPVLKFKDQGLVLDVMCKPGBSD 600
DB 541 SLTVVALCNMHQFIDEBPDMFEKQFVPPHPPPLRYRBPVLKFKDQGLVLDVMCKPGBSD 600
QY 601 PCLKVAAPVLGATGAPADSOHESGHGGLDQDGEARPALDGAALQPLLHTYKASPSDMPR 660
DB 601 PCLKVAAPVLGATGAPADSOHESGHGGLDQDGEARPALDGAALQPLLHTYKASPSDMPR 660
QY 661 DSGIYSSVPSSELSPLMEGLSTDOTETSSLTRESVSSSGLGEEPPPALPSGLSSGSC 720
DB 661 DSGIYSSVPSSELSPLMEGLSTDOTETSSLTRESVSSSGLGEEPPPALPSGLSSGSC 720
QY 721 KADLCGRSTYDELHAAVAP 738
DB 721 KADLCGRSTYDELHAAVAP 738

```

RESULT 5
AAU09951
ID AAU09951 standard; protein; 738 AA.

XX AAU09951;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (IL-17) receptor like protein substitution #1.

XX Interleukin 17, IL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-Alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;
 KW hepatic; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 45 /label= Gly, Pro or Ala

PN MO200168859-A2.

PD 20-SEP-2001.

PF 15-MAR-2001; 2001MO-US008678.

PR 16-MAR-2000; 2000US-0189816P.

PR 28-NOV-2000; 2000US-00724460.

PA (AMGE-) AMGEN INC.
 XX Jing S;
 XX WPI; 2001-611392/70.
 DR Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 PS Claim 18; Page; 158pp; English.
 XX
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anorectic, anti-Alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These
 CC include, for example, immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17R may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17R antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to
 CC information given in claim 18
 CC
 XX
 SQ Sequence 738 AA;
 Query Match 99.8%; Score 3941; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Db 361 CYSKKGQNHMMVQCFAYFLQFCGCEVALDLMEDPSLCREGQREWVIOKIHESQFTIV 420
Qy 421 VCSKGMKTFVDKKNYKHKGSGSGKGEFLVAVAIAEKLROAKOSSSAALESKFIAYVF 480
Db 422 VCSKGMKTFVDKKNYKHKGSGSGKGEFLVAVAIAEKLROAKOSSSAALESKFIAYVF 480
Qy 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
Db 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
Qy 541 SLVVAICNMHQFIDEBPDWFEKQFVPPHPPLRYRREPVLEKFPDGLVNDVWCKPQESD 600
Db 541 SLVVAICNMHQFIDEBPDWFEKQFVPPHPPLRYRREPVLEKFPDGLVNDVWCKPQESD 600
Qy 601 FCILKVAAPVLGATGPADSGHESGHGILDQGEARPALDGSAAIQLPILHTYKAGSPSDMR 660
Db 601 FCILKVAAPVLGATGPADSGHESGHGILDQGEARPALDGSAAIQLPILHTYKAGSPSDMR 660
Qy 661 DSGIYSSVPSSRLSLPLMEGLSTDOTETSLTESVSSSGGLGEEPPALPSKLLSSGSC 720
Db 661 DSGIYSSVPSSRLSLPLMEGLSTDOTETSLTESVSSSGGLGEEPPALPSKLLSSGSC 720
Qy 721 KADLCGRSYTDELHAAVAP 738
Db 721 KADLCGRSYTDELHAAVAP 738

```

RESULT 6
AAU09952
ID AAU09952 standard; protein; 738 AA.

AC AAU09952;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (IL-17) receptor like protein substitution #2.

XX Interleukin 17, IL-17 receptor like protein; immunomodulatory;
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
XX vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;
XX mutein.

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT Misc-difference 227 /label= Phe, Leu, Val, Ile, Ala, Tyr

PN WO200168859-A2.

PD 20-SEP-2001.

PF 15-MAR-2001; 2001WO-US008678.

PR 16-MAR-2000; 2000US-0189816P.

PR 28-NOV-2000; 2000US-00724460.

XX (AMGE-) AMGEN INC.

XX JING S;

DR MPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT psoriasis and glaucoma.

PS Claim 19; Page; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders
CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17R may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17R antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 19
XX

SO Sequence 738 AA;

Query Match 99.8%; Score 3941; DB 4; Length 738;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 MAPWLOLSVFTTVAACINGSLAVALAGSGGAWGVDCGRGVGPASNSGLVNTTFY 60
Db 1 MAPWLOLSVFTTVAACINGSLAVALAGSGGAWGVDCGRGVGPASNSGLVNTTFY 60
Qy 61 DNCTTYLNPVKGHVAADANITISQYACHDQYAVIILWSPGALGIEFLKGFVILIELKS 120
Db 61 DNCTTYLNPVKGHVAADANITISQYACHDQYAVIILWSPGALGIEFLKGFVILIELKS 120
Qy 121 EGRQCOQLIKDPKQINSFKRTGMSOPFLMKETFDYFVKVVPSPSIKESNTHPFF 180
Db 121 EGRQCOQLIKDPKQINSFKRTGMSOPFLMKETFDYFVKVVPSPSIKESNTHPFF 180
Qy 181 RTRACDILLOPNILACKPFRPRNINISOHGSDMVSDPHAPHNCGFPFYLYHYLKHG 240
Db 181 RTRACDILLOPNILACKPFRPRNINISOHGSDMVSDPHAPHNCGFPFYLYHYLKHG 240
Qy 241 PEKRTKQEOETTESCLQNVSPGDIYIELVDNTTRKVMYALPVHSPMAGPIRA 300
Db 241 PEKRTKQEOETTESCLQNVSPGDIYIELVDNTTRKVMYALPVHSPMAGPIRA 300
Qy 301 MAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPREIRLPPKVF 360
Db 301 MAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPREIRLPPKVF 360
Qy 361 CYSKKGQNHMMVQCFAYFLQFCGCEVALDLMEDPSLCREGQREWVIOKIHESQFTIV 420
Db 361 CYSKKGQNHMMVQCFAYFLQFCGCEVALDLMEDPSLCREGQREWVIOKIHESQFTIV 420
Qy 421 VCSKGMKTFVDKKNYKHKGSGSGKGEFLVAVAIAEKLROAKOSSSAALESKFIAYVF 480
Db 421 VCSKGMKTFVDKKNYKHKGSGSGKGEFLVAVAIAEKLROAKOSSSAALESKFIAYVF 480
Qy 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
Db 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540

```


QY 541 SLVVAICNMHOFIDBEPDWEKQFVPHPPPLRYRBPVLEKPNISGLVNDVWCKPSPED 600
 DB 541 SLVVAICNMHOFIDBEPDWEKQFVPHPPPLRYRBPVLEKPNISGLVNDVWCKPSPED 600
 QY 601 FCILKEAPVLTGATGPADSGHESQHGGGLDDGDEARPALDGSALQPLHTVTKAGSPSDMR 660
 DB 601 FCILKEAPVLTGATGPADSGHESQHGGGLDDGDEARPALDGSALQPLHTVTKAGSPSDMR 660
 QY 661 DSGIYDSSVPSSELSPLMEGLSTDQETTSLSLTVSVSSSGGLGEEPPALPSKLSSGSC 720
 DB 661 DSGIYDSSVPSSELSPLMEGLSTDQETTSLSLTVSVSSSGGLGEEPPALPSKLSSGSC 720
 QY 721 KADIGCRSTDELHAAVAP 738
 DB 721 KADIGCRSTDELHAAVAP 738

RESULT 7
 AAU09956
 ID AAU09956 standard; protein; 738 AA.
 AC AAU09956;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (hli-17) receptor like protein substitution #6.
 XX
 KW Interleukin 17, hli-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW heptic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 515
 FT /label= Asp, Glu
 FT
 XX WO200168859-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US008678.
 XX
 PR 16-MAR-2000; 2000US-0189816P.
 PR 28-NOV-2000; 2000US-00724460.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Jing S;
 PI
 DR WPI; 2001-611392/70.
 XX
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 XX
 PS Claim 23; Page; 158pp; English.
 XX
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with

CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
 CC include, for example, immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rlp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17rlp antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to
 CC information given in claim 23
 CC
 XX
 SQ Sequence 738 AA;
 Query Match 99.8%; Score 3941; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPWLTQCSVFPTVNAACNGSQLAAVAGSGGAMGVDTGMRGVGPASNSGLYNTFYK 60
 DB 1 MAPWLTQCSVFPTVNAACNGSQLAAVAGSGGAMGVDTGMRGVGPASNSGLYNTFYK 60
 QY 61 DNGCTTLNPNVGRVADANNTTISQYACHDQVAVTILMSPGALGIBFLKGFVYILBELKS 120
 DB 61 DNGCTTLNPNVGRVADANNTTISQYACHDQVAVTILMSPGALGIBFLKGFVYILBELKS 120
 QY 61 DNGCTTLNPNVGRVADANNTTISQYACHDQVAVTILMSPGALGIBFLKGFVYILBELKS 120
 DB 61 DNGCTTLNPNVGRVADANNTTISQYACHDQVAVTILMSPGALGIBFLKGFVYILBELKS 120
 QY 121 EGRQCOQLIKDKPKOLNSFKRTGMSOPFLMKETFDYFVVPVPPSIKNSNTHPFF 180
 DB 121 EGRQCOQLIKDKPKOLNSFKRTGMSOPFLMKETFDYFVVPVPPSIKNSNTHPFF 180
 QY 181 RTRACDLILQPDNLACKPFMKPRNLNISQHSQSDMOVSPHAPHNIGFRFFYLHYLKHEG 240
 DB 181 RTRACDLILQPDNLACKPFMKPRNLNISQHSQSDMOVSPHAPHNIGFRFFYLHYLKHEG 240
 QY 241 PPKRTCKQEQTEFTTSCILQNVSPGDYIILVDDTNTTRKVMYALKQVHSPMAGPIRA 300
 DB 241 PPKRTCKQEQTEFTTSCILQNVSPGDYIILVDDTNTTRKVMYALKQVHSPMAGPIRA 300
 QY 301 MAITPVLVVISAPATLFTWCKRKKQOENYSHLDESSSSTYTALPRERLRPRKPVFL 360
 DB 301 MAITPVLVVISAPATLFTWCKRKKQOENYSHLDESSSSTYTALPRERLRPRKPVFL 360
 QY 361 CYSSKDGQNHMMVVOCFAYFLDPFCGCEVALDLMEDFSLCRGQREMYQKHESQFTIV 420
 DB 361 CYSSKDGQNHMMVVOCFAYFLDPFCGCEVALDLMEDFSLCRGQREMYQKHESQFTIV 420
 QY 421 VCSKGMKCYFVDKKNYKHKGGGSGKGLFLVAVASAIKRLQAKQSSAALSSTPLAVYF 480
 DB 421 VCSKGMKCYFVDKKNYKHKGGGSGKGLFLVAVASAIKRLQAKQSSAALSSTPLAVYF 480
 QY 481 DYSCEGDVVGILDLSTKTRLMNLPQLCSHLMSRDHGLQEPQHTROGSRNYPFSKSR 540
 DB 481 DYSCEGDVVGILDLSTKTRLMNLPQLCSHLMSRDHGLQEPQHTROGSRNYPFSKSR 540
 QY 541 SLVVAICNMHOFIDBEPDWEKQFVPHPPPLRYRBPVLEKPNISGLVNDVWCKPSPED 600
 DB 541 SLVVAICNMHOFIDBEPDWEKQFVPHPPPLRYRBPVLEKPNISGLVNDVWCKPSPED 600
 QY 601 FCILKEAPVLTGATGPADSGHESQHGGGLDDGDEARPALDGSALQPLHTVTKAGSPSDMR 660
 DB 601 FCILKEAPVLTGATGPADSGHESQHGGGLDDGDEARPALDGSALQPLHTVTKAGSPSDMR 660
 QY 661 DSGIYDSSVPSSELSPLMEGLSTDQETTSLSLTVSVSSSGGLGEEPPALPSKLSSGSC 720

Db 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSLTESVSSSGLGEBBPALPSKILSSGSC 720
 QY 721 KADLGCRSYTDELAHAVP 738
 Db 721 KADLGCRSYTDELAHAVP 738

RESULT 8
 AAU09957 standard; protein; 738 AA.
 AAU09957;
 14-FEB-2002 (first entry)
 Human Interleukin 17 (IL-17) receptor like protein substitution #7.

XX Interleukin 17; IL-17 receptor like protein; immunomodulatory;
 KM anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KM hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KM vasculature; anti-asthmatic; dermatological; renal; osteopathic;
 KM vascular; cytotoxic; anti-leukemic; anti-infectivity; ophthalmological;
 KM hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KM bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KM
 XX
 OS Homo sapiens.
 OS Synthetic.
 Key Location/Qualifiers
 FH Misc-difference 602
 FT /label= Cys, Ala, Ser
 FT
 XX
 PN MO200168859-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 15-MAR-2001; 2001MO-US008678.
 XX
 XX 16-MAR-2000; 2000US-0189816P.
 PR 28-NOV-2000; 2000US-00724460.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX
 PI Jing S;
 XX
 XX WPI; 2001-611392/70.
 DR
 XX
 XX
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 PS
 Claim 24; Page; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytotoxic, anti-leukemic, anti-infectivity and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17r) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia and breast cancer), reproductive disorders (e.g. infertility and

CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17r may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17r antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human Interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to
 CC information given in claim 24
 CC
 XX
 SQ Sequence 738 AA;
 Query Match 99.7%; Score 3937; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPWQLGCVFPTVNAALNGSQLAAVAGSGRAMGVDTGMRGVGPASNSGLYNITFYK 60
 Db 1 MAPWQLGCVFPTVNAALNGSQLAAVAGSGRAMGVDTGMRGVGPASNSGLYNITFYK 60
 QY 61 DKCTTYLANVGVKAVLADQNITISQYACHDQVAVYITLSPGALGIEFLKGFVILBELKS 120
 Db 61 DKCTTYLANVGVKAVLADQNITISQYACHDQVAVYITLSPGALGIEFLKGFVILBELKS 120
 QY 121 EGRQCQQLLKDPKOLNSFKRTGMSOPFLMKFETDFYVYVPPPSIKNSNYHPFF 180
 Db 121 EGRQCQQLLKDPKOLNSFKRTGMSOPFLMKFETDFYVYVPPPSIKNSNYHPFF 180
 QY 181 RTTACDILLQPDNLACKPFMKPRNLNISQHSQDMQVSPDPAHNFGRFPYLAHYKLKHG 240
 Db 181 RTTACDILLQPDNLACKPFMKPRNLNISQHSQDMQVSPDPAHNFGRFPYLAHYKLKHG 240
 QY 241 PPKRTCKQKQBTETTSCLQVNSPDYITIELVDNTTRKMYALKVHSPMAGPIA 300
 Db 241 PPKRTCKQKQBTETTSCLQVNSPDYITIELVDNTTRKMYALKVHSPMAGPIA 300
 QY 301 MATTPVLVYISAPATLFTWCKRKKQOENTYSHLDESSSSTYTAALPRELRPRPKVFL 360
 Db 301 MATTPVLVYISAPATLFTWCKRKKQOENTYSHLDESSSSTYTAALPRELRPRPKVFL 360
 QY 361 CYSSKDGQNHMMVVOCFAYFLQDFGCEVALDLMBDFSLCREGOREWYLOKIHESQFIIV 420
 Db 361 CYSSKDGQNHMMVVOCFAYFLQDFGCEVALDLMBDFSLCREGOREWYLOKIHESQFIIV 420
 QY 421 VCSKGMKTFVDKNTYKHKGGGSGKGLFLVAVSAIAEKLQAKQSSAALSKFTAYVF 480
 Db 421 VCSKGMKTFVDKNTYKHKGGGSGKGLFLVAVSAIAEKLQAKQSSAALSKFTAYVF 480
 QY 481 DYSCEGDVPGIIDLSTKRYLMDNLPQLCSHLSPDHGLQEPQGHTRQSGRRYVFRSKGR 540
 Db 481 DYSCEGDVPGIIDLSTKRYLMDNLPQLCSHLSPDHGLQEPQGHTRQSGRRYVFRSKGR 540
 QY 541 SLVVAICNNHQPIDEBPWFKEQFVFPHPPLRYBPVLEKPSGLVINDVACKGPPESD 600
 Db 541 SLVVAICNNHQPIDEBPWFKEQFVFPHPPLRYBPVLEKPSGLVINDVACKGPPESD 600
 QY 601 FCLTKBAPVYLGATGPADSQHSQHGGLDQDGAARPALDGSALQPLTLTKVKSQSDMR 660
 Db 601 FCLTKBAPVYLGATGPADSQHSQHGGLDQDGAARPALDGSALQPLTLTKVKSQSDMR 660
 QY 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSLTESVSSSGLGEBBPALPSKILSSGSC 720
 Db 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSLTESVSSSGLGEBBPALPSKILSSGSC 720
 QY 721 KADLGCRSYTDELAHAVP 738
 Db 721 KADLGCRSYTDELAHAVP 738

RESULT 9
 AAU09955

ID AAU09955 standard; protein; 738 AA.
 AC AAU09955;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (IL-17) receptor like protein subcltution #5.
 XX
 KM Interleukin 17; IL-17 receptor like protein; immunomodulatory;
 KM anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KM hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KM anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KM vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;
 KM hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KM bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KM
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 385
 FT /label= Cys, Ser, Ala
 XX
 PN MO200168859-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001MO-US008678.
 XX
 PR 16-MAR-2000; 2000US-0189816P.
 PR 28-NOV-2000; 2000US-00724460.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Jing S;
 XX
 DR WPI; 2001-611392/70.
 XX
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 PT
 XX
 PS Claim 22; Page; 158pp; English.
 XX
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17rp antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to

CC Information given in claim 22
 XX
 SQ Sequence 738 AA;
 XX
 Query Match 99.7%; Score 3937; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 MAPWLOLCVFFVFNACVNGSQAIAVAGSGGAAWYDTGCMGVGASRNSGLYNTTFK 60
 DB 1 MAPWLOLCVFFVFNACVNGSQAIAVAGSGGAAWYDTGCMGVGASRNSGLYNTTFK 60
 QY 61 DNGTTLANPVGKRVADDAONITTSOYACHDOYAVTILMSPGALGIFLNGFRYILELKS 120
 DB 61 DNGTTLANPVGKRVADDAONITTSOYACHDOYAVTILMSPGALGIFLNGFRYILELKS 120
 QY 121 EGRQCOOLILKPKOLNSPKRTGMSQPLNMKPEFDYFVKVPPSIKNSNYHPFF 180
 DB 121 EGRQCOOLILKPKOLNSPKRTGMSQPLNMKPEFDYFVKVPPSIKNSNYHPFF 180
 QY 181 RTFACDLILQPDNLACKPFWKPRNINISQHSQDMQVSPHAPNFGFRFFLYLKLKHEG 240
 DB 181 RTFACDLILQPDNLACKPFWKPRNINISQHSQDMQVSPHAPNFGFRFFLYLKLKHEG 240
 QY 241 PFRKRTCKOQTETTSCLQNVSPGDYIIBLVDDNTTRKVMYALKVHSPWAGPIRA 300
 DB 241 PFRKRTCKOQTETTSCLQNVSPGDYIIBLVDDNTTRKVMYALKVHSPWAGPIRA 300
 QY 301 MATVPLVVISAFATLFTWCRKQOENIYSHLDESSSSTYTAALPRERLRPKVP 360
 DB 301 MATVPLVVISAFATLFTWCRKQOENIYSHLDESSSSTYTAALPRERLRPKVP 360
 QY 361 CISSKQGNHNVVOCFAVFLQDFGCEVALDMEDFSICRSGQREWVIOKTHESQITIV 420
 DB 361 CISSKQGNHNVVOCFAVFLQDFGCEVALDMEDFSICRSGQREWVIOKTHESQITIV 420
 QY 421 VCSKGMKVFVDKKNYHKGSGSGKGLFLVAVSAIAKLQAOKSSSALSKFLAVVF 480
 DB 421 VCSKGMKVFVDKKNYHKGSGSGKGLFLVAVSAIAKLQAOKSSSALSKFLAVVF 480
 QY 481 DYSCEGDVGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTQGSRRNFRSKSGR 540
 DB 481 DYSCEGDVGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTQGSRRNFRSKSGR 540
 QY 541 SLVVALCNMHPIDEEPDPFEPFPPPLRYRREPVLEKFDGSLVNDWCKPESD 600
 DB 541 SLVVALCNMHPIDEEPDPFEPFPPPLRYRREPVLEKFDGSLVNDWCKPESD 600
 QY 601 FCILKVAAPVLTGATGPADSGHESQHGGLDODGERAPPLDSSALQPLHTVKAQSPBDMR 660
 DB 601 FCILKVAAPVLTGATGPADSGHESQHGGLDODGERAPPLDSSALQPLHTVKAQSPBDMR 660
 QY 661 DSGIYVSSVPSSELPLMEGLSTDOTETSSLTESVSSSGGLGEERPPALPSGLSSGSC 720
 DB 661 DSGIYVSSVPSSELPLMEGLSTDOTETSSLTESVSSSGGLGEERPPALPSGLSSGSC 720
 QY 721 KADLCGRSYTDEILHAVAP 738
 DB 721 KADLCGRSYTDEILHAVAP 738
 XX
 RESULT 10
 ABB07628
 ID ABB07628 standard; protein; 739 AA.
 XX
 AC ABB07628;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE Human cytokine receptor, Zcytor18 splice variant.
 CC
 CC Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
 CC pulmonary alveolar proteinosis; familial periodic fever; antitumour;

KM erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
 XX Homo sapiens.
 OS
 XX MO200208259-A2.
 XX
 XX 31-JAN-2002.
 PD
 XX 23-JUL-2001; 2001MO-US023253.
 PF
 XX 26-JUL-2000; 2000US-0220747P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Presnell SR, Kuestner RE, Gao Z;
 XX
 XX WPI; 2002-217048/27.
 DR N-PSDB; ABA95035, ABA95036.
 XX
 XX
 PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor growth,
 PT and modulating immune system by binding to endogenous zcytor18 ligand.
 XX
 XX Claim 1; Page 102-106; 119pp; English.
 PS
 XX
 CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which an
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 splice variant
 CC
 XX
 XX Sequence 739 AA;
 SQ
 Query Match 99.2%; Score 3918; DB 5; Length 739;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 734; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 421 VCSKGMKYFVDDKKNYGHKGGGSGKGBELFLVAVSAIAEKLROAKXSSSAALSKFLAVYF 480
 DB 421 VCSKGMKYFVDDKKNYGHKGGGSGKGBELFLVAVSAIAEKLROAKXSSSAALSKFLAVYF 480
 QY 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNRYFRSKSGR 540
 DB 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNRYFRSKSGR 540
 QY 541 SLVVAICMNHOPIDEEPDMFEKQFVFPFPPPLRYRBPVLEKFDGSLVNDVWCKQGPESD 600
 DB 541 SLVVAICMNHOPIDEEPDMFEKQFVFPFPPPLRYRBPVLEKFDGSLVNDVWCKQGPESD 600
 QY 601 FCLKTEAPVLCATGPADSOHESQHGGLDQDGEARPALDGSALOPLLHTVKASPSDMPR 660
 DB 601 FCLKTEAPVLCATGPADSOHESQHGGLDQDGEARPALDGSALOPLLHTVKASPSDMPR 660
 QY 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGIGBEPALPKSLSSGSC 720
 DB 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGIGBEPALPKSLSSGSC 720
 QY 721 KADLCGRSTTDELHAYAP 738
 DB 721 KADLCGRSTTDELHAYAP 738
 RESULT 11
 ADU69242
 ID ADU69242 standard; protein; 739 AA.
 XX
 XX ADU69242;
 AC
 XX
 XX 10-FEB-2005 (first entry)
 DT
 XX
 DE Human SEF amino acid SEQ ID NO.2.
 XX
 XX fibroblast growth factor; SEF; similar expression of FGF genes;
 KM cytostatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
 KM vasotropic; hypotensive; nephrotropic; gene therapy; diagnosis;
 KM prognosis; proliferative disorders; cardiovascular disorders;
 KM renal disease; glomerular disease.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2004235104-A1.
 PN
 XX 25-NOV-2004.
 PD
 XX 07-MAY-2004; 2004US-00842006.
 PF
 XX 08-MAY-2003; 2003US-0469522P.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX
 XX Yang R;
 PI
 XX
 XX WPI; 2004-821320/81.
 DR N-PSDB; ADU69241.
 DR
 XX
 PT New isolated SEF nucleic acid and polypeptide, useful for monitoring,
 PT treating, or diagnosing proliferative and/or differentiative disorders,
 PT e.g. ovarian cancer, breast cancer, or cardiovascular disorder including
 PT arteriosclerosis.
 XX
 XX Claim 1; SEQ ID NO 2; 46bp; English.
 PS
 XX
 CC The invention relates to a novel isolated SEF (similar expression of FGF
 CC genes) nucleic acid molecule (I). An SEF of the invention has cytosstatic,
 CC cardiovascular-gen., antiarteriosclerotic, cardiant, vasotropic,
 CC hypotensive, and nephrotropic activity, and may have a use in gene
 CC therapy. The SEF nucleic acids and polypeptides can be used for
 CC diagnostic assays, prognostic assays, and monitoring clinical trials.
 CC They can also be used for treating a subject at risk of or susceptible to

CC a disorder or having a disorder associated with aberrant or unwanted SRF
 CC expression or activity. The SRF molecules can also be used for
 CC monitoring, treating, or diagnosing proliferative and/or differentiative
 CC disorders, e.g. ovarian cancer, breast cancer, colon cancer, prostatic
 CC cancer, FGF related disorder, cardiovascular disorder including
 CC arteriosclerosis, coronary artery disease, ischemia, reperfusion injury,
 CC restenosis, arterial inflammation, hypertension, endothelial disorder,
 CC and a kidney disorder, e.g. glomerulonephritis, vascular nephropathy,
 CC renal failure, or glomerular disease. The SRF molecules can also be used
 CC as markers of disorders or disease states, as markers for precursors of
 CC disease states, as markers for predisposition of disease states, as
 CC markers of drug activity, or as markers of the pharmacogenomic profile of
 CC a subject. The present sequence represents the SRF amino acid molecule of
 CC the invention.

CC XX
 CC Sequence 739 AA;

Query Match 99.0%; Score 3908; DB 8; Length 739;
 Best Local Similarity 99.2%; Pred. No. 0;

Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAPRLQCSVFETVNAACLSQSLAAGSGRAGVDTGMRGVGPASRNSGLYNTFFKY 60
 DB 1 MAPRLQCSVFETVNAACLSQSLAAGSGRAGVDTGMRGVGPASRNSGLYNTFFKY 60
 QY 61 DNCTTYLNPVKGKVIADQNITTSOYACHQVAVTILMSPGALGIEFLKGRVILEELKS 120
 DB 61 DNCTTYLNPVKGKVIADQNITTSOYACHQVAVTILMSPGALGIEFLKGRVILEELKS 120
 QY 121 EGRQCOOLIKDPKOLNSFRKTGMSOPFLNKKFETDVFVKVPPPSIKNESYHPFF 180
 DB 121 EGRQCOOLIKDPKOLNSFRKTGMSOPFLNKKFETDVFVKVPPPSIKNESYHPFF 180
 QY 181 RTBACDLLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPNFGFRFFLYLKLKHEG 240
 DB 181 RTBACDLLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPNFGFRFFLYLKLKHEG 240
 QY 241 PFRKTCCKOQTETTSCLLOVNSPDYIIEVDNTTRKVMHYALKPHSPAGIRARA 300
 DB 241 PFRKTCCKOQTETTSCLLOVNSPDYIIEVDNTTRKVMHYALKPHSPAGIRARA 300
 QY 301 MATIVPLVISAFAITLFTVMCRKQOENIYSHLDESSSESTYPAALPRELRPRKPVFL 360
 DB 301 MATIVPLVISAFAITLFTVMCRKQOENIYSHLDESSSESTYPAALPRELRPRKPVFL 360
 QY 361 CYSSKDGQNNMNVQCFAYFLQDFCGCEVALDLMEDESLCRGGRVWIOKIHESQPIIV 420
 DB 361 CYSSKDGQNNMNVQCFAYFLQDFCGCEVALDLMEDESLCRGGRVWIOKIHESQPIIV 420
 QY 421 VCSKGMKTFVDKKNYKRGKGGSGKGLFLVAVSAIAEKLRQAKOSSAALSKFIAYVF 480
 DB 421 VCSKGMKTFVDKKNYKRGKGGSGKGLFLVAVSAIAEKLRQAKOSSAALSKFIAYVF 480
 QY 481 DYSCEGDPVGLIDSTYKRLMDNLPOLCSHLHSRHDGLQBRGCHTRGSSRRNYSRSGR 540
 DB 481 DYSCEGDPVGLIDSTYKRLMDNLPOLCSHLHSRHDGLQBRGCHTRGSSRRNYSRSGR 540
 QY 541 SLVYVALCNMHOPIDEBDFWEKOPVPPHPPPLRYREBLEKFDGSLVLDVMCKRGPESD 600
 DB 541 SLVYVALCNMHOPIDEBDFWEKOPVPPHPPPLRYREBLEKFDGSLVLDVMCKRGPESD 600
 QY 601 FCILKEAPVIGATGPADSOHSHGGLDODGEARPALDGSALLOPLLHTYVAGSPSPMPR 660
 DB 601 FCILKEAPVIGATGPADSOHSHGGLDODGEARPALDGSALLOPLLHTYVAGSPSPMPR 660
 QY 661 DSGIYSSVSSSRLSLPLMEGLSTDOTETSLTESVSSSGLAGREBPALPSKLLSGSC 720
 DB 661 DSGIYSSVSSSRLSLPLMEGLSTDOTETSLTESVSSSGLAGREBPALPSKLLSGSC 720
 QY 721 KADLGCRSYTDELAAVAP 738
 DB 721 KADLGCRSYTDELAAVAP 738
 QY 738 KADLGCRSYTDELAAVAP 738
 DB 738 KADLGCRSYTDELAAVAP 738

RESULT 12

ID ADM23600 standard; protein; 739 AA.

XX ADM23600;

XX 10-MAR-2005 (first entry)

XX Human IL-17RLM.

XX Neuroprotective; Immunosuppressive; Cytostatic; IL-17RLM;

XX rheumatoid arthritis; asthma; carcinoma.

XX Homo sapiens.

XX CN1463982-A.

XX 31-DEC-2003.

XX 28-JUN-2002; 2002CN-00123447.

XX 28-JUN-2002; 2002CN-00123447.

XX (UYOI) UNIV QINGHUA.

XX Xiong S, Chang Z, Fu X;

XX WPI; 2004-248693/24.

XX N-PSDB; ADM23599.

XX New polynucleotide encoding IL-17RLM polypeptide, useful in preparing a
 PT composition for treating e.g., neurological or autoimmune disease, such
 PT as rheumatoid arthritis or asthma, or kidney- or testis-related
 PT carcinoma.

XX Disclosure; SEQ ID NO 2; 14bp; Chinese.

XX The present invention relates to a new isolated IL-17RLM polynucleotide.
 CC The polynucleotide encoding the IL-17RLM polypeptide is useful in
 CC preparing a composition for treating an individual in need of an
 CC increased or decreased level of IL-17RLM polypeptide, e.g. neurological
 CC or autoimmune disease, such as rheumatoid arthritis or asthma, or kidney-
 CC or testis-related carcinoma. The present sequence represents the amino
 CC acid sequence of human IL-17RLM.

XX Sequence 739 AA;

Query Match 99.0%; Score 3908; DB 8; Length 739;
 Best Local Similarity 99.2%; Pred. No. 0;

Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAPRLQCSVFETVNAACLSQSLAAGSGRAGVDTGMRGVGPASRNSGLYNTFFKY 60
 DB 1 MAPRLQCSVFETVNAACLSQSLAAGSGRAGVDTGMRGVGPASRNSGLYNTFFKY 60
 QY 61 DNCTTYLNPVKGKVIADQNITTSOYACHQVAVTILMSPGALGIEFLKGRVILEELKS 120
 DB 61 DNCTTYLNPVKGKVIADQNITTSOYACHQVAVTILMSPGALGIEFLKGRVILEELKS 120
 QY 121 EGRQCOOLIKDPKOLNSFRKTGMSOPFLNKKFETDVFVKVPPPSIKNESYHPFF 180
 DB 121 EGRQCOOLIKDPKOLNSFRKTGMSOPFLNKKFETDVFVKVPPPSIKNESYHPFF 180
 QY 181 RTBACDLLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPNFGFRFFLYLKLKHEG 240
 DB 181 RTBACDLLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPNFGFRFFLYLKLKHEG 240
 QY 241 PFRKTCCKOQTETTSCLLOVNSPDYIIEVDNTTRKVMHYALKPHSPAGIRARA 300
 DB 241 PFRKTCCKOQTETTSCLLOVNSPDYIIEVDNTTRKVMHYALKPHSPAGIRARA 300
 QY 301 MATIVPLVISAFAITLFTVMCRKQOENIYSHLDESSSESTYPAALPRELRPRKPVFL 360
 DB 301 MATIVPLVISAFAITLFTVMCRKQOENIYSHLDESSSESTYPAALPRELRPRKPVFL 360

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:|||||
Db 301 VAITPLVVISAPATLFTVWCRKQOENIYSHLDESSSESTYTALPRRLPRKXVFL 360
Qy 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEBPSLCREGRENVYOKIHESQFIY 420
Db 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEBPSLCREGRENVYOKIHESQFIY 420
Qy 421 VCSKGMKTFVDKKNYKHGKGGSGKGLFLVAVSAIAEKLROAKOSSAALSKFIAYVF 480
Db 421 VCSKGMKTFVDKKNYKHGKGGSGKGLFLVAVSAIAEKLROAKOSSAALSKFIAYVF 480
Qy 481 DVSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTQGSRRNYFRSKSGR 540
Db 481 DVSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTQGSRRNYFRSKSGR 540
Qy 541 SLTYVALCMNHQFIDEEBPDWFEKQFVPPHPLRYREPVLEKFSGLVNDVMCKPESD 600
Db 541 SLTYVALCMNHQFIDEEBPDWFEKQFVPPHPLRYREPVLEKFSGLVNDVMCKPESD 600
Qy 601 FCLEKAPVYLGAATGPADSOHESQHGGLDQDEARPALDGSALQPLHTYKAGSPSDMPR 660
Db 601 FCLEKAPVYLGAATGPADSOHESQHGGLDQDEARPALDGSALQPLHTYKAGSPSDMPR 660
Qy 661 DSGIYDSSVPSSELSPLMEGLSTDQETTSSTLESVSSSGLGEBEPALPSKLSSGSC 720
Db 661 DSGIYDSSVPSSELSPLMEGLSTDQETTSSTLESVSSSGLGEBEPALPSKLSSGSC 720
Qy 721 KADLCGRSTYDELAHAVAP 738
Db 721 KADLCGRSTYDELAHAVAP 738

```

RESULT 13

ABB07626 standard; protein; 753 AA.

AC ABB07626;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 amino acid sequence.

KM Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KM erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

PN WO200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-05023253.

PR 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

DR WPI; 2002-217048/27.

DR N-PSDB; ABA95031, ABA95032.

PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor growth,
 PT and modulating immune system by binding to endogenous zcytor18 ligand.

PS Claim 1; Page 2; 11pp; English.

CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The

CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
 CC and localize Zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human Zcytor18 amino acid sequence

XX Sequence 753 AA;

Query Match 98.8%; Score 3901; DB 5; Length 753;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

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Qy 1 MAPWLQLCSVFETVNAALNGSQLAAVAGSGRAGVDTGMR-----GVGP 46
Db 1 MAPWLQLCSVFETVNAALNGSQLAAVAGSGRAGVDTGMRKAAARPRLCVANEVGP 60
Qy 47 AARNSGLVNITTKYNDCTTYLNPVGKHYADQNTTISYACHDQVATYILMSRGLGTE 106
Db 47 AARNSGLVNITTKYNDCTTYLNPVGKHYADQNTTISYACHDQVATYILMSRGLGTE 120
Qy 61 AARNSGLVNITTKYNDCTTYLNPVGKHYADQNTTISYACHDQVATYILMSRGLGTE 120
Db 61 AARNSGLVNITTKYNDCTTYLNPVGKHYADQNTTISYACHDQVATYILMSRGLGTE 120
Qy 107 PLKGRVILIELSGRQCOQLILNDPKQINSFRKTEGSEOPFLNMKEETDYPKVPVF 166
Db 121 PLKGRVILIELSGRQCOQLILNDPKQINSFRKTEGSEOPFLNMKEETDYPKVPVF 180
Qy 167 PSIKNESNYHPPFRTTRACDILLQPDNLACKPMKPRNLINISQHSQDQVSDHAPHNFG 226
Db 181 PSIKNESNYHPPFRTTRACDILLQPDNLACKPMKPRNLINISQHSQDQVSDHAPHNFG 240
Qy 227 FRPFLHYKLGKHSRPRKRTCKQEBOTETTSCLQNVSRBGVITILVYDNTTRKVMYA 286
Db 241 FRPFLHYKLGKHSRPRKRTCKQEBOTETTSCLQNVSRBGVITILVYDNTTRKVMYA 300
Qy 287 LKPVSPMAGPIRAMAIVPLVVISAPATLFTVWCRKQOENIYSHLDESSSESTYTNA 346
Db 301 LKPVSPMAGPIRAMAIVPLVVISAPATLFTVWCRKQOENIYSHLDESSSESTYTNA 360
Qy 347 LPRERLPRPKVFLCYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEBPSLCREGRE 406
Db 361 LPRERLPRPKVFLCYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEBPSLCREGRE 420
Qy 407 WYIOKIHESQFIYVCSKGMKTFVDKKNYKHGKGGSGKGLFLVAVSAIAEKLROAKQ 466
Db 421 WYIOKIHESQFIYVCSKGMKTFVDKKNYKHGKGGSGKGLFLVAVSAIAEKLROAKQ 480
Qy 467 SSSAALSKFIAYFPDSCGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTR 526
Db 481 SSSAALSKFIAYFPDSCGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTR 540
Qy 527 QGSRRNYFRSKSGRSLYVALCMNHQFIDEEBPDWFEKQFVPPHPLRYREPVLEKFSGL 586
Db 541 QGSRRNYFRSKSGRSLYVALCMNHQFIDEEBPDWFEKQFVPPHPLRYREPVLEKFSGL 600
Qy 587 VLNDVMCKPESDPLCKVKEAAVILGATGPADSOHESQHGGLDQDEARPALDGSALQPL 646
Db 601 VLNDVMCKPESDPLCKVKEAAVILGATGPADSOHESQHGGLDQDEARPALDGSALQPL 660
Qy 647 LHTVAGSPDMRPRSGIYDSSVPSSELSPLMEGLSTDQETTSSTLESVSSSGLGEBE 706
Db 661 LHTVAGSPDMRPRSGIYDSSVPSSELSPLMEGLSTDQETTSSTLESVSSSGLGEBE 720
Qy 707 PPALPSKLSSGSCRADLGCRSTYDELAHAVAP 738
Db 721 PPALPSKLSSGSCRADLGCRSTYDELAHAVAP 752

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RESULT 14

ABB07627 standard; protein; 753 AA.

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XX AC ABB07627;
XX 20-MAY-2002 (first entry)
XX Human cytokine receptor, Zcytor18 variant sequence.
XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;
XX erythroleukemia; chromosome 3p14.3; gene therapy; variant.
XX Homo sapiens.
XX Key Location/Qualifiers
XX FH Misc-difference 269 /label= T269M
XX FT /note= "wild-type Thr is replaced with Met"
XX FT Misc-difference 750 /label= V750A
XX FT /note= "wild-type Val is replaced with Ala"
XX PN WO200208259-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001MO-US023253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO ) ZYMOGENETICS INC.
XX PI Presnell SR., Kuestner RE, Gao Z;
XX DR MPI; 2002-217048/27.
XX DR N-PSDB; ABA95033, ABA95034.
XX PT New cytokine receptor polypeptide designated zcytor18, useful for
XX PT inhibiting cell proliferation associated with psoriasis or tumor growth,
XX PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX PS Disclosure; Page 94-98; 119pp; English.
XX CC The invention relates to an isolated cytokine receptor polypeptide
XX CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX CC standard recombinant methodology. The polypeptides can be used to inhibit
XX CC cell proliferation associated with psoriasis or tumor growth. The
XX CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX CC and localize Zcytor18 gene expression in tissue samples. The probes are
XX CC also useful for detecting gross aberrations in chromosome 3 in which
XX CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX CC linkage-based testing of pulmonary alveolar proteinosis, familial
XX CC periodic fever and erythroleukemia, and erythroleukemia associated with
XX CC polymorphisms of cytokine receptors. The present sequence represents a
XX CC human Zcytor18 variant amino acid sequence
XX SQ Sequence 753 AA;
Query Match 98.6%; Score 3891; DB 5; Length 753;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 732; Conservative 1; Mismatches 5; Indels 14; Gaps 1;
QY 1 MAPWLOLCGVFTVNAALNGSOLAVALAGSGRAMGVDTQGM-----GVGP 46
DB 1 MAPWLOLCGVFTVNAALNGSOLAVALAGSGRAMGVDTQGM-----GVGP 60
QY 47 ASRNSGLNITFYNDCTTYLNPVGKIVADANITISQYACHDQVAVITLMSPALGIE 106
DB 61 ASRNSGLNITFYNDCTTYLNPVGKIVADANITISQYACHDQVAVITLMSPALGIE 120
QY 107 FLKGFVILBELKSEGRQCOQLIKDPKQNLNSFKRTGMESQFLMMKFTDYFVAVVPP 166

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DB 121 FLKGFVILBELKSEGRQCOQLIKDPKQNLNSFKRTGMESQFLMMKFTDYFVAVVPP 180
QY 167 PSTKNSNTHPPFFTRACDILLQPNLACKPFWKPRNINISQHGSDMOVSFPAHANG 226
DB 181 PSTKNSNTHPPFFTRACDILLQPNLACKPFWKPRNINISQHGSDMOVSFPAHANG 240
QY 227 FRFFYLHYLKHGEPKRTCKQEQTEETTSCLQNVSGDYIIELVDTNTTRKMYHA 286
DB 241 FRFFYLHYLKHGEPKRTCKQEQTEETTSCLQNVSGDYIIELVDTNTTRKMYHA 300
QY 287 LKRVHSPMAGPIRAMAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 346
DB 301 LKRVHSPMAGPIRAMAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 360
QY 347 LPERLRPPRPKYFLCYSSHDGQNMNVVOCFAVFIQDFCGCEVALDLMEDFSICREGORE 406
DB 361 LPERLRPPRPKYFLCYSSHDGQNMNVVOCFAVFIQDFCGCEVALDLMEDFSICREGORE 420
QY 407 WVIQKHESQFTIIVCSKGMKTVDDKQYKHKGGGSGKGLFLVAVSAIAEKLRQAQ 466
DB 421 WVIQKHESQFTIIVCSKGMKTVDDKQYKHKGGGSGKGLFLVAVSAIAEKLRQAQ 480
QY 467 SSSAALSKFIAYVFDYSCGDPVGLDLSTKTRLMQNLPLQCSHLSPDHGLQEPQHT 526
DB 481 SSSAALSKFIAYVFDYSCGDPVGLDLSTKTRLMQNLPLQCSHLSPDHGLQEPQHT 540
QY 527 QGSRNRYFRSKGSLIYVAINCMHQFIDEPPMFEKQVFPFHPPLRYEPVLEKEDSL 586
DB 541 QGSRNRYFRSKGSLIYVAINCMHQFIDEPPMFEKQVFPFHPPLRYEPVLEKEDSL 600
QY 587 VANDWCKRPSPDFCLKTRAPVLCATGPADSOHSGHGLQDQDGAAPALDGSALQPL 646
DB 601 VANDWCKRPSPDFCLKTRAPVLCATGPADSOHSGHGLQDQDGAAPALDGSALQPL 660
QY 647 LHTVKAQSPDMPRDSIGYDSSVPSSELSLPLMEGLSTQETSTLTSVSSSGLGEBE 706
DB 661 LHTVKAQSPDMPRDSIGYDSSVPSSELSLPLMEGLSTQETSTLTSVSSSGLGEBE 720
QY 707 PPALPSKLLSSGCKVADLCGRSYTDLAAVAP 738
DB 721 PPALPSKLLSSGCKVADLCGRSYTDLAAVAP 752
RESULT 15
AEB55654
ID AEB55654 standard; protein; 738 AA.
XX AEB55654;
AC 22-SEP-2005 (first entry)
XX Human DCSR8 polypeptide.
DB Protein engineering; cytokine receptor; DNA cytokine receptor subunit;
XX DCSR8; Interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
XX interstitial lung disorder; asthma; allergy; atherosclerosis;
XX gastrointestinal-gen.; anti-inflammatory; antiaesthetic; anti-allergic;
XX antiproliferative; antileukemic; respiratory-gen.; immunosuppressive;
XX antitumor; DCSR8 agonist; DCSR8 antagonist; IL-17C antagonist;
XX IL-17C agonist; human; DCSR8; receptor; antisense therapy; RNAi therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX FH Misc-difference 34 /label= Gln, Arg, Pro or Leu
XX FT /note= "encoded by CNG"
XX FT Misc-difference 42 /label= Lys, Arg, Thr or Met
XX FT /note= "encoded by ANG"
XX FT Misc-difference 125 /label= Ser, Gly, Arg or Cys
XX FT /note= "encoded by NGC"

```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:26:21 ; Search time 44 Seconds
(without alignments)
1613.818 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948

Sequence: 1 MAPMTQLCGVFFVFNACNG.....SCKADLCGRSYDELAAVAP 738

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2993	75.8	564	T42695	hypothetical prote
2	169.5	4.3	846	T27282	hypothetical prote
3	124	3.1	718	T30113	hypothetical prote
4	115.5	2.9	901	F83781	transposase (88) /
5	114	2.9	757	T09081	telomere-associate
6	114	2.9	2946	T00867	hypothetical prote
7	112.5	2.8	663	A39897	GTPase-activating
8	110	2.8	3788	T13960	beige protein homo
9	110	2.8	917	T04661	hypothetical prote
10	109.5	2.8	3942	T42730	Basoon protein -
11	109	2.8	3788	T30851	lysosomal traffick
12	108	2.7	535	T17212	hypothetical prote
13	108	2.7	535	T17212	vesicle transport
14	106.5	2.7	638	D86477	protein F1504.27 l
15	105.5	2.7	970	S63059	hypothetical prote
16	105.5	2.7	1007	T24643	hypothetical prote
17	104	2.6	536	T16124	hypothetical prote
18	103.5	2.6	998	S37627	protein-tyrosine k
19	103	2.6	641	T05497	hypothetical prote
20	103	2.6	1462	B36182	protein-tyrosine-P
21	103	2.6	1571	T14155	zinc finger protei
22	102.5	2.6	938	T49071	protein kinase - m
23	102.5	2.6	1639	T50119	probable sensory t
24	102	2.6	664	T51247	ARR2 protein (lipo
25	101.5	2.6	806	JN0612	protein kinase B-r
26	101.5	2.6	807	I51153	protein kinase B-r
27	101	2.6	786	T39585	ubiquitin protein
28	101	2.6	813	B47485	ABR protein 2 - hu
29	101	2.6	859	A49307	98K GTPase-activat

30	101	2.6	930	2	A84688	Argonaute (AGO1)-1
31	101	2.6	1275	2	A39885	nucleotide exchange
32	100.5	2.5	822	2	A47485	ABR protein 1 - hu
33	100.5	2.5	963	2	AD2381	type I site-specif
34	100	2.5	901	2	JC6093	dead ringer nuclea
35	100	2.5	2437	2	S53611	MIBP1 protein - ra
36	99.5	2.5	794	2	S59069	213 protein - mous
37	99.5	2.5	938	2	T05533	hypothetical prote
38	99.5	2.5	2251	2	T24490	hypothetical prote
39	99	2.5	820	2	S33794	hypothetical prote
40	98.5	2.5	353	2	T33782	hypothetical prote
41	98.5	2.5	1121	2	T25715	hypothetical prote
42	98	2.5	787	2	T27632	hypothetical prote
43	98	2.5	794	2	T27632	hypothetical prote
44	98	2.5	828	2	A88860	protein ZC518.3 [i
45	98	2.5	984	2	A39753	protein-tyrosine k

ALIGNMENTS

RESULT 1

T42695
hypothetical protein DKFZp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #ext_change 09-Jul-2004

C/Accession: T42695

R/Bioecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A/Reference number: Z22230

A/Accession: T42695

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-564 <AAA>

A/Cross-references: UNIPROT:Q9UFA0; UNIPARC:UPI00006EF02; EMBL:AL133097

A/Experimental source: adult testis; clone DKFZp434N1928

C/Genetics:

A/Note: DKFZp434N1928.1

Query Match 75.8%; Score 2993; DB 2; Length 564;
Best Local Similarity 99.5%; Pred. No. 4.3e-231;
Matches 560; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	176	HPFFETTRACDILLQPDNLACRPFMRRLNLSQHSQSDMVQSFDAHPNPFPTLHYK	235
DB	1	HPFFETTRACDILLQPDNLACRPFMRRLNLSQHSQSDMVQSFDAHPNPFPTLHYK	60
QY	236	LKHGPPKRTCKQBOETTETSCLQNVSPGDIIELVDTNTRKVMHYALKPVS PMA	295
DB	61	LKHGPPKRTCKQBOETTETSCLQNVSPGDIIELVDTNTRKVMHYALKPVS PMA	120
QY	296	GPTRAMATVPLVVISAPATLFTVMCRKQOENIYSHLDESSSTYTAALPRERLPR	355
DB	121	GPTRAMATVPLVVISAPATLFTVMCRKQOENIYSHLDESSSTYTAALPRERLPR	180
QY	356	PKYFLCYSSKQGNHNVVQCPAYFIQDRGCEVALDLMEDSLCEGQRENTYQKIHSS	415
DB	181	PKYFLCYSSKQGNHNVVQCPAYFIQDRGCEVALDLMEDSLCEGQRENTYQKIHSS	240
QY	416	QPIIVVCSKGMKFFVKKYKHKGGSGSGKGLFLVAASATAEKKRQAKOSSSALSKF	475
DB	241	QPIIVVCSKGMKFFVKKYKHKGGSGSGKGLFLVAASATAEKKRQAKOSSSALSKF	300
QY	476	IAVYFDYSCGDVPGILDLSTKRYLMDNLPOLCSHLASRDHGLQEPGQHTROGSRNRYR	535
DB	301	IAVYFDYSCGDVPGILDLSTKRYLMDNLPOLCSHLASRDHGLQEPGQHTROGSRNRYR	360
QY	536	SKSGRSLYALICMHOPIIDBPDWFEKQVPPHPPPLRREPYLKEFGDGLVINDVCKP	595
DB	361	SKSGRSLYALICMHOPIIDBPDWFEKQVPPHPPPLRREPYLKEFGDGLVINDVCKP	420
QY	596	GPSDFCLVFAVPVIGATGPADSGHSHGGLDQDSEAPALDGSAAALPLHTVAGSP	655

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Db      421 GPESDFLKAEAVLIGATGPAQSQHSQHGGLDQGEARPALDGSALQPLHTVKASGP 480
Qy      656 SDMPROSGIYDSSVPSSELSLPLMEGLSTQTERSSLTESVSSSGGEEEPALPSEKLT 715
Db      481 SDMPROSGIYDSSVPSSELSLPLMEGLSTQTERSSLTESVSSSGGEEEPALPSEKLT 540
Qy      716 SSGSKADLCGRSTYDELAHAVAP 738
Db      541 SSGSKADLCGRSTYDELAHAVAP 563

RESULT 2
T27282
hypothetical protein Y64G10A.e - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T27282
R/Accession: R.
submitted to the EMBL Data Library, September 1999
A/Reference number: Z20336
A/Accession: T27282
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-846 <WTL>
A/References: UNIPROT:Q9NAA64; UNIPARC:UPI000007CGB7; EMBL:AL110498; PIDN:CAB54470.
C/Experimental source: clone Y64G10A
A/Gene: CBSP:Y64G10A.e
A/Intons: 106/1; 196/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3
C/Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e

Query Match      4.3%; Score 169.5; DB 2; Length 846;
Best Local Similarity 21.4%; Pred. No. 4.7e-05;
Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;

Qy      85 QVACHDQVATILMSPGALGIEFLKGFVILELSESGROCOQLIKDPKQLNSSFRTG 144
Db      294 QY-CFEEYEVRLDSS---GIWVLSALITKDELRTS-----ITNGRPVQFGEF----- 338

Qy      145 MESOPPLANKFEEDYFVKVVPFSPISKESYHPPFFRTACDLLOPDNLAC-KPPKPR 203
Db      339 ----NFDIIDLDTLIPSVIPISAHN-----GRC-LCVTNGSGCLAAADMKPV 382

Qy      204 NLNISQHSQMOYSPDAHNPGRFYLMYKLGHEGPFKRTCKOBOTETTSCLQNV 263
Db      383 KLT-----RIEKPRTSN-----QTESDGAKEKDKEDTTWT----- 415

Qy      264 SPGDYIIEVDVDTTRKVMH-YALKEVHSPWAGPIRAMAIVPLVVISAPLT--FTVM 320
Db      416 -----WHYVA-----ITGSAIHALFLISVCAGLKCYKXF 445

Qy      321 CRKKQENIYSHLDESSSESTYTAALPRERLRPVFLCYSKGQGMNNTVQCAYF 380
Db      446 NNNKKASNI--HLINENPAFS-HSGSIPL-ILKOSISVLIVY-SHDSAOHEAAVLAEAL 500

Qy      381 LDPGCGEVALDLMEDSLCREGREGVIOKIHESQIIVYCSGKMYFVDKKNYKKG 440
Db      501 LRDVFNINVLHDVDEDDI-BENSAEYINSIVANKYIINISIG-AYF--RTVFRQR- 555

Qy      441 GRGSGKGLFLVAVSAIAEKLRQAKQSSAALSKFIAYVFDYSCGDV--PGILDLSTKY 498
Db      556 -----EPAIERITTRND-----VIDPMQELALQHPCVISCHFSY 591

Qy      499 -----RLMD-NLPOLCSHLHSDGLQSPGHTHQGSHRNFRSKSGSLVYAI 546
Db      592 TNPKYVFPPINRLLQYGISP--NSIMTMTALTTEQPARPQLAGFNQVFAF-----LQAAI 644

Qy      547 CMNHQFIIDEDBDWEK-----QVPPHPPLKRR----- 575
Db      645 SRKLNTYIESDPQWENTHHRVATRVSELAHNTVPL-PSLEKVKVDEDAFGQMETLPI 703

Qy      576 EPLYLEK-----DSGLVLDVWCKPQPSDPCFKVAPVLTGATGPADSQHS 622

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Db      704 DELKEFPAARKDLEVEVLSEVDKLLIEDYKCAFP-----IHVEPTEPEVLBPABEPMER 758
Qy      623 QHGGLDQDGEARPALDGSAA-----LQPL-HTVKASPSDMPRDSCGYDSS-VPSSELS 675
Db      759 AEED-REDEDVDVSVEGQTRIEELQRLIVH-----KDMHNSGNLDSATVYSGSDFS 809

RESULT 3
T30113
hypothetical protein F56D1.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30113
R/Accession: R.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid F56D1.
A/Reference number: Z20737
A/Accession: T30113
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-718 <CHI>
A/Cross-references: UNIPROT:Q10128; UNIPARC:UPI000013C0C4; EMBL:U39997; PIDN:AAA81100.1;
C/Genetic:
A/Gene: CBSP:F56D1.2
A/Intons: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3
C/Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2

Query Match      3.1%; Score 124; DB 2; Length 718;
Best Local Similarity 21.1%; Pred. No. 0.16;
Matches 82; Conservative 63; Mismatches 150; Indels 94; Gaps 19;

Qy      349 REHLRPRP-----KVFLCYSKDGQGMNNTVQCAYFLODFCGEVALDLMEDS 398
Db      398 RDRVRSREVRNIALTFVKMIVYAD-DNDLHTDCYKLVENLRKASCDDPVLDLKIT 456

Qy      399 LCREGQREVTOKIHESQPIIVVCSKMYFYVDKKNYKKGSGSGKGLFLVAVSAIA 458
Db      457 ABQIVPSRMLVQDSSLKXFLIVSDCAEKILDTSETHQVQAPFADLPFAPMEI- 515

Qy      459 EKLQAKQSSAALSKFIAYVFDYSCGDV--GILDLSTKRLMDNLPOLCSHLHSD 515
Db      516 --LRDATHNPPEARKKYAAVRFNY--PHVPMLALINPT-FILPEQPAQLTAFLHNV 570

Qy      516 HGLQSGQHTQSGSRNRYFRSKSGSLY--VAICMHQFIIDEPMPFEKQFV----- 566
Db      571 H-----TERANVTQNISBAQIHENMLCASMMSEFPVNPVWLETMRKQDELA 619

Qy      567 FHPPRLRYRBPVLEKEDSGLVLDVWCKPQPSDPCFKVAPVLTGATGPADSQHSQHG 626
Db      620 LH---LKRQSPVIVPQT-----EED--RIAAISIKYLVLPQALVDS- 657

Qy      627 LDODGEARPALDGSALQPLHTVKASPSDM--PDSGIVDSSVSSSESLPLMGLST 664
Db      658 -DED-----DVLDLP--HNSHQNOLILPPOCG-----PDS- 690

Qy      685 DQETSSLTESVSSSGGEEEPALPSK 713
Db      691 SESDSSSESSESNDG---EDPKTIIVK 716

RESULT 4
F83781
transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus ha
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: F83781
R/Accession: R.
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: AB36501; M0ID:20512582; PMID:11058132
A/Accession: F83781
A/Status: preliminary
A/Molecule type: DNA

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A/Residues: 1-901 <STO>
A/Cross-references: UNIPROT:Q9XB04; UNIPARC:UPI000000CA39B; GB:AP001510; GB:BA000004; NID:
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH1054

Query Match 2.9%; Score 115.5; DB 2; Length 901;
Best Local Similarity 19.8%; Pred. No. 1.1;
Matches 113; Conservative 76; Mismatches 168; Indels 215; Gaps 28;

QY 47 ASRNSGLYNTFKYDCTTYLNPVKGAVIADQNIITISQY-ACHDQYAVTLLMSPGALGI 105
DB 333 ALKESGL-PLPKTLIADAGSSESNVYAMADELFETLIPS----- 371
QY 106 EPLKGFVILIELKSGR-----OCQOL--ILKPKQLANSFKTKGMSOPLANKF 155
DB 372 ---HTFR--OEQKSFAPKGRPHNRCDETDYVWCNCRKVSFKYTKRTDY---GY 423
QY 156 ETDYFV-----KVVP-PSI-----KNESYHPFPRTACDILLQPDNLACKPFWKPR 203
DB 424 ARPKYVTECSCECPKPECTKARGRQVHTNRY-----EELKAKQHQK 471
QY 204 NLNISQHG-----SDMQVSPDAPHNFGFPFYLYLKLKHEGPKRKTCKOETTER 255
DB 472 ---SEEGRTLQYKRTKDVSVFQHVQKQNGFRLLHKG----- 507
QY 256 TSCILQVSPGDYIIELVDTNTTRKVMHTALKPHSPWAGPIRAMAITYPLVIS-AFA 314
DB 508 -----ESVH-----IELGLVALAHNL 524
QY 315 TLFTVMCRKKOENIYSHLDESESESTYTAALPRRLRPKYFLCYSSKDGNNHNV 374
DB 525 KRATVDRSKPEPNTNQHKNEN-----RIKRF-----SRFYVL 558
QY 375 QCF---AYPLQDFGCEVALDLMEDFSLCREGQRENV---IQKHESOPFIIVCSKGMK 427
DB 559 RCFMDSFPFKSDCKQYASFLPD--KLRRGEGNMIEVDLSTYNNQV---KGIN 612
QY 428 YFVDPKKNYKKGKGGSGKGEFLVAVSAI-----AEKLRQAKOSSAALSK 474
DB 613 MPEKEMVGLGPNMGAKSTTISMSLIQPTSGDVLKSGSIHKSKAIRSILGVVPPQ 672
QY 475 FIAYVPDYSCE-----GDVPGLDLSTKYRLMDNPOLCSHLHSRHHGQEPQHTROG 528
DB 673 EIVVHTDLTKRELAFFGKYGLKGEELKPR-WESTQLV-----GLBE-----RON 718
QY 529 SRNRYFSKSGRSIYVACMHQ---FIDEEP 557
DB 719 DRVHTFSGCMKRLNIAVALHBEELIMDEP 750

RESULT 5

T09081
telomere-associated recQ-like helicase - smut fungus (Ustilago maydis) (fragment)
C/Species: Ustilago maydis (corn smut)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09081
R/Sanchez-Alonso, P.; Guzman, P.
Genetics 148, 1043-1054, 1998
A/Title: Organization of chromosome ends in Ustilago maydis: recQ-like helicase motifs
A/Reference number: Z16557; MUID:88198830; PMID:9539423
A/Accession: T09081
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-757 <SNM>
A/Cross-references: UNIPROT:O13399; UNIPARC:UPI000006BCA3; EMBL:AF030885; NID:g2642221;
A/Experimental source: strain FB2
C/Genetics:
A/Gene: UPAStecQ
C/Keywords: DNA binding

Query Match 2.9%; Score 114; DB 2; Length 757;
Best Local Similarity 20.2%; Pred. No. 1.1;

Matches 110; Conservative 56; Mismatches 188; Indels 190; Gaps 27;

QY 254 ETTSCILQVNSPGDYIIELVDTNTTRKVMHTALKPHSPWAGI-----RAMAITYPL- 307
DB 77 ETTILILPTVALRAMAKLADVNN---IRYHWQF-GSKKAAPYLVSTEAATLAFKE 131
QY 308 -----VISAFAITLFTVMCRKKOENIYSHLDESESESTYTAALP----- 348
DB 132 YANRLDQQLDRIVIDECHLTTANSYRSNMQLAMHVDVETQYWLTAITLPIREDA 191
QY 349 -BERLAPRPKV-----LCYSSKDGQNNHNVQCF-AYPLQDFGCEVALDLMEDF 397
DB 192 FISHNLTKFLIYRESSTNRLCYSVTAHRSNGMTCYAVRVVD--ECRARDIY--- 246
QY 398 SLCREGQRENVITQKHESOPFIIVCSKGMKYFYDK-----KNYKKGKGRGS----- 444
DB 247 ---NGQRD-----RIIYCYTS--KELVARILEMGLCAAYSSESGSEADKAAIIQ 290
QY 445 ---GKGEFLVAVSAIAEKLQAKOSSAALSKFLAVYFDPYCEGDPVIL--DLSTKY 498
DB 291 DWICGKSPVIVATSA-----LGVGFDPVHVRVFIHLGLPDLITDF 331
QY 499 -----RLMDNLPOLCSHLHSRHHGLOBPQHTRQSGSRNRYFS 536
DB 332 SQSSGRAGRDGMABESTLLAGPQLDRAP--ASGKASAEKGVAPG---ADKEMQLYRS 387
QY 537 KSGRSLYVALCNMHQPTDEEPMFEKQFVPPHPLRYRPEVLEKFDGLVNDWCKPG 596
DB 388 RK---YCLRGLVSLQLDQKRDW-----RMWCEGDLQCSVC 419
QY 597 PESDFCLKVAAPVLGANTGPADSOH---ESQHGGLDDGEPALDGAALQPLHITYKAG 653
DB 420 PGNHP-----QARGPDQFHTAPAGAPSTQSGSRHPMGSGS--HPSNR----- 463
QY 654 SPEDMPRDSGITDSSVPSSE--LSLPLMEGLSTQETSTSLTESVSSS---SGLGESEPPA 709
DB 464 -----GSHRPSHGSHSPHSHSHSHSGS--HPSIHSGGCGGRKQKQPD 510
QY 710 LPK 713
DB 511 PPS 514

RESULT 6

T00867
hypothetical protein At2g45540 [imported] - Arabidopsis thaliana
N/Alternate names: hypothetical protein F17K2.7
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00867; G84891
R/Rounsailey, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.T.; Brandon, R.C.; Sykes, S.
submitted to the EMBL Data Library, March 1998
A/Description: Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence.
A/Reference number: Z14207
A/Accession: T00867
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2946 <ROU>
A/Experimental source: cultivar Columbia
R/Lin, X.; Kaul, S.; Rounsailey, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: G84891
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2946 <STO>
A/Cross-references: UNIPARC:UPI000000AA39B; GB:AE002093; NID:g2979554; PIDN:AA06163.1; G8
C/Genetics:
A/Gene: F17K2.7; At2g45540

A. Map position: 2
A. Intcons: 652/1; 913/3; 1165/3; 1210/3; 1245/3; 1283/3; 1309/2; 1336/3; 1438/3; 1638/2;
2449/2; 2481/3; 2643/1; 2890/3; 2931/3

Query Match	2.9%	Score 114	DB 2	Length 2946
Best Local Similarity	18.8%	Pred No. 8.3		
Matches 162	Conservative 105	Mismatches 315	Indels 282	Gaps 40

QY	2	APMLOLGVFFVVAANCLNGSOLAVAAAG--SGAMGWIDTCGRMGVPAENSLXNITPKY	60
Db	393	ATWITYESFADTLNATATAAATAAAAAAKSGK-----TSMSAAAAAALAG-----	439
QY	61	DNCTTYLNPVGGKVIADAQNTITSQYACHDOVAVTILWSPGALGIEPLKGRFVILIELKS	120
Db	440	-EGTAMHBRLEFSLADNQGIEAYFHA-----QFL-----VYESGSG	475
QY	121	EGR-----QC-----QQLIKPKQKQNSFRKRTGMSOPFLMMKET	157
Db	476	KGRSSSLHFTHAFKQCYFIGLEHSCKQGLGKAESBLRYIDSLVESRPF-----	528
QY	158	DYFVXVVPFPEIKNESNHYHPFF-----RTRACOLLQ--PDNLACKPF	199
Db	529	-----DFFPIISK-----PLSFCCIGNPPPTMAGLQRRRQCLFLAMGCVYIFKXPI	576
QY	200	WKPRNLNISQHGSDMQVSPFDHAPHNFGRRFFLYAKLKHEGFFKAKTKQKOBOTETTS-	257
Db	577	GPERMARILASRGSDVLPCCFGNGA---GLPWLATNDYVEN-----KAESSITLADI	624
QY	258	-----CLLQNVSPQDYIIELVDDNTNTRK-----VMHYA--LKPYHSPMA-----	295
Db	625	GGYTHLYLHPCLLSGRFCPD--ASLSGAAGTIRRAEVLGOVHVAITRKPFVESFWALLAYG	682
QY	296	GPIRAMATV-----PLVVISAEATLETVN-----CRKKQ	325
Db	683	GPMSLPLPTVSSVHKDSLPCGLNPLSLSTVTLTAAPFRISVAIOHPGNNBELCRTOG	742
QY	326	QE---NIYSHDEBSEBSSTYTAALPRBRRLRPRPVFLCYSKQOQNMNMYQCFAYFLQ	382
Db	743	PEILARILSYLHSLASLDRKHGVEEEL--VAALVSLCQSQK--INHVLKQVLFRTLL	799
QY	383	DFCCGEVALLDMEDPFLCREGQREWVIOKIHESQFTIIVCSKMK-----YF	429
Db	800	D-----LKITW---SLCNYGLQKTLISLQDMVPTFAATPAMDAAIGLLDGCRCRTMM	849
QY	430	VDKKN---YKHKGCGRSGKGELFLVAVSAIAEQLRQAKOSSAA--LSKFIAYFPYS	483
Db	850	ISEKSEETTFPLDQNTRWQGEINALIDELVLIETLMGAASPLAADLRLGLFIISP	909
QY	484	CEGDVPGILIDSTKTRLMDNL--POLCSHLHSRDHGLQE---PQOHTROGSRNRYFRSK	537
Db	910	QPNQVARTLHMLRYLVQPNNAARQAMFPEAVFTTSGIETLVLLOREAKTGEDNVLAMGR	969
QY	538	SGRSLYVAICNMHQFIDEPPWFEKQVFPFHPPLRYREBPVLEKFPDGLVNDV--MCKRG	596
Db	970	SGKR-----SSTDPSEKS--PYN-----BSGSYKQUDSNPHDIEIFDLPG	1008
QY	597	PESDPCLEVAEPVYGATG--PADSQHESQHGLDDQGEARPALDGSAAIQLPLHTYKASSP	655
Db	1009	PDGN--SVEDDNVGSILVNPESVROEKHG-----STP	1038
QY	656	SDMPRDSGIYDVSVSSELSLPLMGLSTDQETSLTESVSSSGLGS---BEPPA--	709
Db	1039	VVCOSDVSISINSINTERLS-----AEIGISLISADBARNNVNVVNDSDAVV	1087
QY	710	-----LBSKLSSGSCAKDLCGRS	728
Db	1088	VGIRLRIGALISSGHLPDPDARS	1111

RESULT 7
A39897
GTPase-activating protein rap1GAP short form - human
C:Species: Homo sapiens (man)

CjDate: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 05-Oct-2004
CjAccession: A39897
R:Rubinfeld, B.; Mumentstu, S.; Clark, R.; Conroy, L.; Wett, K.; Crosier, W.J.; McCormick
Cell 65, 1033-1042, 1991
A>Title: Molecular cloning of a GTPase activating protein specific for the Krev-1 protein
A:Reference number: A39897; MUID:9156304; PMID:1504317
A:Accession: A39897
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-663 <RUB>
A:Cross-references: UNIPROT:P47736; UNIPARC:UPI0000013381A; GB:M64788; MID:9190855; PIDN:
CjSuperfamily: Rapi GTPase-activating protein

Query Match	2.8%	Score 112.5	DB 2	Length 663
Best Local Similarity	19.7%	Pred. No. 1.2		
Matches 144	Conservative 80	Mismatches 261	Indels 247	Gaps 33

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153 MKEFDYEVKVVPPFPIKSNESVHPFFRTRACDILLQPD----- 192
Db 21 LKTEBDY-----IPYSV-----HEVLGREGPPRLILLQFGGWIIEGTMHETISIPETE 70
Qy 193 -----NLACKP-----FMKPRNLNISOHSDMQVSPDHAPHNFGFRFFYLHYK 235
Db 71 FLQSPPTKYKLECNPTARIYRKHFLGKEHFN-----YSLDTA-----LGHVLFSLKYD 119
Qy 236 L-----KHGPPFRKTKCKQEQTTETTSCLLQNNVSPGYIIELVDDTNTTRKVMYALKPVH 291
Db 120 VIGDQEHRLRLRTKCRTHYDVIPIISCLTEPRPVVMQAKLVCEBDVNVDR-----FYBVL 173
Qy 292 SPWAGPIRAMAITYVLVVIS---APATLFTWOCRKQOENIYSHLBESSESTYTAALP 348
Db 174 YPKAS---RLIYTPREHVISNNPKFGVITYQKLGQTSBEE-----LBSITNEESPAPVFLE 225
Qy 349 REBLRPRKPVLCYSSKQGNHMANVQCFAYFLQDFCGCEVALDLWE---DFSICR-- 401
Db 226 -----FLGQKYK-----LQDFKFGRGDLYTHGQTGESVCNFR 260
Qy 402 -----EGQREWYIQKHESQFIIVVCSKMKTYVDK-----KQYK 436
Db 261 NKEIMFHVSTKLPYTEGDAQOOLQRKHINDIVAV-----VFQDENTPFPVPMIASNFL 314
Qy 437 H-----KGGGRSGSGKGLFLVAVSAIAB-----KLROAKOSSAALSKFEIA 477
Db 315 HAYVVVQAEQGG--PDGFLYKVSVTARDVPPFGPPLPDPAVFRKGPBEOELLTKLIN 371
Qy 478 VYFDYSC-EGDVPGIILDISTKRYLMDNLDPOLCSHLSRD-HGLQEPQHTROGSRNRYF- 534
Db 372 A--EVACYKAEKFAKLEBTRAALETLEYBEL-HINSQMWGLGQDDEKKNENSGCGGFF 428
Qy 535 -----RSGSGSGL-----YVAICMNHQFIIDEBDWE---KQVPVPHRPLR 573
Db 429 ESFKRKVIRSQSGMDAMGLSNKKPMTVSTSHSGSFAPNNDLAKAAGISLIVPKSPTRK 488
Qy 574 YREPVLKRFDSGLVYNDVCKPQPSDFCLKYEAPVIGATGPAQSOHSGHGLDQGEA 633
Db 489 KSGPGRSRRSSAIGIENT-----QEVQEKESPPAQKTP--DSGHVSGEPSE----- 535
Qy 634 RPALDGSALQPLILHTVYKAGSPSDMPRDSGIYDSVPSSELS-----LPLMEGLSTDQTE 688
Db 536 ---NSSTQSSPEMPTTKNRFAETAQBARALADQFSSSSASASFASVBEETEGVDGSDTG 591
Qy 689 TSS-----LTESYSSSG-----LGEEBPALPSKL 714
Db 592 LESVSSSGTPHNRDSFIYSTWLEDVSITSGSSGSPGPRSFPHDAGKLGDPACPEIKIOL 651
Qy 715 LSSGCKRADLGC 726
Db 652 EASEQHMPOLGC 663

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RESULT 8
T13960
beige protein homolog - rat

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T13960
 R/Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.
 submitted to the EMBL Data Library, November 1998
 A/Description: Deletion in the beige gene of the beige rat due to recombination between
 A/Reference number: Z17637
 A/Accession: T13960
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-3788 <MOR>
 A/Cross-references: UNIPROT:Q922X9; UNIPARC:UPI00000587B; EMBL:AB020019; NID:d1241953;
 A/Experimental source: strain DA; spleen
 C/Genetics:
 A/Gene: beige

Query Match 2.8%; Score 112.5; DB 2; Length 3788;
 Best Local Similarity 19.9%; Pred. No. 16;
 Matches 146; Conservative 98; Mismatches 260; Indels 231; Gaps 40;

QY 20 GSOLAVAGSGRAMGVDTGCMR--GVGPASRNSGLYNTFKDNTCTYLANPVGKAVIAD 77
 DB 651 GERTLOGTLCAGSGSCGLPSPSYRFOGILP---SSGSDFLMKDALRAYONFIPOE--DR 705
 QY 78 AONITISOVACH--DOVAVTIIMSFGALGIBFLKGFVILBELKSEG---RQCQOLILK 131
 DB 706 LHNTQJASHICNLIQKNVIVOW-----KLNYITFPVQLQRCVELVHHCQQLSI- 754
 QY 132 DPKOLNSFRRTGMEQOPFAMKPEF--DYFVKVVP-----PPSITKN-----ESN 174
 DB 755 -----TSAQTHMSQGLQYLPQEVGLQYILKTLPIILKSRVIRDLFSCNGVNHIELN 807
 QY 175 Y-----HPR-FRTTRACDILLQPDNLACRPFKPKRNLTISQHSQMSQVSDHAHPNFGF 227
 DB 808 YLDGIRSHSLKAEETLVLSLGEQCKRAAVPGV--DELIDIQEILSSISV----- 853
 QY 228 RPFYLYKLGHEPFRKTKCKQEGTETTSCLLQNSPQDYIIELVDTTTRKVMHYAL 267
 DB 854 -----GSLHKK-----QOASTDSPCSLKK-----FYASLRITDPRKRTVHQ-- 890
 QY 288 KPVHSPWAGPIRAMAIVPLVVISAPATLFTVMCRKKQENITVSHLDESSSESTY--TA 345
 DB 891 -----DHNTINIFLCVAF-----LCVSGEADSDRESAN--ESEDTSIGYSTA 932
 QY 346 ALPERLRPRPKVFLCYSSKQGMHNVV---QCFAYFLQDFCGCEVALDLWEDFSLCR 401
 DB 933 SEPLSHMLPRLSL-----ENVVLPSPRCLHH-----AADIW---SMCR 967
 QY 402 EGGRBNV--IQKHESQFI---IVGSKGKMTFVQKQYKHKGGSGSGKGLF----- 450
 DB 968 -----WYMLNSVFOKQFHLRGFOYCHE-LIFMIIOKLFPSHTEDEGRROGEGSVNKNQ 1021
 QY 451 -LVAVASIAKLRQAKSSAALSKPIAVYFDVSCBQDVPGLD-----LSTK----- 497
 DB 1022 GLWRISOPEMILKEDVSSSTAPEPGFLKKSADRVSELSQMLPTSAQOLATYSTIGEA 1081
 QY 498 -----YRLMDNLPOLCSH---LHSRDHGLQEPGQHTROGSHRNRYFRSKGR 540
 DB 1082 KTFPMQSESTCLOSIRLLESILAIILCHSABASQCKMELPSPQ-----SL 1126
 QY 541 SLVVALCNMHOPIDEEP-----DWFEKQFVFPHPPLRYRPRVLEKPDGSLVYN 589
 DB 1127 SLNNITCELDHDSQSKVAETELAKPLFDALLRVALGNHSAIDLPGDVTYEKSHPS--E 1183
 QY 590 DWACKCPESDPCUKVY-----APVLGATG--PADSQHSQHGGLQDGEARPALDG-S 640
 DB 1184 RYLSQGR---DFSEBAEDSQCSKLGLGEEGRTADESNPDEGETDDGVELPBAEGFS 1240
 QY 641 AALQP--LHHTVXAG 653
 DB 1241 GSIVPNNLLESLTHG 1255

RESULT 9

T04661
 hypothetical protein F8D20.70 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T04661
 R/Bevan, M.; Rose, M.; Hempel, S.; Ertlman, K.D.; Jesse, T.; Hejnen, L.; Vos, P.; Mewes,
 submitted to the Protein Sequence Database, July 1998
 A/Reference number: Z15381
 A/Accession: T04661
 A/Molecule type: DNA
 A/Residues: 1-917 <BEV>
 A/Cross-references: UNIPROT:O81789; UNIPARC:UPI00000A12E3; EMBL:AL031135
 A/Experimental source: cultivar Columbia; BAC clone F8D20
 C/Genetics:
 A/Map position: 4
 A/Intons: 13/3; 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3; 685/
 A/Note: F8D20.70
 C/Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70

Query Match 2.8%; Score 110; DB 2; Length 917;
 Best Local Similarity 17.9%; Pred. No. 3;
 Matches 162; Conservative 129; Mismatches 294; Indels 322; Gaps 40;

QY 19 NSGOLAVA-AGSGRAMGVDTG-----W-RGVGPAS 48
 DB 92 NSGRVSVGYSNGDILWISIPSKGECSPSSAMICKNLGYKSEKIPASLKWYABGKAS 151
 QY 49 R-----NSGLYITFKYDNTCTYLANPVGNV---TADAONI--TISOVACHQVAVTIL 97
 DB 152 RYVVISSSSNSLQVVLNDETERMTKGLHVEPCADMEMIADVNEGSKHQDFLVL 211
 QY 98 WSPGALGI--EFLKGFVILBELKSGRQCQQLLDPKQOLNSFKRTGMEQOP--FLNM 153
 DB 212 GKSGRYAYVDYVIMIKYLLQSGKSSPSLPKETVVKLPFSQSSSITWGEKELTPSHLNL 271
 QY 154 KEPTDY-----FVKVVPSPISINESN---YHFEF-----FTRACDILLQPDNLACK- 197
 DB 272 SDE-DVAQLKADAVPLPFTYTPKSSRSNHPFGFVKVKNVYITGHCDDGTISVWDMTCSP 330
 QY 198 -----PMPKPR-NLINSQHG-----SDMOVSDHAHPNFGFRFYLYLKH-- 238
 DB 331 PIVLPLKQIDPDVSRGKAALTALHYDSNGLVSGDHNGVRLRYRPEBYLTENSF 390
 QY 239 ---EGPFKR-----KTCQEQETETTSCLQNVSP-----GDYIIELVDTNTT 279
 DB 391 IFFQSLKKGNNHIVQSVKIKLGTSTTCIQKQNSKHLAIGSDGHSLEVID----- 445
 QY 280 RKMVHALKPYHSPMAGPIRAMAIVPLVVISAPATLFT----- 318
 DB 446 -----ALTPVY-----LOVSLVDIEBANVLYKHLASDICPGIISLQFESCIV 488
 QY 319 -----VMCKKQENITVSHLDESSSESTYTAALPRELRPRPKVFLCYSSKQGMHNM 372
 DB 489 QGPEKAVLVVAMEDSSVFA-LDSDTGMIMGTMIYK-----KPKVLYNQIILDK- 538
 QY 373 VVOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKHESQFIIVCS----- 423
 DB 539 -----QDTSG-----NGFPTSRES-----IYEBISIRQPSVLVCSBRAIYISL 577
 QY 424 ---KGMKTFVQKQYKHKG-----GGRGSGKELPLVAVSALAE-----KLAQAK 466
 DB 578 AHVVOGVKVKLAKKKSSSPICSAFTYGTSGV--LTLVFTDGTVEIRSLPELSQLKQ 634
 QY 467 S-----SSAALSKPIAVYFDVSCBQD-----VPGIILSTKRLMDNLPOLC 598
 DB 635 TSIRGFTYSSPKNSLPETITISAMGDLLVMNNGDELLVSSVLPQKRTFRVLVESH----- 630
 QY 509 SHLSRDHGLQEPGQHTROGSR-----NYFRSKSGSLVYVAICNMHOPIDEEPWFEK 562
 DB 691 NRYVKKONSVCHEGIIITSSSPREKSMFGSVFRTKSKRTTDPRESSKETIEBELSKFST 750
 QY 563 QFVPF-----HPPPLRYRPRVLEKPDGSL----- 586

Db 751 ANPMMNNVNSREINTITREVEDEBELDIDIDIDHHPNQOQOEKKEGIIISGSKK 810
Qy 587 VLNDWCKPPEDEDFCLKVAEAPVLCATGAPDSCQESQHGSL-----DQDGEA 633
Db 811 MARFNFNFKCKLQOMAKNKKSVV---TYDEKKEBKNGATVDQIKKKYGTSSDEMGAA 866
Qy 634 RPLDGSALQPLHTVTKAGSPSDMPDSCGIYDSSVPSSELSPLMEGLSTDOTETSSLT 693
Db 867 KMA-----QSKIQD-----NLKKGIGISLRTTEWEDTA 894
Qy 694 ESYSSSS 700
Db 895 KSFSSTA 901
RESULT 10
T42730
Basoon protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T42730
R/Desc: S.; Samartli-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A/File: Basoon, a novel zinc-finger CAG/glutamine-repeat protein selectively localized
A/Reference number: Z2249; MUID:98345363; PMID:9679147
A/Accession: T42730
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-3942 <DIR>
A/Cross-references: UNIPROT:O88737; UNIPARC:UP10000029B58; EMBL:Y17034; NID:G3413809; PI
C/Genetics:
A/Map position: 9P1
A/Intons: 72/2; 208/3; 505/3; 675/3; 2869/3; 3582/1; 3851/3; 3886/1; 3930/1
A/Note: basoon
C/Function:
A/Description: may be involved in cytomatrix organization at the site of neurotransmitter
A/Note: component of the presynaptic cytoskeleton
C/Keywords: coiled coil; zinc finger
Query Match 2.8%; Score 109.5; DB 2; Length 3942;
Best Local Similarity 19.0%; Pred. No. 29;
Matches 56; Conservative 28; Mismatches 111; Indels 99; Gaps 9;
Qy 502 DNIPOLCSHLHSDHGLQIEFGQHTQSSRRNYFRSKSGSLVVAIC-----NMHOFIDE 556
Db 3535 DTCPPOFCS-----SHSMRDVQEHVKQGPRAHAYKREGEYMLDSDHCVSDSEAYHLGQEE 3589
Qy 557 PDMPFK-----QVFPFHPPLRYRNPVLEKFDGSLVL 588
Db 3590 TDMFDKRDARSDRFHNGHTVSSSQKGRPAHSHYDDBP---EEGLMPPHDEGPG 3645
Qy 589 NDWVCK-----PGESDFCLKVEAPVL 610
Db 3646 RHNSAKENRHSDHGRHSGHAGEPGRRAAKPHARMGRHEARPHQAS-----PAPAM 3700
Qy 611 -----GATPADSQHESQ-----HGLDQDEARPLDGSALQPLHTVTKAGSPSDMP 659
Db 3701 QKKQGPYPSADYSSQSSRAPSAVNHASQSKGRQAHGTSPALQPKADTQAPOMQGRQ 3760
Qy 660 RBDGIYVSSVPSSELSPLMEGLSTDOTETSSLTSSVSSSSSGICEEPRLPLPK 713
Db 3761 AADPGQSQPPSSKQT---PSGTASRQPTQOQOQOQOQOQGLGQAPQAPSQ 3811
RESULT 11
T30851
lysosomal trafficking regulator, long splice form - mouse
N/Alternate names: beige protein homolog
C/Species: Mus musculus (house mouse)
C/Date: 23-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30851

R/Barbosa, M.D.F.S.; Tchernev, V.T.; Kingmore, S.F.
submitted to the EMBL Data Library, September 1996
A/Description: Two bg or not two bg? longest isoform of mouse Lysc (beige) gene.
A/Reference number: Z20903
A/Accession: T30851
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3788 <BAR>
A/Cross-references: UNIPROT:P97412; UNIPARC:UP10000028F2F; EMBL:U70015; NID:G1813541; PI
C/Genetics:
A/Experimental source: strain C57BL/6J
A/Map position: 1
C/Keywords: alternative splicing
Query Match 2.8%; Score 109; DB 2; Length 3788;
Best Local Similarity 19.8%; Pred. No. 30;
Matches 157; Conservative 104; Mismatches 282; Indels 250; Gaps 45;
Qy 20 GSQIAVAGSGSGRAMGVDTGWR--GVGPASRNSGLNYTPKYDNTCTYLANPVKHIAD 77
Db 651 GRTLGITLGAAPTSGLPSPSTRFGILP---SSGSEDLMKYDALVQSVFQGE--DR 705
Qy 78 AQNTTISOYACH--DQAVTITMSPGALGIEPLKGFVILELKSEG---RQOQQLIK 131
Db 706 LHNIGIYANHCNLLQKGNVVGW-----KLNYIFNPVLQGVLELHHCQQLSIP 755
Qy 132 DPKQNLNSFKTKGMEQPFLLMKFET--DYFVAVVP-----FPGIKN-----EEN 174
Db 756 S-----AQTHMCSQLKQVLPQEVLAQVTLKTLPLKRSVIRDLFSLSCNGVNHIIELN 807
Qy 175 Y-----HPF--PRTACDCLLQPDNLACKPFMKPRLNLSIQHSDMQVSFDHAPNFGF 227
Db 808 YLDGIRSHLKAPEITIVLGEQKDAALDV--DGLIIOQELBELSV----- 853
Qy 228 RFFYLHYKLHSGPFRKTKCKOQTETTSCLLQNVSPEDYIIELVDDNTTRKVMYAL 287
Db 854 -----GPSLHK-----QNASDPSCLRK-----FYASLREPPPKKTKTH--- 889
Qy 288 KPVNSWAPRIRAMATVPLVVISAPATLPTWCKRQKQOENIYSHDESSBSSTYTAAL 347
Db 890 QDVA-----INTINLFLCVAF-----LCYSKEADS-----DRESANESBDTSGY 928
Qy 348 PRERLAPRKVFLCYSSKQDQNNMNV---OCFAVFLDPGCEVALDLMEDFSLCREG 403
Db 929 DSRPSRPLSHMLPCLSLD-----VLPSPRLGNH-----ADIIW---SWCK--- 967
Qy 404 QREWV--IQKHESQFI-----IVCSKGMKYFVDKKNYHKGSGSGKGELE---L 451
Db 968 ---WYMLNSVFOKQFNRILGFGVCHL-LIFMILIQLFPSHTEDQGRQSGEMSRNEOEL 1023
Qy 452 VAVSAIAELKRAQKSSSAAALSKFIIVPDYSGEGVPEIL--DLSTKRYLMDN----- 503
Db 1024 IRIS-----YPELTLLKGVSSSATAEDLGLFKSADSVFGQS 1060
Qy 504 ---LPQLCSHLHSDHGLQIEFGQHTQSSRRNYFRSKSGSLVVAICNMHOFIDEPRWF 560
Db 1061 QPVLTSAQIYATF---SVPGF-----KRAFMSQOSETSLQSTRLESILD----- 1104
Qy 561 EKQFVFNHPPLRYRNPVLEKFDGSLVLNDWVCK-----PGESDFCLKVEAPVL 605
Db 1105 -----ICLHSAKACQOQMELELPSQGLSVENIICELAEHLSSQKVAETELAKPLFDALNRY 1160
Qy 606 EAVPLG---ATGPADS-----QHSQHGGLDDQGEARPLDGSALQPLHTVTKAGSPSD 657
Db 1161 ---ALGNHSADLGPDAVTEKSHPSSEELISQPGDSSEABDSQCCSLKILGEBEYED 1217
Qy 658 M---PRDSGIYDSSVPSSELSPLMEGLSTDOTETSSLTSSVSSSSGSGE---EPPPALP 711
Db 1218 SSSNPEDVDTQDDGV---ELN--PEAEGFS--GSIVSNLNLBNTLH---GEIITPILCMIG 1268
Qy 712 SKLLSSGSCAKDL 724

Db 1269 LMLASAKKADV 1281

RESULT 12

T17212

hypothetical protein DKFZp434P211.1 - human (fragments)

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T17212

R:Roucka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18723

A:Accession: T17212

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-488;489-535 <POU>

A:Cross-references: UNIPROT:Q9NTG6; UNIPARC:UPI000017C18F; UNIPARC:UPI000017C190; EMBL.A

A:Experimental source: adult testis; clone DKFZp434P211

A>Note: the cDNA sequence contains a -1 frameshift near codon 488

C:Genetics:

A>Note: DKFZp434P211.1

Query Match 2.7%; Score 108; DB 2; Length 535;

Best Local Similarity 23.5%; Pred. No. 2;

Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 460 KLRQAKQS-SALSKFIAYFDYSCGDVPGI-----IDLSTKRLMDNLPQ 506

DB 103 RYVQTSQTWSSTCTRNNAISSSYSTGCLPKRRGPASSHCQLTLSSKTVSEDRPQ 162

QY 507 LGSILHSRHDGLOE--PGQHTRQSGRRNFRSKSGSLVYAIQNMHQFIDEEPDMFEKQ 564

DB 163 NVSSGHTQCKAKADIAPGQLT--LRNDSTSEASRP-----STKXP-----PLPPRRG 210

QY 565 VPEFH-PPPL-----RYREPVLEKFDGSLVLDVM--CKRGPESDFLKYEA 608

DB 211 EPLMLPEPLBEGRYVYVBDLRKEKAPKINSALQVEDAISDCPRSSH---TLSSL 267

QY 609 VLGATG-PADSGHSGHGLDQGEARPALDSALQPLHTYKAGSPSMP-----RD 661

DB 268 ATGASGLPVAISKAPS---MDAQETHKSGDCLGLDPLASA--AGVPSTAPMSGKKHR 321

QY 662 SG-IYSSVPSSESLPLMEGSTDQETNSLTESVSSSGLGEERPPALPSCLSSG 718

DB 322 PGLPESSDP-----LPATSSDSQDSAQVYSLT-----PAPPPASMDAG 361

RESULT 13

I49239

vesicle transport protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004

C:Accession: I49239

R:Tellam, J.T.; McIntosh, S.; James, D.E.

J. Biol. Chem. 270, 5857-5863, 1995

A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neurona

A:Reference number: I49238; PMID:95197608; PMID:7890715

A:Accession: I49239

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-592 <RBS>

A:Cross-references: UNIPROT:Q60770; UNIPARC:UPI00000284B1; EMBL:U19521; NID:9642027; PII

A:Genetics:

A:Gene: munc-18c

C:Superfamily: vacuolar protein sorting protein VPS45

Query Match 2.7%; Score 108; DB 2; Length 592;

Best Local Similarity 18.5%; Pred. No. 2.3;

Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;

QY 307 LVVISAFTLFTWCKRKKQ-----ENIYSHLDEBSESSTYALPRRLRP 357

DB 34 IMLDEFTTKLSSCCNMIDLBEGITVIENTYKREPPVROMALYF-----ISPTK 86

QY 358 VFLCYSSKQGNHNVQCFAYFLQDFC-----GCE----- 388

DB 87 SYDCFLRDFSGSEKKYKAYIYFTDFCPDSLFPNKIKASCSSIRCKEINISFIQESQ 146

QY 389 -VALDLMEDPFLC-----REGREWVIOKIHESQFIYVC-----SKGMKY----- 428

DB 147 VTLVDVPDAFYCYSPDPBNARKVYVMAEMQ--IVYVCAITLDNPGVRYSKFLDNA 204

QY 429 ----FVDDK--NYK--HKGGRGSGKEBLV-----AVSAIAEKLQAKOSSAALS 473

DB 205 SKLAQLVERKELBDYKIDKEGLIKGTQSLIIDRGFPDVSIVLHEL----- 252

QY 474 KPIAYVED-----YSCG-DVPGIL-----DLSTKYR-----LMDNLPQLCSHL 512

DB 253 TFOAMAYDILLPIENDTYKTKTDGKEKAVLEEDDDLMVVRHHAIVAEIIPKMEIS 312

QY 513 SRDHGLQEGQHTRQSGRRNFRSKSGSLVYAIQNMHQFIDEEPDMFEKQVFPHPPL 572

DB 313 STK-----KATGKTSLSALITQLMCKMFRKQISKQV-----HL 348

QY 573 RYREPVLEKPE-----DSGLVLDVMCKRGPESDFLKYE 606

DB 349 NLAEDCMNFKLNIKELCKTEODLAGTDAEGQVYKDSMLVLLPVLL--NKHNDCKIR 406

QY 607 APVLGATGPAADSGHSGHGLDQGEARPALDSALQPLHTYKAGSPSMPRD--SGTY 665

DB 407 AVLLTYFGINGTEEN-----LDRLIHNVKIEDSDMIKRWSHLG 446

QY 666 DSVPSSESLPLMEGSTDQET 687

DB 447 VPIVPSQAKPLKRSARET 468

RESULT 14

D86477

protein P1504.27 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: D86477

R:Theologis, A.; Eckert, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shum, P.; Southwick, A.M.; Sun, H.; Tallon, I

ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Accession: D86477

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-638 <STO>

A:Cross-references: UNIPROT:Q9LQF8; UNIPARC:UPI00000AB3A1; GB:AE005172; NID:98778345; PII

A:Genetics:

A:Gene: P1504.27

A:Map position: 1

Query Match 2.7%; Score 106.5; DB 2; Length 638;

Best Local Similarity 19.4%; Pred. No. 3.4;

Matches 94; Conservative 63; Mismatches 175; Indels 153; Gaps 24;

QY 80 NITISQYACHDOVAATILWSPGALGIEFPGFVILEKSGRQCOQLILDPKOLNS 139

DB 275 DIKYGQYSHLDQCFVYNS-----KCATHEWVWDGKELFMIISBDETDIDP 322

QY 140 FKRTGESQPLNMKEETDYFKVVPF---SIKESNYPFFPFRACDILLQPDNLAC 196

DB 323 FNNLG-----DGFIKHFCHKRLKLNKHNDGARDTEKQCRAC---IYP---IYS 364

QY 197 KPPMKRNLNISOHG--SDMVSPDHAHPNPGFRFPYLIHYKLNKHEP--FKRTCKQEOGT 252

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Db      365 HQYHCKKCNVSLHEVCAGSLRDLDAHNN-----HTLLISPSGKCCSACGREST 416
Qy      253 TETTSCLLVNSPGDYIIEIVDDTTTRKVMYALKVHSPMAGPIRAMAITYPLVVIS 312
Db      417 GFSYIC--SNKGCODFVLAV-----RCISYLEVFIRHSEH-----PIPISTG 457
Qy      313 FALFLVWCKKQKQENIYSHLDESSSE--SSTYTA--LPRE--RLRPRKVPFLCYSGK 367
Db      458 YNSKDELICKVCKKRCIGALQCTLCFTWCYSCAIIPEIHYKFPDKHPLTSCGESAD- 516
Qy      368 QNHMNVVQCFAYFLADPFCGCEVALDLMEDPSLCREGREWIOKIHESQPIIVVCSKGM 427
Db      517 -----NRYWCEV-----CEKQIDPKEMFYTCNK-----CCITIH-----LHCIFGSS 553
Qy      428 YFVDDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKEFIAVVPDYSCED 487
Db      554 VFM-----KPG-----SIFFDYGKVQ 570
Qy      488 VPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQERPGQHTROGSRNN--YPRSKSGSLY-V 544
Db      571 V-----FRNNSYTRQLCYMCHNCTGL-----IFEGYRNNATTYNHSNRSTHRM 616
Qy      545 AICNM 549
Db      617 IFCSL 621

```

RESULT 15

863059

hypothetical protein YNL118c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein N1917

C:Species: *Saccharomyces cerevisiae*

C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 05-Oct-2004

C:Accession: S63059; S59701; S67340

R:De Antoni, A.; D'Angelo, M.; Dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63047

A:Accession: S63059

A:Molecule type: DNA

A:Residues: 1-970 <DEA>

A:Cross-references: UNIPROT:P53550; UNIPARC:UPI000000056F; EMBL:Z71394; NID:G1302044; PI

R:Experimental source: strain S288C

R:Tzagoloff, A.A.

submitted to the EMBL Data Library, June 1995

A:Description: Suppressor of a yeast pet mutant.

A:Reference number: S59701

A:Accession: S59701

A:Molecule type: DNA

A:Residues: 1424,'L',426-970 <TZA>

A:Cross-references: UNIPARC:UPI0000168DB7; EMBL:LA3065; NID:G870733; PID:G870734

A:Experimental source: strain D273-10B

R:De Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.

submitted to the EMBL Data Library, February 1996

A:Description: The DNA sequence of cosmid 14-13b from chromosome XIV of *Saccharomyces ce*

A:Reference number: S67327

A:Accession: S67340

A:Molecule type: DNA

A:Residues: 1-970 <DAN>

A:Cross-references: UNIPARC:UPI000000056F; EMBL:Z69382; NID:G1183941; PID:e221828; PID:G

C:Genetics:

A:Gene: SGD:PSU1

A:Cross-references: SGD:S0005062; MIPS:YNL118C

A:Map position: 14L

F:129-163/Domain: mult domain homology <MUT>

Query Match 2.7%; Score 105.5; DB 2; Length 970;

Best Local Similarity 19.7%; Pmed No. 7.6; Indels 213; Gaps 30;

Matches 112; Conservative 72; Mismatches 171; Indels 213; Gaps 30;

Qy 260 LQNVSPGDYIIE--LV-----DQNTTRKVMYALKVHSPW--AGPIRAMAITYP 306

Db 9 LENVTSVDRLELDLVRFINCNEDLSVERELFHE-----EASWFTYDFIKLMPPTLP 64

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Qy      307 LVVISAFAFLFVWCKKQKQENIYSHLDESSSSSTYTAAP-----RERLR----- 353
Db      65 SLKISFAQLIITKLCPLWKMDI--RVDAALQOFSTKYSIFVRGAITRENLSKLLVQ 122
Qy      354 -----PRPVLFCYSSKQGNMNVVQCFAYFLADPFCGCEVALDLMEDPSLCREGO 404
Db      123 GRESWSWSPGKTI-----SKD-----ENDIDCIREVKE-----EIGFDLTD----- 160
Qy      405 REMVIOKIHESQPIIVVCSKGMKTFVDKKNYKKGSGSGKGEFLVAV--VSAI----- 457
Db      161 -----YIDNDFI-----ERNIOGNK-----IFLISGSEVFNFKKQ 194
Qy      458 -----AEKLR--QAKOSSAALSKEFIAVVPDY-----CEGD 487
Db      195 VNEIDKIKWEPDFPKLSKTYMYSNITKYLLINSMMRPLSMWLHQROIKNEDQLKSTAEQ 254
Qy      488 VPGIIDLSTKYRLMDNLPOLCSHLHSR-----DHGLQEPGQHTR 526
Db      255 LKLLIGI--TKEBQIDPGRLEMLMTAVQANNNNAVNSGQVPSQELQHLKEQSGEHQ 313
Qy      527 QGSRNRYFRSKSGSLYVAICNMQPIDEEDPWFQVFPFHPPPLRYEPEVLEKEDSG- 585
Db      314 QKDQSSFSQOQPSIFPSL-----SEPPANNKNTI--PPTW-----PMANVEMSNP 358
Qy      586 ---LVNDVCKKPGP-----ESDFCLKVBAV-----LGATGPADSGHESQHGGLDQ 631
Db      359 QLEFATNQGPPAPFPFPMLEPLTNNNSANPIPTVPFPNPAFPNPAFGVPMNHN----- 412
Qy      632 EARPALDGSAAALQPLHTYKAGSPSDMPDPSGIYDSSVPSBSLSPLMEGLSTDQETSS 691
Db      413 -----LSGPAVQGP-----SLPPAPLPDPSG--YSSSSPGQL-----D 445
Qy      692 LRESVSSSGLGEBEPPALPSKLLSGS 719
Db      446 IINSKKPDSNVOSKKPKL--KILQKGT 471

```

Search completed: March 1, 2006, 10:30:58
 Job time : 49 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:24:46 ; Search time 232 Seconds

(without alignments)
2244.310 Million cell updates/sec

Title: US-10-616-788-2

Sequence: 1 MAPWLCVFFVFNACLSG.....SCRADLCGRSYTDELHVAAP 738

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3912	99.1	739	2	Q8NFS0 HUMAN
2	3908	99.0	739	2	Q8NFM7 HUMAN
3	3716	94.1	707	2	Q58E27 HUMAN
4	3706	93.9	707	2	Q6RVF4 HUMAN
5	3681.5	93.2	728	2	Q6UW15 HUMAN
6	3396.5	86.0	738	2	Q8JZL1 MOUSE
7	3158	80.0	595	2	Q8N113 HUMAN
8	2993	75.8	564	2	Q9UPA0 HUMAN
9	2893	71.6	741	2	Q7T217 CHICK
10	2828	71.6	697	2	Q8AV76 CHICK
11	2665.5	67.5	594	2	Q8K447 MOUSE
12	2606.5	66.0	582	2	Q8R5J8 MOUSE
13	1966	49.8	745	2	Q8OHC9 BRARE
14	1957	49.6	745	2	Q8OHC6 BRARE
15	1335	33.8	470	2	Q4RLH0 TESTING
16	1325.5	33.6	445	2	Q4VBV6 BRARE
17	543	13.8	109	2	Q8HXE8 MACFA
18	313	7.9	864	1	I17RA_HUMAN
19	298	7.5	864	1	I17RA_MOUSE
20	202	5.1	769	2	Q69H03 CIOIN
21	169.5	4.3	846	2	Q9NA64_CABEL
22	165	4.2	50	2	Q4T7L3 TESTING
23	153.5	3.9	831	2	Q6OX85 CAEBR
24	134.5	3.4	502	1	I17RB_HUMAN
25	127.5	3.2	443	2	Q5NUI0_FUGRU
26	127.5	3.2	443	2	Q6IGL7_CAEBR
27	124.5	3.2	990	2	Q7PWU5_ANOGA
28	124	3.1	718	1	YSO2_CABEL
29	121.5	3.1	1190	2	Q6H470_ORYSA
30	120.5	3.1	1081	2	Q5NRP3_SOLDE
31	120	3.0	1376	2	Q4N457_THERA

32	117.5	3.0	617	2	Q8K4C1 MOUSE	Q8K4C1 mus musculus
33	117.5	3.0	2317	2	Q4SH16 TESTING	Q4SH16 tetradon n
34	115.5	2.9	637	2	Q6AZ51_RAT	Q6AZ51 rattus norv
35	115.5	2.9	901	2	Q9KE04_BACHD	Q9KE04 bacillus ha
36	115	2.9	726	2	Q6A063_MOUSE	Q6A063 mus musculu
37	115	2.9	859	1	MYRI1_HUMAN	Q6A063 mus musculu
38	115	2.9	859	1	MYRI1_HUMAN	Q6A063 mus musculu
39	115	2.9	1202	2	Q4OEP5_LEIMA	Q4OEP5 leishmania
40	114	2.9	539	2	Q4NSA6_THERA	Q4NSA6 theileria p
41	114	2.9	757	2	Q13399_USTMA	Q13399 ussilaago ma
42	114	2.9	2946	2	Q64634_ARATH	Q64634 arabidopsis
43	113.5	2.9	549	2	Q8KGB4_CHLYR	Q8KGB4 chlorobium
44	113	2.9	4736	2	Q7YT99_MYTGA	Q7YT99 mytilus gal
45	112.5	2.8	562	2	Q9J755_HUMAN	Q9J755 homo sapien

ALIGNMENTS

Query Match	Score	99.1%	Score	3912	DB 2	Length	739
Best Local Similarity	99.3%	Pred. No.	2.7e-284				
Matches	733	Conservative	1	Mismatches	4	Indels	0
Gaps	0						
QY	1	MAPWLCVFFVFNACLSG	QY	1	MAPWLCVFFVFNACLSG	QY	1
DB	1	MAPWLCVFFVFNACLSG	DB	1	MAPWLCVFFVFNACLSG	DB	1
QY	61	DNCTTYLNPVQKVIADQNIITTSOYACHDOQVAVTILMSGALIGRFLVLEBLKS	QY	61	DNCTTYLNPVQKVIADQNIITTSOYACHDOQVAVTILMSGALIGRFLVLEBLKS	QY	61
DB	61	DNCTTYLNPVQKVIADQNIITTSOYACHDOQVAVTILMSGALIGRFLVLEBLKS	DB	61	DNCTTYLNPVQKVIADQNIITTSOYACHDOQVAVTILMSGALIGRFLVLEBLKS	DB	61
QY	121	EGROCOQQLIKDPKOLNSFFRTGMSQPLNKFETDYVKKVPPSPINSSNTHPFF	QY	121	EGROCOQQLIKDPKOLNSFFRTGMSQPLNKFETDYVKKVPPSPINSSNTHPFF	QY	121
DB	121	EGROCOQQLIKDPKOLNSFFRTGMSQPLNKFETDYVKKVPPSPINSSNTHPFF	DB	121	EGROCOQQLIKDPKOLNSFFRTGMSQPLNKFETDYVKKVPPSPINSSNTHPFF	DB	121
QY	181	RTAACPDLLOPDLNACPKPKNLNLSQHSQMOVSFDAPNPGFRFFYLKLGHEG	QY	181	RTAACPDLLOPDLNACPKPKNLNLSQHSQMOVSFDAPNPGFRFFYLKLGHEG	QY	181
DB	181	RTAACPDLLOPDLNACPKPKNLNLSQHSQMOVSFDAPNPGFRFFYLKLGHEG	DB	181	RTAACPDLLOPDLNACPKPKNLNLSQHSQMOVSFDAPNPGFRFFYLKLGHEG	DB	181
QY	241	PFKRTCKOQOTTEITTSCLQONVSPGDIIELVDTNTTRKVMHAYALKPHSPWAGIRA	QY	241	PFKRTCKOQOTTEITTSCLQONVSPGDIIELVDTNTTRKVMHAYALKPHSPWAGIRA	QY	241
DB	241	PFKRTCKOQOTTEITTSCLQONVSPGDIIELVDTNTTRKVMHAYALKPHSPWAGIRA	DB	241	PFKRTCKOQOTTEITTSCLQONVSPGDIIELVDTNTTRKVMHAYALKPHSPWAGIRA	DB	241
QY	301	MAITVPLVVISAPATLFTVNCRRKQDENIYSHLDESSSSSTYTAALPRRLPRPVFL	QY	301	MAITVPLVVISAPATLFTVNCRRKQDENIYSHLDESSSSSTYTAALPRRLPRPVFL	QY	301
DB	301	MAITVPLVVISAPATLFTVNCRRKQDENIYSHLDESSSSSTYTAALPRRLPRPVFL	DB	301	MAITVPLVVISAPATLFTVNCRRKQDENIYSHLDESSSSSTYTAALPRRLPRPVFL	DB	301
QY	361	CYSKSGQGNMNVVQCAYFLQDFCGCEVALDLMDEPSLCREQRENVVICKIHESQITIV	QY	361	CYSKSGQGNMNVVQCAYFLQDFCGCEVALDLMDEPSLCREQRENVVICKIHESQITIV	QY	361
DB	361	CYSKSGQGNMNVVQCAYFLQDFCGCEVALDLMDEPSLCREQRENVVICKIHESQITIV	DB	361	CYSKSGQGNMNVVQCAYFLQDFCGCEVALDLMDEPSLCREQRENVVICKIHESQITIV	DB	361

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Db      361  CYSKQGNHNNVVOCAFYLDPCCGEVALDLMEDPFLCRGQRENVIOKIHESQFTIV 420
Qy      421  VCSKGMKFFVDKKNYGHKGSGSGKGLFLVAVSAIAEKLQAKQSSAALSKFLAVYF 480
Db      421  VCSKGMKFFVDKKNYGHKGSGSGKGLFLVAVSAIAEKLQAKQSSAALSKFLAVYF 480
Qy      481  DYSCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRQGSRRNYFRSKGR 540
Db      481  DYSCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRQGSRRNYFRSKGR 540
Qy      541  SLVVAICNNHOFIDEEPWFKEQFVPPHPPRYRREPVLEKFPDGLVLDVWCKPGEPSD 600
Db      541  SLVVAICNNHOFIDEEPWFKEQFVPPHPPRYRREPVLEKFPDGLVLDVWCKPGEPSD 600
Qy      601  FCLKVEAPVIGATGPADSOHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSDMPR 660
Db      601  FCLKVEAPVIGATGPADSOHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSDMPR 660
Qy      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTRESVSSSGIGEEPPALPSKLLSSGSC 720
Db      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTRESVSSSGIGEEPPALPSKLLSSGSC 720
Qy      721  KADLGCRSYTDELHAAVAP 738
Db      721  KADLGCRSYTDELHAAVAP 738

RESULT 2
Q8NFM7_HUMAN PRELIMINARY; PRT; 739 AA.
ID Q8NFM7
AC Q8NFM7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein long form.
GN Name=IL17RD; Synonyms=IL17RLM;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Euteleostomi; Euteleostomi; Primates; Catarrhini; Hominiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Kong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "Self inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling."
RL J. Biol. Chem. 278:50273-50282(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
RA Chen Y., Liu L., Fu X.Y., Chang Z.J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL: AF949408; AAM74077.1; -; mRNA
DR Ensembl; ENSG00000144730; Homo sapiens.
DR HGN; HGNC:17616; IL17RD.
DR GO; GO:0004888; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
KW Receptor.
SQ SEQUENCE 739 AA; 82441 MW; BCD2A95261B0277 CRC64;

Query Match 99.0%; Score 3908; DB 2; Length 739;
Best Local Similarity 99.2%; Pred. No. 5,4e-284;
Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Db      61  DNCCTYLNPGKVIADANQITISQVACHDQAVAVTILMSGALGIEFLKGFVILEELKS 120
Qy      121  EGRQCOQILKDPKQINSFKRTGMSQPLNMFETDVFYKVPVPSIKNSNTYPPFF 180
Db      121  EGRQCOQILKDPKQINSFKRTGMSQPLNMFETDVFYKVPVPSIKNSNTYPPFF 180
Qy      181  RTKACDILLQPDNLACKPFMKPRNLNLSOHGSDMQVSPHAPNPFRRFFLYLKJKEG 240
Db      181  RTKACDILLQPDNLACKPFMKPRNLNLSOHGSDMQVSPHAPNPFRRFFLYLKJKEG 240
Qy      241  PPRKRTCKOQETETTSCLQNVSPGDYIIEVDDTNTTRKVMYALKEVHSPWAPPIRA 300
Db      241  PPRKRTCKOQETETTSCLQNVSPGDYIIEVDDTNTTRKVMYALKEVHSPWAPPIRA 300
Qy      301  MATTVPLVVISAPATLFTWCKRKQOENYSHLDESSSSSTYTAALPREBLRPRKVL 360
Db      301  MATTVPLVVISAPATLFTWCKRKQOENYSHLDESSSSSTYTAALPREBLRPRKVL 360
Qy      361  CYSKQGNHNNVVOCAFYLDPCCGEVALDLMEDPFLCRGQRENVIOKIHESQFTIV 420
Db      361  CYSKQGNHNNVVOCAFYLDPCCGEVALDLMEDPFLCRGQRENVIOKIHESQFTIV 420
Qy      421  VCSKGMKFFVDKKNYGHKGSGSGKGLFLVAVSAIAEKLQAKQSSAALSKFLAVYF 480
Db      421  VCSKGMKFFVDKKNYGHKGSGSGKGLFLVAVSAIAEKLQAKQSSAALSKFLAVYF 480
Qy      481  DYSCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRQGSRRNYFRSKGR 540
Db      481  DYSCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRQGSRRNYFRSKGR 540
Qy      541  SLVVAICNNHOFIDEEPWFKEQFVPPHPPRYRREPVLEKFPDGLVLDVWCKPGEPSD 600
Db      541  SLVVAICNNHOFIDEEPWFKEQFVPPHPPRYRREPVLEKFPDGLVLDVWCKPGEPSD 600
Qy      601  FCLKVEAPVIGATGPADSOHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSDMPR 660
Db      601  FCLKVEAPVIGATGPADSOHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSDMPR 660
Qy      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTRESVSSSGIGEEPPALPSKLLSSGSC 720
Db      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTRESVSSSGIGEEPPALPSKLLSSGSC 720
Qy      721  KADLGCRSYTDELHAAVAP 738
Db      721  KADLGCRSYTDELHAAVAP 738

RESULT 3
Q58E27_HUMAN PRELIMINARY; PRT; 707 AA.
ID Q58E27
AC Q58E27
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IL17RD protein.
GN Name=IL17RD;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Euteleostomi; Euteleostomi; Primates; Catarrhini; Hominiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Testis;
RX MEDLINE=23988257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
RA Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.T., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Bullyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalloe D.E.,
 RA Schmech A., Schein J.B., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RG NIH MGC Project;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC038369; AAI38369.1; -; mRNA.
 SQ SEQUENCE 707 AA; 79495 MW; 128A84EA4CF0C476 CRC64;
 Query Match 94.1%; Score 3716; DB 2; Length 707;
 Best Local Similarity 99.7%; Pred. No. 1.3e-269;
 Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 41 WRGVGPAASRNSGLYNTFKYDNCCTTYLNPVKGKVIADAQNTTISQVACHQDVAVTILMSP 100
 DB 9 WQGVGPAASRNSGLYNTFKYDNCCTTYLNPVKGKVIADAQNTTISQVACHQDVAVTILMSP 68
 QY 101 GAGIIEFLKGFVILBELSEGRQCOQLIKDPKQUNSSFKRTGMSQPLNKKFETDYF 160
 DB 69 GAGIIEFLKGFVILBELSEGRQCOQLIKDPKQUNSSFKRTGMSQPLNKKFETDYF 128
 QY 129 VKVVPFSSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNLSQSGSDMQVSFDH 220
 DB 161 VKVVPFSSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNLSQSGSDMQVSFDH 220
 QY 221 APNHFGRFPYLYLKYKLHSGFPFKRTCKOQTETTSCLLQNVSPGYIIELVDDNTTTR 280
 DB 189 APNHFGRFPYLYLKYKLHSGFPFKRTCKOQTETTSCLLQNVSPGYIIELVDDNTTTR 248
 QY 281 KVMHYALKPVHSPWAGPIRAMAIVPLVVISAPATLFTWCRKQOENIYSHLDESSSES 340
 DB 249 KVMHYALKPVHSPWAGPIRAMAIVPLVVISAPATLFTWCRKQOENIYSHLDESSSES 308
 QY 341 STTTAALPRERLRPRKPVFLCYSSKQGNMNVVQCFAYFLDPCGCEVALDLMBDFSLC 400
 DB 309 STTTAALPRERLRPRKPVFLCYSSKQGNMNVVQCFAYFLDPCGCEVALDLMBDFSLC 368
 QY 401 REGOREVNIQKHESQFIIVVCSKGMKYFYDKKNYKHGGGSGKGEFLVAVSAIAEK 460
 DB 369 REGOREVNIQKHESQFIIVVCSKGMKYFYDKKNYKHGGGSGKGEFLVAVSAIAEK 428
 QY 461 LROAKOSSSAALSKFLAVYFDYSCGEGVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQ 520
 DB 429 LROAKOSSSAALSKFLAVYFDYSCGEGVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQ 488
 QY 521 PCQHTQSGRRNRYFRSKSGSLVYALCNMHOPIDEBDPMFEKQFVFHPPLRYRBPVLE 580
 DB 489 PCQHTQSGRRNRYFRSKSGSLVYALCNMHOPIDEBDPMFEKQFVFHPPLRYRBPVLE 548
 QY 581 KFDPSGLVNDVMCKPESBDFCLKVEAPVLGATGPADSGHESQHGGLDDGEARPALDGS 640
 DB 549 KFDPSGLVNDVMCKPESBDFCLKVEAPVLGATGPADSGHESQHGGLDDGEARPALDGS 608
 QY 641 AALQPLHTYKASPSMPRDSGIYDSSVPSSELSLPLMEGLSDTDQETSSLTESVSSS 700
 DB 609 AALQPLHTYKASPSMPRDSGIYDSSVPSSELSLPLMEGLSDTDQETSSLTESVSSS 668
 QY 701 GLGSEBPALPSKLSSGSCKADLGCRSYTDELHAIVAP 738
 DB 669 GLGSEBPALPSKLSSGSCKADLGCRSYTDELHAIVAP 706

RESULT 4
 ID O6RVF4_HUMAN PRELIMINARY; PRT; 707 AA.
 AC O6RVF4;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE SEP splice variant b.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testes;
 RX PubMed=14742870; DOI=10.1073/pnas.0307952100;
 RA Preger E., Ziv I., Shabtay A., Sher I., Tang M., Dawid I.B.,
 RA Altuvia Y., Ron D.;
 RT "Alternative splicing generates an isoform of the human Sef gene with
 RT altered subcellular localization and specificity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:1229-1234 (2004).
 DR EMBL: AY489047; AAS15051.2; -; mRNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO: GO:0006954; P:inflammatory response; IEA.
 DR InterPro: IPR000157; TIR.
 SQ SEQUENCE 707 AA; 79493 MW; 7D3BE21E038F17E CRC64;
 Query Match 93.9%; Score 3706; DB 2; Length 707;
 Best Local Similarity 99.4%; Pred. No. 7.1e-269;
 Matches 694; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 41 WRGVGPAASRNSGLYNTFKYDNCCTTYLNPVKGKVIADAQNTTISQVACHQDVAVTILMSP 100
 DB 9 WQGVGPAASRNSGLYNTFKYDNCCTTYLNPVKGKVIADAQNTTISQVACHQDVAVTILMSP 68
 QY 101 GAGIIEFLKGFVILBELSEGRQCOQLIKDPKQUNSSFKRTGMSQPLNKKFETDYF 160
 DB 69 GAGIIEFLKGFVILBELSEGRQCOQLIKDPKQUNSSFKRTGMSQPLNKKFETDYF 128
 QY 129 VKVVPFSSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNLSQSGSDMQVSFDH 220
 DB 161 VKVVPFSSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNLSQSGSDMQVSFDH 220
 QY 221 APNHFGRFPYLYLKYKLHSGFPFKRTCKOQTETTSCLLQNVSPGYIIELVDDNTTTR 280
 DB 189 APNHFGRFPYLYLKYKLHSGFPFKRTCKOQTETTSCLLQNVSPGYIIELVDDNTTTR 248
 QY 281 KVMHYALKPVHSPWAGPIRAMAIVPLVVISAPATLFTWCRKQOENIYSHLDESSSES 340
 DB 249 KVMHYALKPVHSPWAGPIRAMAIVPLVVISAPATLFTWCRKQOENIYSHLDESSSES 308
 QY 341 STTTAALPRERLRPRKPVFLCYSSKQGNMNVVQCFAYFLDPCGCEVALDLMBDFSLC 400
 DB 309 STTTAALPRERLRPRKPVFLCYSSKQGNMNVVQCFAYFLDPCGCEVALDLMBDFSLC 368
 QY 401 REGOREVNIQKHESQFIIVVCSKGMKYFYDKKNYKHGGGSGKGEFLVAVSAIAEK 460
 DB 369 REGOREVNIQKHESQFIIVVCSKGMKYFYDKKNYKHGGGSGKGEFLVAVSAIAEK 428
 QY 461 LROAKOSSSAALSKFLAVYFDYSCGEGVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQ 520
 DB 429 LROAKOSSSAALSKFLAVYFDYSCGEGVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQ 488
 QY 521 PCQHTQSGRRNRYFRSKSGSLVYALCNMHOPIDEBDPMFEKQFVFHPPLRYRBPVLE 580
 DB 489 PCQHTQSGRRNRYFRSKSGSLVYALCNMHOPIDEBDPMFEKQFVFHPPLRYRBPVLE 548
 QY 581 KFDPSGLVNDVMCKPESBDFCLKVEAPVLGATGPADSGHESQHGGLDDGEARPALDGS 640
 DB 549 KFDPSGLVNDVMCKPESBDFCLKVEAPVLGATGPADSGHESQHGGLDDGEARPALDGS 608

Qy 641 AALQPLHTYKAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTDQETSTSLTESVSSS 700
 Db 609 AALQPLHTYKAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTDQETSTSLTESVSSS 668
 Qy 701 GLGEEPPALPSKLLSSGSCCKADIGCRSYTDELHAHAV 738
 Db 669 GLGEEPPALPSKLLSSGSCCKADIGCRSYTDELHAHAV 706

RESULT 5
 Q6UW15_HUMAN PRELIMINARY; PRT; 728 AA.
 ID Q6UW15_HUMAN PRELIMINARY; PRT; 728 AA.
 AC Q6UW15;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE I117Rhom.
 GN ORFNames=UNO6115;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brueh J.,
 Chen Y., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 Lewis L., Liao D., Mark M.R., Robbie B., Sanchez C., Schoenfeld J.,
 Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vages A.,
 Vanden R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
 Yansua D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 Wood W.I., Godowski P.J., Gray A.M.;
 RA "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358774; AA089134.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006954; P:inflammatory response; IEA.
 DR InterPro; IPR00157; TIR.
 SQ SEQUENCE 728 AA; 81310 MW; 4AD9J3F8B1C78C6 CRC64;

Query Match 93.24; Score 3681.5; DB 2; Length 728;
 Best Local Similarity 97.54; Pred. No. 5.1e-267;
 Matches 694; Conservative 2; Mismatches 3; Indels 13; Gaps 1;

Qy 40 GMRGVGPASNSGLNITFTKYDNCCTYLANVGVKAVIADAONITISQYACHDQVAVITLMS 99
 Db 16 GEGGVGPASNSGLNITFTKYDNCCTYLANVGVKAVIADAONITISQYACHDQVAVITLMS 75
 Qy 100 PGLAGTIFELGPFVILEELSEBGRQCOQLIKPKOLNSFKRTGMSQSFILMKKFTDY 159
 Db 76 PGLAGTIFELGPFVILEELSEBGRQCOQLIKPKOLNSFKRTGMSQSFILMKKFTDY 135

Qy 160 FVKVVPSPISIKNSNYPFFRTRACDILLQPDNLACKPFMKPRLNISO----- 209
 Db 136 FVKVVPSPISIKNSNYPFFRTRACDILLQPDNLACKPFMKPRLNISOHGSDMQVSPD 195
 Qy 210 ---HGSDMQVSPDHPNPGFRPFYLYLKLKHSGPFRTCKQKQETSTSLCLQNVSPG 266
 Db 196 HADHGSMDQVSPDHPNPGFRPFYLYLKLKHSGPFRTCKQKQETSTSLCLQNVSPG 255

Qy 267 DYIIELVDNTTRKVMHVALKPVHSPWAGIRAMATVTLVYISAFATLFTWCRKQKQ 326
 Db 256 DYIIELVDNTTRKVMHVALKPVHSPWAGIRAMATVTLVYISAFATLFTWCRKQKQ 315

Qy 327 ENIYSHLDESSSSSTYTAALPRERLPRPKVFLCYSSKDGONHNMVVOCPAFVLODFCG 386

Db 316 ENIYSHLDESSSSSTYTAALPRERLPRPKVFLCYSSKDGONHNMVVOCPAFVLODFCG 375
 Qy 387 CEVALDLMEDFSICREGRQEWYOKTHESQFIIVVCSKGMKYFVDKKNKHKGGSGSK 446
 Db 376 CEVALDLMEDFSICREGRQEWYOKTHESQFIIVVCSKGMKYFVDKKNKHKGGSGSK 435

Qy 447 GELFLVAVASIAEKLRQAKQSSSAALSKFLAVFDVSCBGDPGLDLSTKRYLMDNLQ 506
 Db 436 GELFLVAVASIAEKLRQAKQSSSAALSKFLAVFDVSCBGDPGLDLSTKRYLMDNLQ 495

Qy 507 LCSHLHSDHGLQEPQHTQSGRRNYPFSKSGRSIYVAICMWHQPIDEBPMFEKQFVP 566
 Db 496 LCSHLHSDHGLQEPQHTQSGRRNYPFSKSGRSIYVAICMWHQPIDEBPMFEKQFVP 555

Qy 567 FHPPELRYPPEVLEKDSGLVNDVWCKGPPSDFLKXTEAPVLTGATGPAQSDHESQHG 626
 Db 556 FHPPELRYPPEVLEKDSGLVNDVWCKGPPSDFLKXTEAPVLTGATGPAQSDHESQHG 615

Qy 627 LPDQGEARPALDGSALQPLHTYKAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTDQ 686
 Db 616 LPDQGEARPALDGSALQPLHTYKAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTDQ 675

Qy 687 TETSSLTESVSSSGLGEEPPALPSKLLSSGSCCKADIGCRSYTDELHAHAV 738
 Db 676 TETSSLTESVSSSGLGEEPPALPSKLLSSGSCCKADIGCRSYTDELHAHAV 727

RESULT 6
 Q8JZL1_MOUSE PRELIMINARY; PRT; 738 AA.
 ID Q8JZL1_MOUSE PRELIMINARY; PRT; 738 AA.
 AC Q8JZL1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Transmembrane protein (Interleukin 17 receptor-like protein long form).
 GN Name=I117rd; Synonyms=I117rlm, Sef;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21959295; PubMed=11960706; DOI=10.1016/S0925-4773(02)00018-7;
 RA Lin W., Furchauer M., Thise B., Thise C., Jing N., Ang S.-L.;
 RT "Cloning of the mouse Sef gene and comparative analysis of its
 RL expression with Pgf8 and Spfy2 during embryogenesis.";
 RL Mech. Dev. 113:163-168(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
 RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
 Liu L., Chen Z.;
 RT "Sef inhibits PC-12 cell differentiation by interfering with Ras-
 RT mitogen-activated protein kinase MAPK signaling.";
 RL J. Biol. Chem. 278:50273-50282(2003).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
 Chen Y., Liu L., Fu X.Y., Chang Z.J.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF459444; AAM28441.1; -; mRNA.
 DR EMBL; AF494210; AAM74079.1; -; mRNA.
 DR Ensembl; ENSMUSG0000040717; Mus musculus.
 DR MGI; MGI:2159727; I117rd.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO:0008270; F:zinc ion binding; IEA.
 DR InterPro: IPR000157; TIR.
 DR InterPro: IPR007087; ZnF_C3H2.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_1.
 DR Receptor; Transmembrane.
 SQ SEQUENCE 738 AA; 82347 MW; D8CE66230E3B8226 CRC64;

Query Match 86.0%; Score 3396.5; DB 2; Length 738;
 Best Local Similarity 86.6%; Pred. No. 1.2e-245;
 Matches 642; Conservative 38; Mismatches 54; Indels 7; Gaps 4;

QY 1 MAPWLOCSVEFTYVNAAGSQAQVAAGSGRAGVDTCCGWRGYPGASRNGLYNTYKY 60
 DB 1 MAPWLOCSVEFTYVNAAGSQAQVAAGSGRAGVDTCCGWRGYPGASRNGLYNTYKY 60
 QY 61 DNCTTYLNPVKGAVIADQNTTISQVACHDQVAVTILMSPALGIEFLKGRVILEIKS 120
 DB 61 DNCTTYLNPVKGAVIADQNTTISQVACHDQVAVTILMSPALGIEFLKGRVILEIKS 120
 QY 121 EGRQCOOLIKDPKQNLSPKRTGMSOPFLNMKFEVDYFKVYPPPSIKNESYHPPF 180
 DB 121 EGRQCOOLIKDPKQNLSPKRTGMSOPFLNMKFEVDYFKVYPPPSIKNESYHPPF 180
 QY 181 RTACADLLQPDNLACKPFWKPRMLNISOHSDMVAFDHPQNGFRGFRVLYKLKHEG 240
 DB 181 RTACADLLQPDNLACKPFWKPRMLNISOHSDMVAFDHPQNGFRGFRVLYKLKHEG 240
 QY 241 PPRKRTKQRTETTSCLQNVSPGYIIEVDVTRTKVMYALKPVHSPWAGPIRA 300
 DB 241 PPRKRTKQRTETTSCLQNVSPGYIIEVDVTRTKVMYALKPVHSPWAGPIRA 300
 QY 301 MATVPLVISAFTLTVMCRKQOENIYSHLDESESSSTYTAALPRELRPRVFL 360
 DB 301 MATVPLVISAFTLTVMCRKQOENIYSHLDESESSSTYTAALPRELRPRVFL 360
 QY 361 CYSKQDQNMNVQCFAYFLQDFCGCEVALDLMEDSLCREGQREWIYOKIHESQPIY 420
 DB 361 CYSKQDQNMNVQCFAYFLQDFCGCEVALDLMEDSLCREGQREWIYOKIHESQPIY 420
 QY 421 VCSKGMKYFYDKKXKFKGSGRSGKELFLVAVSAIAEKLRQKQSSAALSKFIAYVF 480
 DB 421 VCSKGMKYFYDKKXKFKGSGRSGKELFLVAVSAIAEKLRQKQSSAALSKFIAYVF 480
 QY 481 DYCCEGVPGILDLSTYKRLMDNLPOICSHLSHSDHQLQEP-GQHTQSGRRNYFRKSG 539
 DB 481 DYCCEGVPGILDLSTYKRLMDNLPOICSHLSHSDHQLQEP-GQHTQSGRRNYFRKSG 539
 QY 539 RSLVYALCNMHQFIDEEDPMEKQFVPHPEPLRYREPVLEKPSGLVINDVMCKPGPES 599
 DB 539 RSLVYALCNMHQFIDEEDPMEKQFVPHPEPLRYREPVLEKPSGLVINDVMCKPGPES 599
 QY 600 DFLKVEAPVLTGAPADSOH--ESQHGILDQDEARPALDGSNALLPLHTTVAGSPSD 657
 DB 600 DFLKVEAPVLTGAPADSOH--ESQHGILDQDEARPALDGSNALLPLHTTVAGSPSD 657
 QY 658 MPRDSGIVDSVPSSESLPLMEGLSTDQETSSLTSSVSSSGLGEEBPPALPSKLLSS 717
 DB 658 MPRDSGIVDSVPSSESLPLMEGLSTDQETSSLTSSVSSSGLGEEBPPALPSKLLSS 717
 QY 718 GSCKADLCRSYDELTAHAVP 738
 DB 718 GSCKADLCRSYDELTAHAVP 738
 QY 738 GSCKADLCRSYDELTAHAVP 738
 DB 738 GSCKADLCRSYDELTAHAVP 738

RESULT 7
 Q8N113_HUMAN PRELIMINARY; PRT; 595 AA.
 ID Q8N113_HUMAN PRELIMINARY; PRT; 595 AA.
 AC Q8N113; (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Interleukin 17 receptor-like protein short form (Hypothetical protein DKFp434L0320).

GN Name=IL17RLM; Synonym=DKEP434L0320;
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Testis;
 RG The German cDNA Consortium;
 RA Ottensmeyer B., Obermaier B., Deutschenbauer S., Schapp A.,
 RA Mewes H.W., Weil B., Amid C., Oanger A., Fob G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF494211; AAM74080.1; -; mRNA.
 DR EMBL; AL833913; CAD38769.1; -; mRNA.
 DR Ensembl; ENSG00000144730; Homo sapiens.
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro: IPR000157; TIR.
 DR Hypothetical protein; Receptor.
 SQ SEQUENCE 595 AA; 66846 MW; 7E6BB64F73B2112 CRC64;

Query Match 80.0%; Score 3158; DB 2; Length 595;
 Best Local Similarity 99.5%; Pred. No. 6.9e-228;
 Matches 591; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 145 MESQFLAMKFEVDYFKVPPPSIKNESYHPPFRTACDILLQPDNLACKPFWKPRN 204
 DB 1 MESQFLAMKFEVDYFKVPPPSIKNESYHPPFRTACDILLQPDNLACKPFWKPRN 204
 QY 205 LNIISOHSDMVAFDHPQNGFRFYLHYKLKHEGPKKTKQEGTETTSCLQNV 264
 DB 205 LNIISOHSDMVAFDHPQNGFRFYLHYKLKHEGPKKTKQEGTETTSCLQNV 264
 QY 61 LNIISOHSDMVAFDHPQNGFRFYLHYKLKHEGPKKTKQEGTETTSCLQNV 120
 DB 61 LNIISOHSDMVAFDHPQNGFRFYLHYKLKHEGPKKTKQEGTETTSCLQNV 120
 QY 265 PGDIYIEVDVTRTKVMYALKPVHSPWAGPIRAVAIVPLVISAFTLTVMCRK 324
 DB 265 PGDIYIEVDVTRTKVMYALKPVHSPWAGPIRAVAIVPLVISAFTLTVMCRK 324
 QY 325 QOENIYSHLDESESSSTYTAALPRELRPRVFLCYSSKQDQNMNVQCFAYFLQDF 384
 DB 325 QOENIYSHLDESESSSTYTAALPRELRPRVFLCYSSKQDQNMNVQCFAYFLQDF 384
 QY 385 CGCEVALDLMEDSLCREGQREWIYOKIHESQPIIIVCSKGMKYFYDKKXKFKGSG 444
 DB 385 CGCEVALDLMEDSLCREGQREWIYOKIHESQPIIIVCSKGMKYFYDKKXKFKGSG 444
 QY 445 GKGELFLVAVSAIAEKLRQKQSSAALSKFIAYVDPYSCGEGVPGILDLSTYKRLMDNL 504
 DB 445 GKGELFLVAVSAIAEKLRQKQSSAALSKFIAYVDPYSCGEGVPGILDLSTYKRLMDNL 504
 QY 505 POLCSHLSHSDHQLQEPGQHTQSGRRNYFRSAGSLVYALCNMHQFIDEEDPMEKQF 564
 DB 505 POLCSHLSHSDHQLQEPGQHTQSGRRNYFRSAGSLVYALCNMHQFIDEEDPMEKQF 564
 QY 565 VPHAPPPLRYREPVLEKPSGLVINDVMCKPGPESDCLKVEAPVLTGAPADSOHSDH 624
 DB 565 VPHAPPPLRYREPVLEKPSGLVINDVMCKPGPESDCLKVEAPVLTGAPADSOHSDH 624
 QY 625 GGLDQGEARPALDGSNALLPLHTTVAGSPSPMPDSGIVDSVPSSESLPLMEGLST 664
 DB 625 GGLDQGEARPALDGSNALLPLHTTVAGSPSPMPDSGIVDSVPSSESLPLMEGLST 664
 QY 685 DQETSSLTSSVSSSGLGEEBPPALPSKLLSSGSKADLCRSYDELTAHAVP 738
 DB 685 DQETSSLTSSVSSSGLGEEBPPALPSKLLSSGSKADLCRSYDELTAHAVP 738
 QY 738 GSCKADLCRSYDELTAHAVP 738
 DB 738 GSCKADLCRSYDELTAHAVP 738

RESULT 8

Q9UFA0 HUMAN PRELIMINARY; PRT; 564 AA.
 ID Q9UFA0;
 AC Q9UFA0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp434N1928 (Fragment).
 GN Name=DKFZp434N1928;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxId=9606;
 RN NCBIOTIDE SEQUENCE.
 RP TISSUE=Testis;
 RC Bloecher H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
 RA Wiemann S.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL133097; CAB61408.1; -; mRNA.
 DR PIR; T42695; T42695.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR000157; TIR.
 KM Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E86C CRC64;

Query Match 75.8%; Score 2993; DB 2; Length 564;
 Best Local Similarity 99.5%; Pred. No. 1.5e-215;

Matches 560; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

176 HPPFRTACDILLQPNLACKPFWKPRNINISQHSQDMQVSPDHADPHNGFRFPYLHYK 235
 1 HPFFRTACDILLQPNLACKPFWKPRNINISQHSQDMQVSPDHADPHNGFRFPYLHYK 60
 236 LKHEGPKRTKCOEOTETTSCILQNVSPGDIYIELVDNTTRKVMYALKPVHSPWA 235
 61 LKHEGPKRTKCOEOTETTSCILQNVSPGDIYIELVDNTTRKVMYALKPVHSPWA 120
 296 GPTRAMATVPLVYISAFATLFTVMCRKQOENITSHLDESSSESTYTAALPRELRPR 355
 121 GPTRAVATVPLVYISAFATLFTVMCRKQOENITSHLDESSSESTYTAALPRELRPR 180
 356 PKYFLCYSSKQGNHNVVOCFAFYLDPCGCEVALDLMEDFSLCREGQEWYIOKIHES 415
 181 PKYFLCYSSKQGNHNVVOCFAFYLDPCGCEVALDLMEDFSLCREGQEWYIOKIHES 240
 416 QPITIVVCSKMKTPVDKQNTKHKGGSGKGEFLVAVASIAEKLRAQAOSSAALSKP 475
 241 QPITIVVCSKMKTPVDKQNTKHKGGSGKGEFLVAVASIAEKLRAQAOSSAALSKP 300
 476 IAYYFDVSCGSDVPGIIDLSTKRYLMONLPCOLCSHLSDHGLQEPQHTROGSRNRYFR 535
 301 IAYYFDVSCGSDVPGIIDLSTKRYLMONLPCOLCSHLSDHGLQEPQHTROGSRNRYFR 360
 536 SKGSRSLVYALCMNHQPIDEBPWFEXQVPPFHPPLRYREPVYLEKFDGSLVINDVWCKP 595
 361 SKGSRSLVYALCMNHQPIDEBPWFEXQVPPFHPPLRYREPVYLEKFDGSLVINDVWCKP 420
 596 GPSSDFCLKATBAPYLATGPADSQHSQHGGLDGDGAPALDGSALQPLTLTVKAGSP 655
 421 GPSSDFCLKATBAPYLATGPADSQHSQHGGLDGDGAPALDGSALQPLTLTVKAGSP 480
 656 SDMPROSGITDSSVPSSELSLPLMEGLSTDOTETSSLTESVSSSSGAGEEPALPESKL 715
 481 SDMPROSGITDSSVPSSELSLPLMEGLSTDOTETSSLTESVSSSSGAGEEPALPESKL 540
 716 SSGSKADLCRSYTDLHAAP 738
 |||||

DB 541 SSGSKADLCRSYTDLHAAP 563

RESULT 9

Q7T2L7 CHICK PRELIMINARY; PRT; 741 AA.
 ID Q7T2L7;
 AC Q7T2L7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FGF signalling antagonist SRF.
 GN Name=DKFZp434N1928;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxId=9031;
 RN NCBIOTIDE SEQUENCE.
 RP MEDLINE=22660508; PubMed=12766772; DOI=10.1038/nb989;
 RX Kawakami Y., Rodriguez-Leon J., Koch C.M., Buscher D., Itoh T.,
 RA Rava A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
 RA Schwarz M.F., Asahara H., Izpisua Belmonte J.C.;
 RT "Wk3 mediates the cellular response to FGF8 signalling in the
 vertebrate limb."
 RL Nat. Cell Biol. 5:513-519 (2003).
 DR EMBL; AY278204; AAP70001.1; -; mRNA.
 DR Ensembl; ENSGALG0000005499; Gallus gallus.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006954; P:inflammatory response; IEA.
 DR InterPro; IPR000157; TIR.
 SQ SEQUENCE 741 AA; 83553 MW; 64B8E88241AC60CF CRC64;

Query Match 73.3%; Score 2893; DB 2; Length 741;
 Best Local Similarity 73.5%; Pred. No. 7.1e-208;

Matches 545; Conservative 79; Mismatches 112; Indels 6; Gaps 5;

1 MAPWILQCVFFTVNACLSQSLAVAGSG--RAMGVDTGMRGVSPARNSGLYNTF 58
 1 MAPGRILGAFLLALAFCCGRRLAEAGSPGRGAADACGGRGLSSTKNGILNITF 60
 59 KDNCTTYLNPVGVIAADQNTTISQVACHQDAVATLMSFGALGIEFLKGFVILEEL 118
 61 KDNCTPYLNSGVKIVIGDVNTTISQVACHQDAVATLMTANAIGIEFLRFRVILEEL 120
 119 KSGRCCQQLIKDPQLNSSFRTGMSQPLNKKFEFDYVKKVPFSSINSESYHFF 178
 121 KSGRCCQQLIKDPQLNSSFRTGMSQPLNKKFEFDYVKKVPFSSINSESYHFF 180
 179 PFTTRACDILLQPNLACKPFWKPRNINISQHSQDMQVSPDHADPHNGFRFPYLHYK 238
 181 PFTTRACDILLQPNLACKPFWKPRNINISQHSQDMQVSPDHADPHNGFRFPYLHYK 240
 239 EGFPRKTKCOEOTETTSCILQNVSPGDIYIELVDNTTRKVMYALKPVHSPWAGPI 298
 241 EGFPRKTKCOEOTETTSCILQNVSPGDIYIELVDNTTRKVMYALKPVHSPWAGPI 300
 299 RAMATVPLVYISAFATLFTVMCRKQOENITSHLDESSSESTYTAALPRELRPRPV 358
 301 RAMATVPLVYISAFATLFTVMCRKQOENITSHLDESSSESTYTAALPRELRPRPV 360
 359 FLCYSSKQGNHNVVOCFAFYLDPCGCEVALDLMEDFSLCREGQEWYIOKIHESQPI 418
 361 FLCYSSKQGNHNVVOCFAFYLDPCGCEVALDLMEDFSLCREGQEWYIOKIHESQPI 420
 419 IVCSSKMKTPVDKQNTKHKGGSGKGEFLVAVASIAEKLRAQAOSSAALSKPIAV 478
 421 IVCSSKMKTPVDKQNTKHKGGSGKGEFLVAVASIAEKLRAQAOSSAALSKPIAV 479
 479 YPDSGCEGSDVPGIIDLSTKRYLMONLPCOLCSHLSDHGLQEPQHTROGSRNRYFR 538
 480 YPDSGCEGSDVPGIIDLSTKRYLMONLPCOLCSHLSDHGLQEPQHTROGSRNRYFR 539
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QY 539 GRSLYVACNMHOFIDEEPDMFEKQFVFPFPPRLRYREPVLEKFDGLVINDVWCKEPE 598
DB 540 GRSLYVACNMHOFIDEEPDMFEKQFIPFLPHPLHYSEPMWEKDSGLVINDVWCKEAD 599
QY 599 SDPCLKVEAPVLGATGADPSOHESQHGGLDQDGEARP-ALDGSANLOPLHTTVKAGSPSD 657
DB 600 DDFLTKTDVNIISA-GSSDSHCIIQHLNLTGEDVETQDIQSGSSVLPALHVAASNLKD 658
QY 658 MPBDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSSGLGEEPPALPS-KLIS 716
DB 659 MPBDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSSGLGEEPPALPS-KLIS 718
QY 717 SGSCKADLCGRSYDELAHAVP 738
DB 719 PGICKALHCHIRHDELQAIAP 740

RESULT 10
Q8AV76_CHICK PRELIMINARY; PRT; 697 AA.
ID Q8AV76_CHICK PRELIMINARY; PRT; 697 AA.
AC Q8AV76_CHICK PRELIMINARY; PRT; 697 AA.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Self protein (Fragment).
GN Name=SRF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Facial mesenchyme;
MEDLINE=2651784; PubMed=12765832; DOI=10.1016/S0968-0004(03)00067-7;
RA Novatchkova M., Leibbrandt A., Werzowa J., Neubueser A.,
RA Bisenhaber P.;
RT "The STR-domain superfamily in signal transduction, development and
RT immunity.";
RL Trends Biochem. Sci. 28:226-229(2003).
DR EMBL; AJ508679; CAD48485.1; -; mRNA.
DR Ensembl; ENSGALG0000005499; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
FT NON TER
SQ SEQUENCE 697 AA; 79259 MW; D288939E17272FC3 CRC64;

Query Match 71.6%; Score 2828; DB 2; Length 697;
Best Local Similarity 75.5%; Pred. No. 4.9e-203;
Matches 527; Conservative 75; Mismatches 92; Indels 4; Gaps 4;

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DB 301 YGALPVERLRPRPKVFCICSSSDCKHINIVICPAFLQDFGCEVALDMLDELKICKE 360
QY 403 GQREWVIOKIHESQFIIIVVCSKMKTFVDKXNKHKGSGSGKGLFLVAVASIAEKLR 462
DB 361 SOKEMILKIKINESQFIIIVVCSKMKTFVEKXNKHKGSGKGLFLVAVASIAEKLR 420
QY 463 QAKOSSAALSKRTIAYPDVSCGDPVGLIDLSITKRLMNLNOLCSHLSRPHGOEPG 522
DB 421 QAKONSN-DICKRTIAYPDVSCGDPVGLIDLSITKRLMNLNOLCSHLSRPHGOEPG 479
QY 523 QHTROGSRNRYPRSKGSLIYVACNMHOFIDEEPDMFEKQFVFPFPPRLRYREPVLEK 582
DB 480 VFPVNSKRTYPRSKGSLIYVACNMHOFIDEEPDMFEKQFIPFLPHPLHYSEPMWEK 539
QY 583 DSGLVINDVWCKEPESDFLKVEAPVLGATGADPSOHESQHGGLDQDGEARPALD-GSA 641
DB 540 DSGLVINDVWCKEADDFLTKTDVNIISA-GSSDSHCIIQHLNLTGEDVETQDIQSGSS 598
QY 642 ALQPLHTTVKAGSPDMPRDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSG 701
DB 599 VLPPLHVAASNLKMPRDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSG 658
QY 702 LGSEEPALPS-KLISSGCKADLCGRSYDELAHAVP 738
DB 659 LGSEEPALPS-KLISSGCKADLCGRSYDELAHAVP 696

RESULT 11
Q8K447_MOUSE PRELIMINARY; PRT; 594 AA.
ID Q8K447_MOUSE PRELIMINARY; PRT; 594 AA.
AC Q8K447_MOUSE PRELIMINARY; PRT; 594 AA.
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein short form.
GN Name=IL17rd; Synonyms=IL17rlm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA PubMed=12958313; DOI=10.1074/jbc.M306936200;
RX Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RX Liu L., Chang Z.;
RT "Self-inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
DR EMBL; AF494209; AAM74078.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Receptor.
SQ SEQUENCE 594 AA; 66780 MW; EABE6B55DF4EC3 CRC64;

Query Match 67.5%; Score 2665.5; DB 2; Length 594;
Best Local Similarity 84.6%; Pred. No. 5.9e-191;
Matches 505; Conservative 35; Mismatches 50; Indels 7; Gaps 4;

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Db 61 LINSQSGDMHVSFDHAPQNFGRGFHVLTKLKHGEFRRRTCRQDQNTETTSCLQNVS 120
Qy 265 PGQYIIELVDDTTTRKVMYIALKPNVSPMAGPIRAMAIVPLVISAFTLPTVMCRKK 324
Db 121 PGQYIIELVDDSTTRKMAQYVYKVSQSPMAGPIRAVAITVPLVISAFTLPTVMCRKK 180
Qy 325 QQENITSHLDESSSESTYTAALPRELTPRPKYFLCYSSKDGONHNNVQCFAYFLQDF 384
Db 181 QQENITSHLDESBESSTYAAALPRDLTPQPKYFLCYSNKDGONHNNVQCFAYFLQDF 240
Qy 385 CGCEVALDLMEDFSCLCEGGEWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHGGGRGS 444
Db 241 CGCEVALDLMEDFSCLCEGGEWMAIOKIHESQFIIVVCSKGMKYFVDKKNYKHGGGRGS 300
Qy 445 GKRELPLVAVSAIAEKLRQAKQSSSALSKFIAYFPYSCGDPVPGILDLSTKRLMDNL 504
Db 301 AQGEFFLVAAVAIAEKLRQAKQSSSALSKFIAYFPYSCGDPVPGILDLSTKRLMDNL 360
Qy 505 POLCSHLSDHGLQEP--GGHTQCSRRNTFRSKSGSLVYALCNMHQFIDEBDMFEKQ 563
Db 361 PELCAHLHS--GGEVLYGQHPGHSRRNTFRSKSGSLVYALCNMHQFIDEBDMFEKQ 417
Qy 564 FVPEHPPEPLRYRREPVLKFPDGLVNDVMCKPGEPSDFCLKVEAPVLGATGPADSOH--E 621
Db 418 FIFQHPHPVRYQEPVLEKFPDGLVNDVIAKPGESDFCRKVEACVLGAAPADSVSYLE 477
Qy 622 SQHGGLDQDGEAPALPDGSAALQPLHTVYKAGSPSDMPRDSGIYDSSVPSSELSPLMEG 681
Db 478 SQHVGLDQDDEAPSCSAPALQPLHTAVKAGSPSEMPRDSGIYDSSVPSSELSPLMEG 537
Qy 682 LSTPDQETTSILTVSSSSGSGEPEEPALPSKLLSSGSKADLCGRSYTELHAAVAP 738
Db 538 LSPDQETTSILTVSSSSGSGEPEEPALPSKLLSSGSKADLCGRSYTELHAAVAP 593

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RESULT 12

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08R5J8 MOUSE
ID 08R5J8_MOUSE PRELIMINARY: PRT: 582 AA.
AC 08R5J8_MOUSE
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Similar expression to FGF protein (Fragment).
GN Name=117rd; Synonyms=Self;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21824237; PubMed=11802165; DOI=10.1038/nb750;
RA Furlan M., Lin W., Ang S.L., Thibse B., Thibse C.;
RT "Self is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signaling";
RL Nat. Cell Biol. 4:170-174(2002).
DR EMBL; AF424604; ALU79530.1; -; mRNA.
DR MGI; MGI:2159727; I117rd.
DR GO; GO:0016020; C:nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR00157; TIR.
DR InterPro; IPR007087; ZnF_C2H2.
DR PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 1.
FT NON TER 1 1
SQ SEQUENCE 582 AA; 65263 MW; 5666B2981C4268 CRC64;

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Query Match 66.0%; Score 2606.5; DB 2; Length 582;
 Best Local Similarity 84.4%; Pred. No. 1.5e-186;
 Matches 494; Conservative 35; Mismatches 49; Indels 7; Gaps 4;

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Qy 157 TDYFVAVPEPSTIKNESNYHPFFRTRACDLLLQPDNLACKPEWKRININISQHSQDMQV 216
Db 1 TDYFVAVPEPSTIKNESNTHPPFFRTRACDLLLQPDNLACKPEWKRININISQHSQDMQV 60
Qy 217 SFDHAPNFGPREFVLYHYLKLKHGEPKRYTKQEQTEFTTSCILQNVSPQDYIIELVDDT 276
Db 61 SFDHAPQNGFGFHYLYLKLKHGEPKRYTKQEQTEFTTSCILQNVSPQDYIIELVDDT 120
Qy 277 NTRTKMYHAKLPVNSPMAGPIRAMAIVPLVISAFTLPTVMCKKQENITSHLDE 336
Db 121 NTRTKAAQTVVNSVQSPMAGPIRAVAITVPLVISAFTLPTVMCKKQENITSHLDE 180
Qy 337 SSESSTYTAALPRELTPRPKYFLCYSSKDGONHNNVQCFAYFLQDFCGCEVALDLMED 396
Db 181 SPSSSTYAAALPRDLTPQPKYFLCYSNKDGONHNNVQCFAYFLQDFCGCEVALDLMED 240
Qy 397 FSLCREGGEWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHGGGRSGKBLFLVAVSA 456
Db 241 FSLCREGGEWMAIOKIHESQFIIVVCSKGMKYFVDKKNYKHGGGRSGEAGFEFLVAVSA 300
Qy 457 IAEKLRQAKQSSSALSKFIAYFPDYSCEGDPVPGILDLSTKRLMDNLQOLCSHLSDH 516
Db 301 IAEKLRQAKQSSSALSKFIAYFPDYSCEGDPVPGILDLSTKRLMDNLQOLCSHLSDH 357
Qy 517 GLQEP--GGHTQCSRRNTFRSKSGSLVYALCNMHQFIDEBDMFEKQFVPEHPPELRYR 575
Db 358 GGEVLYGQHPGHSRRNTFRSKSGSLVYALCNMHQFIDEBDMFEKQIIFQHPHPVRYQ 417
Qy 576 EPLKFPDGLVNDVIAKPGESDFCRKVEACVLGAAPADSVSYLESQHGVLDDQDEA 633
Db 418 EPLKFPDGLVNDVIAKPGESDFCRKVEACVLGAAPADSVSYLESQHGVLDDQDEA 477
Qy 634 RPLDQSAALQPLHTVYKAGSPSDMPRDSGIYDSSVPSSELSPLMEGISTOTETSSILT 693
Db 478 QPSCDSAPALQPLHTAVKAGSPSEMPRDSGIYDSSVPSSELSPLMEGISTOTETSSILT 537
Qy 694 ESYVSSSGGLGEBEPPALPSKLLSSGSKADLCGRSYTELHAAVAP 738
Db 538 ESYVSSSGGLGEBEPPALPSKLLSSGSKADLCGRSYTELHAAVAP 581

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RESULT 13

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08QHU9 BRAR
ID 08QHU9_BRAR PRELIMINARY: PRT: 745 AA.
AC 08QHU9_BRAR
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Self.
GN Name=117rd; Synonyms=Self;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
OX RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21824236; PubMed=11802164; DOI=10.1038/nb749;
RA Tsang M., Friesel R., Kudoh T., David I.;
RT "Identification of Self, a novel modulator of FGF signaling";
RL Nat. Cell Biol. 4:165-169(2002).
DR EMBL; AF364103; AAU76112.1; -; mRNA.
DR EMBL; ENSDARG0000005754; Danio rerio.
DR ZFIN; ZDB-GENE-020320-5; I117rd.
SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98D84 CRC64;

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Query Match 49.8%; Score 1966; DB 2; Length 745;
 Best Local Similarity 52.4%; Pred. No. 2.3e-138;
 Matches 391; Conservative 111; Mismatches 198; Indels 46; Gaps 10;


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Db      7 LAHFMAASCLFLCYTASVNG-----GKRGNSDKCSYKQGTQTSMSDEGARKLGV 56
Qy      58 FKXDNCTTYLNPVKHVIADAQNTTISQYACHDVAVTILMSPALGIEPLKGRVILIE 117
Db      57 FRDNCNVNNSPLGKAHIEVNNTTFSHLSDSQAAVVMWMAASPLGIEHVKGRVYLED 116
Qy      118 LKSEGRCCOOLILKDPKOLNSFKRTGMSQPLANKFEFDYFVKVVPFSPKESNYHP 177
Db      117 KNEBRKCOCHLILKDPKOLNFSYKTIKMSQPFSSLAFFEDYVWRIYVFPFPLNDSFPP 176
Qy      178 FFRTRACDILLDPNLACKPFPKPNLNTISQHSQDQVSDHAPHNFGFRFLYATK 237
Db      177 SFLRTNSCEVLGPDNLVCKPFPKPNLNTISQHSQDQVSDHAPHNFGFRFLYATK 236
Qy      238 HEGPFRKTKCKOQETTTSCLLQNSPGDYIIELVDTTTRKVMHAYALKPVSMPAGP 297
Db      237 QGEPFRLKCKPQNGPKTKCVLDVTPGYALIELRDSNTRQOTYHNSQVHSPWAGP 296
Qy      298 IRMAITVPLVISAFAITFTWCRKQKQENIYSHLDESSSSTYTAALPRELRPRK 357
Db      297 IRMAITVPLVISAFAITFTWCRKQKQENIYSHLDESSSSTYTAALPRELRPRK 356
Qy      358 VPLCYSSKQDQNMNVQCAVFLQDPCGCEVALDMEDESLCREGOREWVIOKIHESQF 417
Db      357 IFLCYSSRDGAKHLAVIQSFAFLQDPCGCEVALDMEDESLCREGOREWVIOKIHESQF 416
Qy      418 IIVVCSGKMYFYDKNYKHKGGK-----GSGKGLFLVAVSAIAETLROAKQ 466
Db      417 IIVVCSGKGLHFKYKHKGGKATSKENKREPSADSSSSSRDLFIYASAIISGLKXEHQ 476
Qy      467 SSSAALSKFLAVYFDVSCGEGDVPGLDSTKYRLMDLPLQCSHLHSRDHGLQEPGHTR 526
Db      477 KSS-DLSRFMSYFEDYSHETDVPSTLSLAPFKLMDLPLQCFARLSRQSLTDREPOPP 535
Qy      527 QGSRNRYFRKSGSLYVAICNMHOFIDEERDPEKQFVFPHPPLRYRREPVLEKPSGL 586
Db      536 NVSKRNYFCKSGSLYVAIYNMHQHTQEPDWEKELM---PPPLNKRTTPEKVDGSL 592
Qy      587 VLANDVCKPESDPCLKVEAPVL-----GATGPADSGHESQHGGLDODGEARPALDG 639
Db      593 VLANDVCKPESDPCLKVEAPVL-----GATGPADSGHESQHGGLDODGEARPALDG 642
Qy      640 SAALQPLHTVAKGSPDMRDGSIYDSSVPSSELPLMEGLSTQDTETSSLTESVSS 699
Db      643 AGSCRPLHTDGSASPEMPRDSGIYDSSVPSSELPLMDGLSPDHADNSLADSVSS 702
Qy      700 SGLGEPPALPESKLSGSS-CRADL 724
Db      703 SGLGEPPAVSSLHCTAHTICRADL 728

RESULT 14
Q8QHJ6 BRARE PRELIMINARY; PRT; 745 AA.
ID Q8QHJ6 BRARE PRELIMINARY; PRT; 745 AA.
AC Q8QHJ6;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DB FGF signaling antagonist Sef.
GN Name=117rd; Synonym=ssef;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_Taxid=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fierthauer M., Lin W., Ang S.L., Thise B., Thise C.;
RA MEDLINE=21824237; PubMed=11802165; DOI=10.1038/nbt750;
RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signaling".
RL Nat. Cell Biol. 4:170-174(2002).
RN [2]

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RP NUCLEOTIDE SEQUENCE.
RA Fierthauer M., Lin W., Siew-Ian A., Thise B., Thise C.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401232; AAL78817.1; -; mRNA.
DR Ensembl; ENSDARG0000005754; Danio rerio.
DR ZFIN; ZDB-GENE-020320-5; 1117rd.
SQ SEQUENCE 745 AA; 83437 MW; 75BB9EDCC08A4652 CRC64;

Query Match 49.6%; Score 1957; DB 2; Length 745;
Best Local Similarity 52.1%; Pred. No. 1,1e-137;
Matches 389; Conservative 113; Mismatches 198; Indels 46; Gaps 10;

1 MAPMLQCSVFETVNACTNSQLAAVAGSGRAGVDTGCMR-GVGPASRNSGL--YNIT 57
Db      7 LAHFMAASCLFLCYTASVNG-----GKRGNSDKCSYKQGTQTSMSDEGARKLGV 56
Qy      58 FKXDNCTTYLNPVKHVIADAQNTTISQYACHDVAVTILMSPALGIEPLKGRVILIE 117
Db      57 FRDNCNVNNSPLGKAHIEVNNTTFSHLSDSQAAVVMWMAASPLGIEHVKGRVYLED 116
Qy      118 LKSEGRCCOOLILKDPKOLNSFKRTGMSQPLANKFEFDYFVKVVPFSPKESNYHP 177
Db      117 KNEBRKCOCHLILKDPKOLNFSYKTIKMSQPFSSLAFFEDYVWRIYVFPFPLNDSFPP 176
Qy      178 FFRTRACDILLDPNLACKPFPKPNLNTISQHSQDQVSDHAPHNFGFRFLYATK 237
Db      177 SFLRTNSCEVLGPDNLVCKPFPKPNLNTISQHSQDQVSDHAPHNFGFRFLYATK 236
Qy      238 HEGPFRKTKCKOQETTTSCLLQNSPGDYIIELVDTTTRKVMHAYALKPVSMPAGP 297
Db      237 QGEPFRLKCKPQNGPKTKCVLDVTPGYALIELRDSNTRQOTYHNSQVHSPWAGP 296
Qy      418 IIVVCSGKMYFYDKNYKHKGGK-----GSGKGLFLVAVSAIAETLROAKQ 466
Db      417 IIVVCSGKGLHFKYKHKGGKATSKENKREPSADSSSSSRDLFIYASAIISGLKXEHQ 476
Qy      467 SSSAALSKFLAVYFDVSCGEGDVPGLDSTKYRLMDLPLQCSHLHSRDHGLQEPGHTR 526
Db      477 KSS-DLSRFMSYFEDYSHETDVPSTLSLAPFKLMDLPLQCFARLSRQSLTDREPOPP 535
Qy      527 QGSRNRYFRKSGSLYVAICNMHOFIDEERDPEKQFVFPHPPLRYRREPVLEKPSGL 586
Db      536 NVSKRNYFCKSGSLYVAIYNMHQHTQEPDWEKELM---PPPLNKRTTPEKVDGSL 592
Qy      587 VLANDVCKPESDPCLKVEAPVL-----GATGPADSGHESQHGGLDODGEARPALDG 639
Db      593 VLANDVCKPESDPCLKVEAPVL-----GATGPADSGHESQHGGLDODGEARPALDG 642
Qy      640 SAALQPLHTVAKGSPDMRDGSIYDSSVPSSELPLMEGLSTQDTETSSLTESVSS 699
Db      643 AGSCRPLHTDGSASPEMPRDSGIYDSSVPSSELPLMDGLSPDHADNSLADSVSS 702
Qy      700 SGLGEPPALPESKLSGSS-CRADL 724
Db      703 SGLGEPPAVSSLHCTAHTICRADL 728

RESULT 15
Q4RLH0 TETNG PRELIMINARY; PRT; 470 AA.
ID Q4RLH0 TETNG PRELIMINARY; PRT; 470 AA.
AC Q4RLH0;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAR15020, whole genome shotgun sequence.

```

DE (fragment).
GN ORFNames=GSTENG0032492001;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Catolico L., Poulat J., De Berardinis V.,
RA Cnaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Querier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
RT Genome duplication in the teleost fish Tetradodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CAAB0105020; CAG10762.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 470 470
SQ SEQUENCE 470 AA; 53660 MW; 0FB99F24436E5124 CRC64;

Query Match 33.8%; Score 1335; DB 2; Length 470;
Best Local Similarity 54.8%; Pred. No. 2,6e-91;
Matches 259; Conservative 67; Mismatches 133; Indels 14; Gaps 4;

QY 105 IEFKGFVILIEBKSGRQCOQILKDPKQLNSSFRTGMSQPLNMFETDYPVKV 164
DB 1 IEHVKGFRVYLEDKNPEGRKCOHLKDPQLNFSHKNTKLSQPFAGLTFDTDMVRVY 60
QY 165 PFPISIKRESYHPPFPFTRACDILLDPDNLACRPFWRKRLNLSOHGSDMQVSFDHAPHN 224
DB 61 PFPISLNNESFPFPFTRNCEVLLGSDSLVCKRPFWRKRLNLSOHGSDMQVSFDHAPHN 120
QY 225 FGRFPFLYHKLHGEQPKKTCQEQETETTSCLQNVSPGDIIELVDTMTTRKVMH 284
DB 121 FGRFALYLYIKLQDGFPRKQCKRCPGPAWMLRALTKCPTTSSNVLSFLDMLITTLQLSR 180
QY 285 YALKPVHSPWAGPIRAMAIVPLVVISAFATL-FTVWCRRKQENIYSHLDESSSESTY 343
DB 181 YKFPY--FWAGPIRAMAIVPLVVISAFATL-FTVWCRRKQENIYSHLDESSSESTY 237
QY 344 TALLPBRRLAPRRVFLCYSSKQGNMNVQCPAYFLDPCCGEVALDLMEDPSLCREG 403
DB 238 SAALNPERPWRPRKRVFLCYSNRQDPKHSNVIQSFAYFLDPCCGEVALDLMEDPSLCREG 297
QY 404 QREWVIOKHESQPIIIVGSKMKYFVDKKNYKHKGGRSGK-----GELFLVAVSA 456
DB 298 QMSWLSRQLDEADPIITVCGRLRYEKRKSGSPVSRQSGSLPPAASMGDLFFVSVSV 357
QY 457 IAEKLRQAKS---SSAALSKFIAVVPDYSCEGDVPGILDLSTYRLMDNLPOLCSHLHS 513
DB 358 IAEKLRQAKS---SSAALSKFIAVVPDYSCEGDVPGILDLSTYRLMDNLPOLCSHLHS 417
QY 514 RDHGLQEPGQHTKQSGRRATFRSKSGSLYVAICNMHGFIDEEDPWFQKQVP 566
DB 418 SSGSLAESLSLPVNVSRNRYFRSKSGSLYVAICNMHGFIDEEDPWFQKQVP 470

Search completed: March 1, 2006, 10:30:09
Job time : 237 secs

Db 241 GTGATGCTGACGCGCCAGAAATATCATCATGCGCATGATGCTTGCCATGACGAAAGTGGCA 300
Qy 301 GTACCAATCTTTGTGTGTCCTCCAGGGGCTCTGCGCATGGAATCTTGAAGAGATTTCCGGTA 360
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Qy 361 ATATGAGAGAGTGAAGTGGAGGGAGACAGTGGCCAACTGATCTTCAAAAGATCCG 420
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Qy 421 AAGCACTCAACAGTATGCTTCAAAAGATCTGAAATCTCACTTCTTGAATATG 480
Db 421 AAGCACTCAACAGTATGCTTCAAAAGATCTGAAATCTCACTTCTTGAATATG 480
Qy 481 AAATTTGAAACGGAATATTTCTTAAAGTGTGCTTCTTCTTCAATTAATAAGCAAGC 540
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Qy 541 AATTACACGCTTCTTCTTGAACCGGAGCTGTGACCTGTGTTAAGCGCGGCAAT 600
Db 541 AATTACACGCTTCTTCTTGAACCGGAGCTGTGACCTGTGTTAAGCGCGGCAAT 600
Qy 601 CTAGCTTGAACCTCTTCTGGAAGCTCGGAACCTGAAATCAATCAGCAGATGGCTCGAC 660
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Db 661 ATGCAAGTGTCTTCTGACCAAGCAAGCACTTGGCTTCCGTTCTTCTTCAATCTTCAAC 720
Qy 721 TACAACTCAAGACGAAGGACCTTCAAGCGAAAGCTGTAAAGACGAGCAACTCA 780
Db 721 TACAACTCAAGACGAAGGACCTTCAAGCGAAAGCTGTAAAGACGAGCAACTCA 780
Qy 781 GAGACGACAGTGTCTCTTCAAAATGTTTCTCAGGGATTAATTAATGAGTGTG 840
Db 781 GAGACGACAGTGTCTCTTCAAAATGTTTCTCAGGGATTAATTAATGAGTGTG 840
Qy 841 GATGACATTAACAAACAAAGAAAGTATGATTAATGCTTAAAGCAGTGCATCCCG 900
Db 841 GATGACATTAACAAACAAAGAAAGTATGATTAATGCTTAAAGCAGTGCATCCCG 900
Qy 901 TGGGCGGGGCGCATGAGGCAATGAGCATGAGTGCATGCTGATGATGATGAGATTC 960
Db 901 TGGGCGGGGCGCATGAGGCAATGAGCATGAGTGCATGCTGATGATGATGAGATTC 960
Qy 961 GCGACGCTCTTCACTGTGATGTGCGCGCAAGAACAAACAAAGAAATATATTTCACTTTA 1020
Db 961 GCGACGCTCTTCACTGTGATGTGCGCGCAAGAACAAACAAAGAAATATATTTCACTTTA 1020
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Db 1621 TCCGAGGCAAGTCAAGGCGGCTCCCTATGATGTCGCAATTTGCAATGCAACGATTTAT 1680
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Db 1741 TACCGGAGCCAGTCTTGGAGAAATTTGATTTGGGCTTGGTTTAAATGATGATGTC 1800
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Db 2221 CAGCGGATGCGCTTGTGAACAAACGAAAGATCTTAAGATTCAGTGTGCTG 2280
Qy 2281 CCTCCCTCTGATTTCCCGAGCTCATCTCCGTGTTCATGAGCACTTGAAGCTGAGTCT 2340
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Oy		2461	TGTCGAATAAGCTCGACAAACAGCTTGCCAAAATTTGGTAAAGCTTAGATCAAGACTGTG	2520
Db		2461	TGTCGAATAAGCTCGACAAACAGCTTGCCAAAATTTGGTAAAGCTTAGATCAAGACTGTG	2520
Oy		2521	GTCGAGAGGTAGGAGGAAATATGTAAAGAAAAACAGAAAGATACCTGCACTAATCATTTCA	2580
Db		2521	GTCGAGAGGTAGGAGGAAATATGTAAAGAAAAACAGAAAGATACCTGCACTAATCATTTCA	2580
Oy		2581	GACTTCATTAGAGCTCTGCAAACTTGTGCTGTTGGTATATGGCTCAGCTGAATTTGAAATGC	2640
Db		2581	GACTTCATTAGAGCTCTGCAAACTTGTGCTGTTGGTATATGGCTCAGCTGAATTTGAAATGC	2640
Oy		2641	TTTGTGAAAAAAGGACCTTTTAACAATCAATAGCACAGAAATCAAAGTGCAGCTATCTGG	2700
Db		2641	TTTGTGAAAAAAGGACCTTTTAACAATCAATAGCACAGAAATCAAAGTGCAGCTATCTGG	2700
Oy		2701	AATCATGTGTGATATTCGACATPATGTCTCATTTATTTTTGATGTAAATTTACATGCC	2760
Db		2701	AATCATGTGTGATATTCGACATPATGTCTCATTTATTTTTGATGTAAATTTACATGCC	2760
Oy		2761	ATGGGTGTAAATATAAGCTTTGAGTCAAAAGTCAAGAAAGTACAGTAATACATGACCT	2820
Db		2761	ATGGGTGTAAATATAAGCTTTGAGTCAAAAGTCAAGAAAGTACAGTAATACATGACCT	2820
Oy		2821	TTTATGAAATGAAAAAATTT	2880
Db		2821	TTTATGAAATGAAAAAATTT	2880
Oy		2881	CTCGAGGGGCCCCAACGCTTACGCCGATACCAGCTTCTTGTATCAAAATGGTCCCCTATAGTA	2940
Db		2881	CTCGAGGGGCCCCAACGCTTACGCCGATACCAGCTTCTTGTATCAAAATGGTCCCCTATAGTA	2940
Oy		2941	GTCGTATATATAAGCTAGGACACTGGCCGTCGTGTTTACAACTGTCGTAACAGGAAAACTGCT	3000
Db		2941	GTCGTATATATAAGCTAGGACACTGGCCGTCGTGTTTACAACTGTCGTAACAGGAAAACTGCT	3000
Oy		3001	AGCTTGGGATCTTTGTGAGAAGAACCTTACTTCTGTGTGTGACATPATTTGACAAACTAC	3060
Db		3001	AGCTTGGGATCTTTGTGAGAAGAACCTTACTTCTGTGTGTGACATPATTTGACAAACTAC	3060
Oy		3061	CTACAGAGATTTAAAGCTCTAAG 3083	
Db		3061	CTACAGAGATTTAAAGCTCTAAG 3083	

RESULT 2
US-10-216-156-1

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; Sequence 1, Application US/10216156
; Publication No. US20030099980A1
; GENERAL INFORMATION:
; APPLICANT: Jinq, Shuduan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/10/216,156
; PRIORITY FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2235)
; US-10-216-156-1
    
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Db	1	TGGCTGGCGGAGCCGACGAGCCATGAGCCCGGTGGCTGGAGCTCTGCTCGTCTTCTTAACG	60	
Qy	61	GTCAACGCTTGTCTTCAACGCTGTGCGAGCTGTGCGCTGTGGCCGCTGGCCGCGCGC	120	
Db	61	GTCAACGCTTGTCTTCAACGCTGTGCGAGCTGTGCGCTGTGGCCGCTGGCCGCGCGC	120	
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Db	121	TGGGGCGGTGCAACACTGTGTGTGAGAGGGAGATGGGGGCAAGCAGACAGAAACATGGGGCTG	180	
Qy	181	TACAAACATCACTTCAAAATATGACATTTGTATACACTACTTGAATTCAGTGGGAAAGCAT	240	
Db	181	TACAAACATCACTTCAAAATATGACATTTGTATACACTACTTGAATTCAGTGGGAAAGCAT	240	
Qy	241	GTGATTTGCTGACGCCAGATATATCAACATCAGCCAGTATGCTTGCATGACCAAGTGCA	300	
Db	241	GTGATTTGCTGACGCCAGATATATCAACATCAGCCAGTATGCTTGCATGACCAAGTGCA	300	
Qy	301	GTCAACATCTTTTGTGTCCCGAGGGGCGCTCGGACATGCAATTCGCGAAAGATTCGGGTA	360	
Db	301	GTCAACATCTTTTGTGTCCCGAGGGGCGCTCGGACATGCAATTCGCGAAAGATTCGGGTA	360	
Qy	361	ATATCTGAGAGAGCTGAAGTGGAGGAGAAAGACATGAGCCAAACATGATTTCTAAAGATTCG	420	
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Qy	421	AAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAAATGCAACTTTCCTGAATATG	480	
Db	421	AAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAAATGCAACTTTCCTGAATATG	480	
Qy	481	AAATTTGAAAGGATATTTTGTAAAGATGTTCCTTTTCTTGCATTTAAAGAAAGC	540	
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Qy	601	CTAGCTTGTAAACCCCTTCTGGAAGCTCTGGAACCTGGAACATCAGCAGCATGTGCTGGAC	660	
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Qy	661	ATGCAAGTGTCTTGTGACACGACACCGCAACATTCGGCTTCGGTTCTTATCTTCAAC	720	
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Qy	781	GAGACGACACAGCTGCTCTTCAAAATGTTTCTCAAGGGATTTATATATGACTGGTG	840	
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Qy	901	TGGGCGGGGCGCACTCAAGCAATGGCCATCAAGTGCACATGATGATATATGCGGATTC	960	
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Qy 1081 CCGCGGCCGGAAGGCTTTTCTCTCTCTATTCAGTAAAGATGGCCAGATATCATGAATATGTC 1140
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Qy 1861 GGAACCAAGGCTCTGAGAGTGAATTTCTGCTTAAAGATGAGGCGCTGTCTTGGGCAAC 1920
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RESULT 3
 US-10-616-788-1
 ; Sequence 1, Application US/10616788
 ; Publication No. US2004004833B1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jang, Shuglian


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Db      1861  GAGCCGCGGAGCTCCAGACGAGAGTCAAGATGAGGAGGCTGAGACCAAGACGGGAGGCGC 1920
Qy      1921  CGGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
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Db      2101  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
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Qy      2461  TGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
Db      2461  TGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
Qy      2521  GTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
Db      2521  GTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
Qy      2581  GACTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Db      2581  GACTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Qy      2641  TTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
Db      2641  TTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
Qy      2701  AATCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
Db      2701  AATCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
Qy      2761  ATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
Db      2761  ATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
Qy      2821  TTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
Db      2821  TTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
Qy      2881  CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2940

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Db      2881  CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2940
Qy      2941  GTCGATTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
Db      2941  GTCGATTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
Qy      3001  AGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3060
Db      3001  AGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3060
Qy      3061  CTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3083
Db      3061  CTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3083

RESULT 4
US-10-842-006-3
; Sequence 3, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SRF Molecule and Uses
; FILE REFERENCE: MP103-071P1M
; CURRENT APPLICATION NUMBER: US/10/842,006
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)...(2241)
US-10-842-006-3

Query Match      100.0%; Score 3083; DB 8; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Db      1  TGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Qy      61  GTCAACGCGCTGCTCAACGCGCTGCGAGCTGCGTGGCGGCTGCGGCGCGG 120
Db      61  GTCAACGCGCTGCTCAACGCGCTGCGAGCTGCGTGGCGGCTGCGGCGCGG 120
Qy      121  TGGGCGCTGCGACACTGTGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db      121  TGGGCGCTGCGACACTGTGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy      181  TACCAATCACTTCAAAATATGACAAATTGTACCACTTGAATCCAGTGGGAGGAGGAGGAGGAG 240
Db      181  TACCAATCACTTCAAAATATGACAAATTGTACCACTTGAATCCAGTGGGAGGAGGAGGAGGAG 240
Qy      241  GTGATGCTGAGCGCCAGAAATATCAATCAACAGAGTATGCTTGCATGACCAAGTGGCA 300
Db      241  GTGATGCTGAGCGCCAGAAATATCAATCAACAGAGTATGCTTGCATGACCAAGTGGCA 300
Qy      301  GTCAACATTTCTTTGGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db      301  GTCAACATTTCTTTGGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy      361  ATACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db      361  ATACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy      421  AAGCAGCTCAACAGTACGCTTCAAAAGAACTGGAATGAACTTCAACCTTCTGGAATAG 480

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Db 421 AAGCAGCTCAACAGTAGCTTCAAAAGAACTGAAATGGAATCTCACTTTCTGAAATAG 480
Qy 481 AATTGGAACGGATTAATTTCTTAAAGTTGTCTCTTTCTTCAATTAAAAAGAAAGC 540
Db 481 AATTTGGAACGGATTAATTTCTTAAAGTTGTCTCTTTCTTCAATTAAAAAGAAAGC 540
Qy 541 AATTACCACTCTTCTTCTTAAAGCCGAGCTGTGACCTGTGTTTACAGCCGGAAT 600
Db 541 AATTACCACTCTTCTTCTTAAAGCCGAGCTGTGACCTGTGTTTACAGCCGGAAT 600
Qy 601 CTAGCTTGTAAACCTTCTTGAAGCCTCGAACCCTGAACATCAAGCAATGAGCTCGAC 660
Db 601 CTAGCTTGTAAACCTTCTTGAAGCCTCGAACCCTGAACATCAAGCAATGAGCTCGAC 660
Qy 661 ATGCAAGTGTCTTCTTGAACCAAGCAAGCAATTTGGCTTCCGTTCTTCTTATCTTCA 720
Db 661 ATGCAAGTGTCTTCTTGAACCAAGCAAGCAATTTGGCTTCCGTTCTTCTTATCTTCA 720
Qy 721 TACAACTCAAGCAAGCAAGCACTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 780
Db 721 TACAACTCAAGCAAGCAAGCACTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 780
Qy 781 GAGACGACGAGCTGCTCTTCAAAATGTTTCTCAAGGGATTATTAATTAGCTGTG 840
Db 781 GAGACGACGAGCTGCTCTTCAAAATGTTTCTCAAGGGATTATTAATTAGCTGTG 840
Qy 841 GATGACATTAACCAACAAAGAAAGTATGATTAATGCTTAAAGCACTGCTCCG 900
Db 841 GATGACATTAACCAACAAAGAAAGTATGATTAATGCTTAAAGCACTGCTCCG 900
Qy 901 TGGGCGGGGCGGCTGAGGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 960
Db 901 TGGGCGGGGCGGCTGAGGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 960
Qy 961 GCGAGCTCTTCACTGTGATGTCGCGCAAGAAACAAAGAAATATATTTCACTTTA 1020
Db 961 GCGAGCTCTTCACTGTGATGTCGCGCAAGAAACAAAGAAATATATTTCACTTTA 1020
Qy 1021 GATGAAGAGAGCTGTGATGTTTCAATACATGACAGCTCCCAAGAGAGGCTCCG 1080
Db 1021 GATGAAGAGAGCTGTGATGTTTCAATACATGACAGCTCCCAAGAGAGGCTCCG 1080
Qy 1081 CCGCGGCGGAGGCTTCTGCTGATATTCAGTAAAGTGGCCAGATCAATGAATGTC 1140
Db 1081 CCGCGGCGGAGGCTTCTGCTGATATTCAGTAAAGTGGCCAGATCAATGAATGTC 1140
Qy 1141 GTCCAGTGTGTCCTACTTCTCTCAGAGCTTCTGTGCTGTGAGGTGCTGTGACCTG 1200
Db 1141 GTCCAGTGTGTCCTACTTCTCTCAGAGCTTCTGTGCTGTGAGGTGCTGTGACCTG 1200
Qy 1201 TGGGAAGACTTCAAGCTGTGAGAGAGGAGAGAAATGGTCAATCCAGAAATCCAC 1260
Db 1201 TGGGAAGACTTCAAGCTGTGAGAGAGGAGAGAAATGGTCAATCCAGAAATCCAC 1260
Qy 1261 GAGTCCCACTTCAATGTTGTGTTTCTCAAGAGTAAAGTATGTTGTGCAAGAAAG 1320
Db 1261 GAGTCCCACTTCAATGTTGTGTTTCTCAAGAGTAAAGTATGTTGTGCAAGAAAG 1320
Qy 1321 AACTACAAACAAAGAGAGTGGCCGAGGCTCGGAGAAAGAGAGAGCTTCTCTGTGAGG 1380
Db 1321 AACTACAAACAAAGAGAGTGGCCGAGGCTCGGAGAAAGAGAGAGCTTCTCTGTGAGG 1380
Qy 1381 GTGTCAAGCAATGCGGAAAGCTCGGCAAGGCAAGATTCGTCCGCGGCGCTCAAG 1440
Db 1381 GTGTCAAGCAATGCGGAAAGCTCGGCAAGGCAAGATTCGTCCGCGGCGCTCAAG 1440
Qy 1441 AAGTTATAGCCGTCTACTTTGATTAATCTCTGAGAGAGAGAGTCCCCGGTATCTAGAC 1500
Db 1441 AAGTTATAGCCGTCTACTTTGATTAATCTCTGAGAGAGAGAGTCCCCGGTATCTAGAC 1500
Qy 1501 CTGAGTACCAAGAGAGAGCTCATGAGCAATCTTCTCAGCTGTGTTCCCACTGACCTCC 1560
Db 1501 CTGAGTACCAAGAGAGAGCTCATGAGCAATCTTCTCAGCTGTGTTCCCACTGACCTCC 1560

Qy 1561 CGAGACCAAGGCTCCAGAGAGCCGGGAGAGCAACGCGACAGGGGACAGAAAGAACTAC 1620
Db 1561 CGAGACCAAGGCTCCAGAGAGCCGGGAGAGCAACGCGACAGGGGACAGAAAGAACTAC 1620
Qy 1621 TTCGGAGAGAGTCAAGGCGGCTCCCTATAGTTCGCAATTTGCAACATGACAGATTAAT 1680
Db 1621 TTCGGAGAGAGTCAAGGCGGCTCCCTATAGTTCGCAATTTGCAACATGACAGATTAAT 1680
Qy 1681 GACGAGAGCCCGAGCTGTGTTCAAAAGCAATTCCTTCCATCTCTCCACCTGCGC 1740
Db 1681 GACGAGAGCCCGAGCTGTGTTCAAAAGCAATTCCTTCCATCTCTCCACCTGCGC 1740
Qy 1741 TACCGGAGAGCTGTGAGAAATTTGATTTGGCTTGGTTTAAATGATCAATGTC 1800
Db 1741 TACCGGAGAGCTGTGAGAAATTTGATTTGGCTTGGTTTAAATGATCAATGTC 1800
Qy 1801 AAACAGAGGCTGAGAGTGAATTCCTGCTAAAGTGAAGGCGCTCTTCTTGGGCAAC 1860
Db 1801 AAACAGAGGCTGAGAGTGAATTCCTGCTAAAGTGAAGGCGCTCTTCTTGGGCAAC 1860
Qy 1861 GGAACAGGCGGACTCCAGACAGAGTCAAGATGAGGAGCTGAGCAAGAGAGGAGG 1920
Db 1861 GGAACAGGCGGACTCCAGACAGAGTCAAGATGAGGAGCTGAGCAAGAGAGGAGG 1920
Qy 1921 CGGCTGCTGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1980
Db 1921 CGGCTGCTGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1980
Qy 1981 AGCCCTCGGAGATGCGGAGGAGCTGAGGATCTATGATCTGCTGTGCTCATCCGAG 2040
Db 1981 AGCCCTCGGAGATGCGGAGGAGCTGAGGATCTATGATCTGCTGTGCTCATCCGAG 2040
Qy 2041 CTGTCTTCTGCACTGATGAGAGAGCTTGAAGAGCAAGAGAGAGAGAGAGAGAG 2100
Db 2041 CTGTCTTCTGCACTGATGAGAGAGCTTGAAGAGCAAGAGAGAGAGAGAGAGAG 2100
Qy 2101 GAGAGGAGTCTCTCTCTTCAAGGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 GAGAGGAGTCTCTCTCTTCAAGGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Qy 2161 CTCTCTCTTCTGAGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 CTCTCTCTTCTGAGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Qy 2221 CAGCGGAGTCCCTTCTTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Db 2221 CAGCGGAGTCCCTTCTTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Qy 2281 CCTCCTCTGATTTCCCAAGCTCATCTCCTGTGAGTGGCCCACTTGAAGTCT 2340
Db 2281 CCTCCTCTGATTTCCCAAGCTCATCTCCTGTGAGTGGCCCACTTGAAGTCT 2340
Qy 2341 CATPACAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Db 2341 CATPACAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Qy 2401 TTAACGAGATCTTGAAGAACTCCCAATTTCTAAATGATGAGAGCTGAAAGGCA 2460
Db 2401 TTAACGAGATCTTGAAGAACTCCCAATTTCTAAATGATGAGAGCTGAAAGGCA 2460
Qy 2461 TGTCAATAGGTTCTGACAAAGCTTGCAGAAATTTGGTTAGTCTTGAATCAAGCTGTT 2520
Db 2461 TGTCAATAGGTTCTGACAAAGCTTGCAGAAATTTGGTTAGTCTTGAATCAAGCTGTT 2520
Qy 2521 GTGGAGAGTAAAGGAGAAATATGTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2580
Db 2521 GTGGAGAGTAAAGGAGAAATATGTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2580
Qy 2581 GACTTCATTTGAGCTGCAAGCTTGTGCTGTTGCTATTTGCTGATTTGAAATTC 2640
Db 2581 GACTTCATTTGAGCTGCAAGCTTGTGCTGTTGCTATTTGCTGATTTGAAATTC 2640

QY 2641 TTTGTGAAAAAGGCACTTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGG 2700
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Db 2641 TTTGTGAAAAAGGCACTTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGG 2700
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QY 2701 AATCCATGTTGTAATTCAGATTAATGTTCTCATTTATTTTGAATGAAATTTACATTGCC 2760
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Db 2701 AATCCATGTTGTAATTCAGATTAATGTTCTCATTTATTTTGAATGAAATTTACATTGCC 2760
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|
QY 2761 ATGGGGTTTAAATAGCTTTGAGTCAAAAGTCAAGAAAGTGAATATATAGAGTACCT 2820
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Db 2761 ATGGGGTTTAAATAGCTTTGAGTCAAAAGTCAAGAAAGTGAATATATAGAGTACCT 2820
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QY 2821 TTTATGAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAA 2880
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Db 2821 TTTATGAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAA 2880
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QY 2881 CTCGAGGGGCCCAAGCTTACGCGTACCGCTTTCTTTGACAAAGTGTCTCTATAGTGA 2940
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|
Db 2881 CTCGAGGGGCCCAAGCTTACGCGTACCGCTTTCTTTGACAAAGTGTCTCTATAGTGA 2940
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|
QY 2941 GTCGTATTTAATAGCTAGGCACTGGCCGTGTTTAAACAGTCTGATCTGGAAAACTGCT 3000
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|
|
Db 2941 GTCGTATTTAATAGCTAGGCACTGGCCGTGTTTAAACAGTCTGATCTGGAAAACTGCT 3000
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|
QY 3001 AGCTTGGGATCTTTGTGAAGAACTTACTTCTGTGGTGTGACATATTTGACAAACTAC 3060
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|
Db 3001 AGCTTGGGATCTTTGTGAAGAACTTACTTCTGTGGTGTGACATATTTGACAAACTAC 3060
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|
QY 3061 CTACAGAGATTTAAAGCTCTTAAG 3083
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Db 3061 CTACAGAGATTTAAAGCTCTTAAG 3083
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RESULT 5
US-10-842-006-1
; Sequence 1, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SER Molecule and Uses
; FILE OF INVENTION: Therefore
; FILE REFERENCE: MP103-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842, 006
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90) ... (2309)
US-10-842-006-1

Query Match 91.5%; Score 2822.4; DB 8; Length 4477;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2826; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TGGCTGGGGAGGAGGCAAGGCAATGAGCCGCTGGCTGAGCTGCTCCGCTCTTTAGG 60
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Db 69 TGGCTGGGGAGGAGGCAAGGCAATGAGCCGCTGGCTGAGCTGCTCCGCTCTTTAGG 128
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|
|
QY 61 GTCAAGCCTGCTCAACGGCTGCGACAGTGTGTGGCCGTGGCGGGTCCGGCCGGCG 120
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|
|
|
Db 129 GTCAAGCCTGCTCAACGGCTGCGACAGTGTGTGGCCGTGGCGGGTCCGGCCGGCG 188
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|
|
QY 121 TGGGAGCTGACACCTGTGGCTGGAGGGAGTGGGGCCAGCCAGCAAGAAACAGTGGGCTG 180
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|
Db 189 CCGGAGCGGACACCTGTGGCTGGAGGGAGTGGGGCCAGCCAGCAAGAAACAGTGGGCTG 248
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QY 181 TACAACATCATCTTCAAAATATGACAATTGTACACCTACTTGAATTCAGTGGGAGACAT 240
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|
Db 249 TACAACATCATCTTCAAAATATGACAATTGTACACCTACTTGAATTCAGTGGGAGACAT 308
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|
|
QY 241 GTGATTTGTCGAGCCCGAAGATATCACCATCAGCCAGTATGCTTGGCATGACAGTGGCA 300
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|
Db 309 GTGATTTGTCGAGCCCGAAGATATCACCATCAGCCAGTATGCTTGGCATGACAGTGGCA 368
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|
|
QY 301 GTACACATCTTTGGCCCCCAGGGGCCCTGGCATCGAATTCCTGAAAGATTTGGGGTA 360
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|
|
Db 369 GTACACATCTTTGGCCCCCAGGGGCCCTGGCATCGAATTCCTGAAAGATTTGGGGTA 428
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|
QY 361 ATACTGAGAGACTGAGTGTGAGGAGAGACAGTGCACAACTGATTTCTAAAGATCCG 420
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Db 429 ATACTGAGAGACTGAGTGTGAGGAGAGACAGTGCACAACTGATTTCTAAAGATCCG 488
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QY 421 AAGCAGCTCAACAGTAGTCTTCAAAAGAACTGGAATGGAATCTCAACTTTCTGAATATG 480
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|
Db 489 AAGCAGCTCAACAGTAGTCTTCAAAAGAACTGGAATGGAATCTCAACTTTCTGAATATG 548
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QY 481 AATTTGAAAAGGATTAATTTGTTAAAGTGTCCCTTTCTTCAATTAAGAAACGAAAGC 540
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Db 549 AATTTGAAAAGGATTAATTTGTTAAAGTGTCCCTTTCTTCAATTAAGAAACGAAAGC 608
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QY 541 AATTACCACTTTCTTCTTTGAAACCCGAGCCTGTGACCTGTGTTACAGCCGGACAAT 600
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Db 609 AATTACCACTTTCTTCTTTGAAACCCGAGCCTGTGACCTGTGTTACAGCCGGACAAT 668
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QY 601 CTAGCTTGTAAACCTTTCTGAAAGCTTGGAACTGGAACATGACGCAAGATGGCTGGAC 660
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Db 669 CTAGCTTGTAAACCTTTCTGAAAGCTTGGAACTGGAACATGACGCAAGATGGCTGGAC 728
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QY 661 ATGCAAGTGTCTCTTGAACAGAGCAAGCAAACTTCCGCTTCCTTCAATCTCAC 720
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Db 729 ATGCAAGTGTCTCTTGAACAGAGCAAGCAAACTTCCGCTTCCTTCAATCTCAC 788
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|
QY 721 TACAAGCTCAACAGAAAGAACTTTCAAGCGAAAGACCTGTGAAGAGAGAACTACA 780
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Db 789 TACAAGCTCAACAGAAAGAACTTTCAAGCGAAAGACCTGTGAAGAGAGAACTACA 848
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|
QY 781 GAGACGACCAAGTGTCTCTTCAAAATGTTTCTCAAGGGAGATTATTAATGAGCTGTG 840
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Db 849 GAGACGACCAAGTGTCTCTTCAAAATGTTTCTCAAGGGAGATTATTAATGAGCTGTG 908
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QY 841 GATGACACTAACAACAAGAAAGTATGATTAATGCTTTAAAGCAGTGAACCTCCCG 900
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Db 909 GATGACACTAACAACAAGAAAGTATGATTAATGCTTTAAAGCAGTGAACCTCCCG 968
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QY 901 TGGGCGGGCCCATGAGAGCCATGAGCCATCAGATGCGCACTGGTAGTCATATCGGCATTG 960
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|
Db 969 TGGGCGGGCCCATGAGAGCCATGAGCCATCAGATGCGCACTGGTAGTCATATCGGCATTG 1028
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|
QY 961 GCGAGCTCTTTCATGTGTATGTGCGCAAGAAACAAGAAATATATATTTCAATTTA 1020
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|
|
Db 1029 GCGAGCTCTTTCATGTGTATGTGCGCAAGAAACAAGAAATATATATTTCAATTTA 1088
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|
QY 1021 GATGAAGAGAGCTGTGAGTCTTCCACATACATGACAGCACTCCCAAGAGAGGCTCCGG 1080
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|
|
|
Db 1089 GATGAAGAGAGCTGTGAGTCTTCCACATACATGACAGCACTCCCAAGAGAGGCTCCGG 1148
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|
QY 1081 CCGGAGCGAAGGTCTTTCTGTGCTATTTCAAGTAAGATGSCCAAAATCAATGATATGTC 1140
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|
Db 1149 CCGGAGCGAAGGTCTTTCTGTGCTATTTCAAGTAAGATGSCCAAAATCAATGATATGTC 1208
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|
|
QY 1141 GTCAAGTGTGCTTCTCTCTCCAGACTTCTGTGTGAGTGTGCTGTGACCTG 1200
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|
|
Db 1209 GTCAAGTGTGCTTCTCTCTCCAGACTTCTGTGTGAGTGTGCTGTGACCTG 1268
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|
QY 1201 TGGGAAAGACTTACGCTCTGTGTGAAGAGGAGAGAAATGGGTATTCAGAAAGATCCAC 1260
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|
|
Db 1269 TGGGAAAGACTTACGCTCTGTGTGAAGAGGAGAGAAATGGGTATTCAGAAAGATCCAC 1328
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|
QY 1261 GAGTCCACAGTTATCATGTGTGTGTTCCAAAGGATATGAATGATCTTTGTGACAAAGAG 1320
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Db 1329 GAGTCCAGTTCAATTTGGTGTTCAGAAAGTATGAAAGTACTTTGGACAGAGAG 1388
Qy 1321 AACTTACAAACAAAGAGGTGGCCGAGGCTCGGGAAAGAGAGCTCTTCTGTGGCG 1380
Db 1389 AACTTACAAACAAAGAGGTGGCCGAGGCTCGGGAAAGAGAGCTCTTCTGTGGCG 1448
Qy 1381 GGTTCAGGCAATTCGGGAAAGCTCCGACAGAGAGTGTTCGGGGGCTCAGC 1440
Db 1449 GTGTCAAGCAATTCGAAAGGCTCCGACAGGCAAGAGTGTTCGGGGGCTCAGC 1508
Qy 1441 AAGTTTATGCGCCCTTACTTGTATTTCTCGAGAGAGAGCTCCCGGTATCTAGAC 1500
Db 1509 AAGTTTATGCGCCCTTACTTGTATTTCTCGAGAGAGAGCTCCCGGTATCTAGAC 1568
Qy 1501 CTGAGTACCAAGTACAGACTCATAGCAATCTTCTCAAGCTGTTCCTCAGCTCC 1560
Db 1569 CTGAGTACCAAGTACAGACTCATAGCAATCTTCTCAAGCTGTTCCTCAGCTCC 1628
Qy 1561 CGAGACACAGGCTTCCAGAGAGCCGGGGGACACACGAGAGAGGACAGAAAGTAC 1620
Db 1629 CGAGACACAGGCTTCCAGAGAGCCGGGGGACACACGAGAGAGGACAGAAAGTAC 1688
Qy 1621 TTCGAGAGCAAGTACAGGCGGCTCCCTATAGCTGCGCAATTTGCAACATGACAGTTAT 1680
Db 1689 TTCGAGAGCAAGTACAGGCGGCTCCCTATAGCTGCGCAATTTGCAACATGACAGTTAT 1748
Qy 1681 GACGAGAGGCGGCTGCTTGAAGAAAGCAAGTTCCTTCCTTCAGCTCCCTCAGCTCCG 1740
Db 1749 GACGAGAGGCGGCTGCTTGAAGAAAGCAAGTTCCTTCCTTCAGCTCCCTCAGCTCCG 1808
Qy 1741 TACCGGAGGCTGCTTGAAGAAATTTGATTCGGGCTGTGTTTAAATGATGATGTC 1800
Db 1809 TACCGGAGGCTGCTTGAAGAAATTTGATTCGGGCTGTGTTTAAATGATGATGTC 1868
Qy 1801 AAACCAAGGCTGAGAGTGAATCTTCCGCTTAAAGTAAAGGCGGCTGTTCTTGGGGCAAC 1860
Db 1869 AAACCAAGGCTGAGAGTGAATCTTCCGCTTAAAGTAAAGGCGGCTGTTCTTGGGGCAAC 1928
Qy 1861 GGAACAGGCGGCTCCAGACAGAGTACAGATGGGGGCTTGAACCAAGCGGGAGGCC 1920
Db 1929 GGAACAGGCGGCTCCAGACAGAGTACAGATGGGGGCTTGAACCAAGCGGGAGGCC 1988
Qy 1921 CGGCTGCTTGAAGGCTGAGGCGGCGGCTTGAACCTCTGCTGCAACAGGTTGAAGCGGC 1980
Db 1989 CGGCTGCTTGAAGGCTGAGGCGGCGGCTTGAACCTCTGCTGCAACAGGTTGAAGCGGC 2048
Qy 1981 AGCCCTCGGACATGCGGGGGAATGAGGATCTATGACTGCTGCTGCTCATCCGAG 2040
Db 2049 AGCCCTCGGACATGCGGGGGAATGAGGATCTATGACTGCTGCTGCTCATCCGAG 2108
Qy 2041 CTGTCTCTGCACTGATGAAAGATCTCGACCGGACAGACAGAAAGTCTTCCCTGACG 2100
Db 2109 CTGTCTCTGCACTGATGAAAGATCTCGACCGGACAGACAGAAAGTCTTCCCTGACG 2168
Qy 2101 GAGAGGCTGCTCTCTTCAAGGCTGTGAGAGAGAACTTCTGCTTCTTCCAG 2160
Db 2169 GAGAGGCTGCTCTCTTCAAGGCTGTGAGAGAGAACTTCTGCTTCTTCCAG 2228
Qy 2161 CTCTCTCTTCTGAGGATGCAAGAGAGATCTGTGTCGCGGACATGATGATGATG 2220
Db 2229 CTCTCTCTTCTGAGGATGCAAGAGAGATCTGTGTCGCGGACATGATGATGATG 2288
Qy 2221 CAGCGGCTGCGCCCTTGTAAACAAAGAGTCTAAGACTTGCACATTTAGCTGCTG 2280
Db 2289 CAGCGGCTGCGCCCTTGTAAACAAAGAGTCTAAGACTTGCACATTTAGCTGCTG 2348
Qy 2281 CTCTCTCTGATTTCCCAAGCTCATCTCTGTGTTGATGAGCCCATTTGAGCTGAGCT 2340
Db 2349 CTCTCTCTGATTTCCCAAGCTCATCTCTGTGTTGATGAGCCCATTTGAGCTGAGCT 2408
Qy 2341 CATACAGAGTATTTGAGAGTAAATGCTGCGAGTACTTGTCTCCCTTCCCAACCT 2400

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Db 2409 CATACAGAGTATTTGAGAGTAAATGCTGCGAGTACTTGTCTCCCTTCCCAACCT 2468
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Db 2469 TTACCGGATATCTTGAACAACTCTCCAAATTTCTTAAATGATATGAGCTCTGAAAGCA 2528
Qy 2461 TGTCCATTAAGTCTGCAACAGCTTGCAGAAATTTGGTATGCTTGTGATCAGAGCTGT 2520
Db 2529 TGTCCATTAAGTCTGCAACAGCTTGCAGAAATTTGGTATGCTTGTGATCAGAGCTGT 2588
Qy 2521 GTGGAGGATGAGGAGAAATATGTAAAGAAAAACAGAAAGATCTGCACTAATCATTC 2580
Db 2589 GTGGAGGATGAGGAGAAATATGTAAAGAAAAACAGAAAGATCTGCACTAATCATTC 2648
Qy 2581 GACTTATTAAGCTCTGCAACCTTTGCTGTTTGTGATTTGGCTAATTTGAATGTC 2640
Db 2649 GACTTATTAAGCTCTGCAACCTTTGCTGTTTGTGATTTGGCTAATTTGAATGTC 2708
Qy 2641 TTTTGAAGAAAGGCACTTTTAAATCATATAGGCAAGAAATCAAGTCCAGTATCTGG 2700
Db 2709 TTTTGAAGAAAGGCACTTTTAAATCATATAGGCAAGAAATCAAGTCCAGTATCTGG 2768
Qy 2701 AATCCATGTTGATTCAGATATATGTTCTCATTTATTTTGAATGAAATTTACATTTGCC 2760
Db 2769 AATCCATGTTGATTCAGATATATGTTCTCATTTATTTTGAATGAAATTTACATTTGCC 2828
Qy 2761 ATGGGTTTAATTAAGCTTTGAGTCAAAAGTCAAGAAAGTACTGAATATACATCACT 2820
Db 2829 ATGGGTTTAATTAAGCTTTGAGTCAAAAGTCAAGAAAGTACTGAATATACATCACT 2888
Qy 2821 TTTTGAAGTGA 2832
Db 2889 TTTTGAAGTGA 2900

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RESULT 6
US-10-608-449-1
; Sequence 1, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: 12003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-608-449-1

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Query Match      91.5%; Score 2822.4; DB 8; Length 4477;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2826; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGGCTGGGAGGAGCGACGCGCAATGGCCCGGTGGCTGCACTGTCTCTCTTTTACG 60
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Qy 61 GTCAAGCTGCTCTCAACGCGCTGCGAGCTGTGTGTGGCGGCTGCGCGCGCGG 120
Db 129 GTCAAGCTGCTCTCAACGCGCTGCGAGCTGTGTGTGGCGGCTGCGCGCGCGG 188
Qy 121 TGGGCGGTGAGACCTGTGTGTGGAGGGAGTGGGGGCGAGCAGAGAAAGTGGGCTG 180
Db 189 CGGGGCGCGAGCACTGTGTGTGGAGGGAGTGGGGGCGAGCAGAGAAAGTGGGCTG 248
Qy 181 TACAACATCACTTCAATATATGCAATTTGATCACTTCACTTGAATTCAGTGGGAGAT 240
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QY 241 GTGATGTCGACGCCAGATATACCATCAGCCAGTATGCTTGCATGACCAAGTGGCA 300
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 Db 309 GTGATGTCGACGCCAGATATACCATCAGCCAGTATGCTTGCATGACCAAGTGGCA 368
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 QY 301 GTGACCAATCTTTGTGTCCCAAGGGGCTCTGGCATGGAATTCCTGAAGGATTTCCGGTA 360
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 Db 369 GTCAACAATCTTTGTGTCCCAAGGGGCTCTGGCATGGAATTCCTGAAGGATTTCCGGTA 428
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 QY 361 ATACTGAGAGCTGAAGTGGAGGGAAGACAGTGCACAACTGAATCTTCAAGAGATCCG 420
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 Db 429 ATACTGAGAGCTGAAGTGGAGGGAAGACAGTGCACAACTGAATCTTCAAGAGATCCG 488
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 QY 421 AAGCACTCAACAGTATGCTTCAAAAGAACGTGAATGGAATCTCACTTCTCTGAATATG 480
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 QY 481 AAATTTGAAACGGATTAATTTCTGAAGGTTGCTCTTTCTCTTCATTAAAAAGAAAGC 540
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 Db 549 AAATTTGAAACGGATTAATTTCTGAAGGTTGCTCTTTCTCTTCATTAAAAAGAAAGC 608
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 QY 541 AATTACACACCTTCTTCTTTAGAACCCGAGCCTGTGACCTGTGTTACAGCCGGAACAT 600
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 Db 909 GATGACACTPAACAAACAAAGAAAGTATGATTAATGCTTAAAGCAGTGCATCCCG 968
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 Db 1209 GTCCAGTGTTCGCTACTTCTCTCAGGACTTCTGTGCTGTGAGGTGCTCTGACCTG 1268
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 Db 1509 AAGTTATGCGCGTCACTTTGATTAATTCCTGAGAGGAGAGTCCCGGTATCTTAGAC 1568
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 Db 1569 CTGAGTACCAAGTACAGACTCATGACAAATCTTCTCACTCTGTGTTCCACTGCACTCC 1628
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 Db 1629 CGAGACACAGGCTCCAGAGAGCCGGGCGAGCACAGCCACAGGGCGAGAGAACTAC 1688
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 QY 1621 TTCGGAGCAAGTCAAGGCGGTCCTTATPAGTTCGCAATTTGCAACATGACCAAGTTATT 1680
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 Db 1689 TTCGGAGCAAGTCAAGGCGGTCCTTATPAGTTCGCAATTTGCAACATGACCAAGTTATT 1748
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 QY 1681 GACAGAGAGCCCGACTGTGTGAAAAAGCATGTTCCTTCATCTTCCTCACTGCGC 1740
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 QY 1741 TACCGGAGCCAGCTTGTGAGAAATTTGATTCGGGCTTGGTTTAAATGATCATATGTC 1800
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 Db 1809 TACCGGAGCCAGCTTGTGAGAAATTTGATTCGGGCTTGGTTTAAATGATCATATGTC 1868
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 QY 1801 AAACCAAGGCTGAGAGTGAATCTTGCCCTTAAAGTATGAGAGCCTGTGTTCTTGGGCAAC 1860
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 Db 1869 AAACCAAGGCTGAGAGTGAATCTTGCCCTTAAAGTATGAGAGCCTGTGTTCTTGGGCAAC 1928
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 QY 1861 GAGACAGCCGACTCCCAAGACAGAGTGCAGCATGAGGAGGCTGTGACCAAGACGGAGAGGCC 1920
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 Db 1929 GAGACAGCCGACTCCCAAGACAGAGTGCAGCATGAGGAGGCTGTGACCAAGACGGAGAGGCC 1988
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 QY 1921 CGGCTCGCCCTTGAGGATGAGCGTACCGCCGCTGCAACCCCTGTGCAACAGGATGAAGCCGCG 1980
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 Db 1989 CGGCTCGCCCTTGAGGATGAGCGTACCGCCGCTGCAACCCCTGTGCAACAGGATGAAGCCGCG 2048
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 QY 1981 AGCCCTCGGACATGCGCGGAGCTCAAGCATCTATGACTGCTGTGCTCATCCGAG 2040
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 Db 2049 AGCCCTCGGACATGCGCGGAGCTCAAGCATCTATGACTGCTGTGCTCATCCGAG 2108
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 QY 2041 CTGTCTTGCACATGAGAGAGACTCTGACGAGACAGACAGAAACGTCTTCCCTGACG 2100
 |||||
 Db 2109 CTGTCTTGCACATGAGAGAGACTCTGACGAGACAGACAGAAACGTCTTCCCTGACG 2168
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 QY 2101 GAGAGCGTGTCTCTCTTCAAGGCTGGGTGAGAGAACTCTCGCTTCTTCCAG 2160
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 Db 2169 GAGAGCGTGTCTCTCTTCAAGGCTGGGTGAGAGAACTCTCGCTTCTTCCAG 2228
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 QY 2161 CTCTCTCTTCTGAGGATGCAAGACAGATCTTGTGTCGCGAGCTACATGATACTC 2220
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 Db 2229 CTCTCTCTTCTGAGGATGCAAGACAGATCTTGTGTCGCGAGCTACATGATACTC 2288
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 QY 2221 CACGGGTGCGCCCTTTGTAAACAAACGAAAGAGTCTAAGACTTGCACTTTAGTGTCTG 2280
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 Db 2289 CACGGGTGCGCCCTTTGTAAACAAACGAAAGAGTCTAAGACTTGCACTTTAGTGTCTG 2348
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 QY 2281 CTTCCCTCTGATTTCCCGAGCTATCTCCGTGTGATGAGCCCACTTGAAGTGAAGTCT 2340
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 Db 2349 CTTCCCTCTGATTTCCCGAGCTATCTCCGTGTGATGAGCCCACTTGAAGTGAAGTCT 2408
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 QY 2341 CATACAGGATTAATTTGAGTGAATGCTGGCAGATCTTGTCTCTGCGCCCAACCT 2400
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 Db 2409 CATACAGGATTAATTTGAGTGAATGCTGGCAGATCTTGTCTCTGCGCCCAACCT 2468
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 QY 2401 TTACCGATATCTTGAACAACTCTCAATTTCTTAAATGATGAGACTTGAAGGCA 2460
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Db 2469 TTACGGATATCTTGAACAACCTCTCCAAATTTCTAAATATATGAGCTCTGAAGGCA 2528
Qy 2461 TGTCCATAAGGTGTGACACAGCTTGGCAATTTGGTATGCTTGGATGAGAGCTGTT 2520
Db 2529 TGTCCATAAGGTGTGACACAGCTTGGCAATTTGGTATGCTTGGATGAGAGCTGTT 2588
Qy 2521 GTGGGAGTATGAGGAAATATGTAAAGAAAACAGGAATATACCTGCACTAATCAATTC 2580
Db 2589 GTGGGAGTATGAGGAAATATGTAAAGAAAACAGGAATATACCTGCACTAATCAATTC 2648
Qy 2581 GACTTCATGAGCTCTGCAAACTTTGCTGTTGTATGCTATGCTTGAATTTGAATGC 2640
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Qy 2641 TTTTGAAAAAAGGCACTTTTAACATCATATGCAAGAAATCAAGTCCAGTCTATCTGG 2700
Db 2709 TTTTGAAAAAAGGCACTTTTAACATCATATGCAAGAAATCAAGTCCAGTCTATCTGG 2768
Qy 2701 AATCCATGTTGTATGCAAGTATATGTTCTCATTTATTTTGTAGTGAATTTACATTTGCC 2760
Db 2769 AATCCATGTTGTATGCAAGTATATGTTCTCATTTATTTTGTAGTGAATTTACATTTGCC 2828
Qy 2761 ATGGGTGTTAAATAGCTTTGAGTCAAAAGTCAAGAAAGTACTGAATATACAGTCACT 2820
Db 2829 ATGGGTGTTAAATAGCTTTGAGTCAAAAGTCAAGAAAGTACTGAATATACAGTCACT 2888
Qy 2821 TTTATGAATGA 2832
Db 2889 TTTATGAATGA 2900

RESULT 7
US-10-343-348-15
; Sequence 15, Application US/10343348
; Publication No. US20040038242A1
; GENERAL INFORMATION:
; APPLICANT: Edmonds, Brian
; APPLICANT: Micanovic, Radmila
; APPLICANT: Ou, Weijia
; APPLICANT: Su, Eric
; APPLICANT: Techang, Sheng-Hung
; APPLICANT: Wang, He
; TITLE OF INVENTION: No. US20040038242A1 secreted proteins and their uses
; FILE REFERENCE: X-14001
; CURRENT APPLICATION NUMBER: US/10/343,348
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 4392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1662)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (82)..()
; OTHER INFORMATION:
; US-10-343-348-15

Query Match 89.4%; Score 2757.4; DB 7; Length 4392;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2805; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

Qy 22 ATGGCCCGGTGCTGACGCTCTGCTCTTCTTTACGGTCAACGCTGCTCAACGCG 81
Db 1 ATGGCCCGGTGCTGACGCTCTGCTCTTCTTTACGGTCAACGCTGCTCAACGCG 60
Qy 82 TCGCAGCTGCTGCGCTGCGGAGGTTCGCGCGCGCGCGTGGGAGCGTCAACCTGTCG 141
Db 61 TCGCAGCTGCTGCGCTGCGGAGGTTCGCGCGCGCGCGTGGGAGCGTCAACCTGTCG 120

Qy 142 TGAAGGAGATGGGGCCAGCCAGAGAAACAGTGGCTGTACACATCACTTCAATAT 201
Db 121 TGAAGGAGATGGGGCCAGCCAGAGAAACAGTGGCTGTACACATCACTTCAATAT 180
Qy 202 GACAAATTTGACCACTCACTTGAATCCAGTGGGGAAGCATGTGTATGCTGACGCCAGAA 261
Db 181 GACAAATTTGACCACTCACTTGAATCCAGTGGGGAAGCATGTGTATGCTGACGCCAGAA 240
Qy 262 ATCCATGACGCGATGATCTTGCATGACCAAGTGGAGTCCATCTTTGCTCCCA 321
Db 241 ATCCATGACGCGATGATCTTGCATGACCAAGTGGAGTCCATCTTTGCTCCCA 300
Qy 322 GGGGCGCTGCGATCGAATTTCTGAAAGATTTGGGTAAATCTGAGAGAGCTGAAGTGC 381
Db 301 GGGGCGCTGCGATCGAATTTCTGAAAGATTTGGGTAAATCTGAGAGAGCTGAAGTGC 360
Qy 382 GAGGGAAGACAGTGCACACATGATTTTAAAGATCCGAAAGCTCAACAGTACTTC 441
Db 361 GAGGGAAGACAGTGCACACATGATTTTAAAGATCCGAAAGCTCAACAGTACTTC 420
Qy 442 AAAAGAACTGGAATGGAATCTCAACCTTTCTGAATATGAATTTGAAACGATTAATTC 501
Db 421 AAAAGAACTGGAATGGAATCTCAACCTTTCTGAATATGAATTTGAAACGATTAATTC 480
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Db 481 GTTAAAGTGTGCTTCTTCTTCTTCAATTAAGAAAGCAATTAACCTTCTCTT 540
Qy 562 AGAACCAGAGCTGTGACCTGTTGTTACAGCGGAGCAATCTAGCTTGAACCTTCTGC 621
Db 541 AGAACCAGAGCTGTGACCTGTTGTTACAGCGGAGCAATCTAGCTTGAACCTTCTGC 600
Qy 622 AAGCTTGGAACCTGTAACATGACAGCAATGCTGGAATGAGTCTTTCACAC 681
Db 601 AAGCTTGGAACCTGTAACATGACAGCAATGCTGGAATGAGTCTTTCACAC 660
Qy 682 GCAACGCAACCTTCCGCTTCCGTTCTTCTTCAATTAAGCAAGTCAAGCAAGAA 741
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1441 GATTATTCCTGCGAGGAGAGAGTCCCGGTATCTTAGAGCTGAGTACCAAGTACAGACTC 1500
1522 ATGGAAGATC-TTCCCTCAGCTCTGTCCGAC-CTGACCTCCGAGACAGCGGCTCAAG 1579
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1561 AGCGGCGGCA-GCAGACGCGCAGAGGCA-GCAGAAAGAACTACTTCGCGAGCAAGTCAAG 1620
1638 CCGGTCTCTATAGTGGGCACTTTGCAACATGACCAAGTTTATGACGAGAGCCGCACTG 1697
1621 CCGGTCTCTATAGTGGGCACTTTGCAACATGACCAAGTTTATGACGAGGCCAGCTG 1680
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1681 GTTGTGAAAGAGATGTTCCCTTCATCTCTGCACTGCGGCTTACCGGAGCAATCTT 1740
1758 GGAGAAATTTGATTCGGGCTTGTGTTTAAATGATGATGATGCAATGCAAGAGGCTGAGAG 1817
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1861 GCAAGGAGATCAGCAATGGGGGCTGAGACCAAGACGGGAGGCGGCGCTGCTTGAACG 1920
1938 TAGCGCGGCTGCAACCCCTGCTGCAACAGGTGAAGCGGAGCGGCTCGGACATGCG 1997
1921 TAGCGCGGCTGCAACCCCTGCTGCAACAGGTGAAGCGGAGCGGCTCGGACATGCG 1980
1998 GCGGGACTGAGGATATGATCTGCTGTGCTGCTCATTCGAGCTGTCTTTCGCACTGAT 2057
1981 GCGGGACTGAGGATATGATCTGCTGTGCTGCTCATTCGAGCTGTCTTTCGCACTGAT 2040
2058 GGAAGAGATCTGACGAGACCAAGACAGAAAGTCTTCCCTGACGAGAGAGGTCTCTCTC 2117
2041 GGAAGAGATCTGACGAGACCAAGACAGAAAGTCTTCCCTGACGAGAGAGGTCTCTCTC 2100
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2101 TTCAAGGCTGTGGGAGAGAGAGCTCTGCTGCTTCTTCCCAAGCTCTCTCTTCTGGGTC 2160
2178 ATGCAAGAGATCTTGTGTTGCGGACGTAACATGTAATCTCAGCGGTGCGCCCTT 2237
2161 ATGCAAGAGATCTTGTGTTGCGGACGTAACATGTAATCTCAGCGGTGCGCCCTT 2220
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2221 GTTAAAGAAAGAAAGTCTTAAAGATTCGACTTTTAACTGTGCTGCTCTCTGATTTCCC 2280
2298 AGCTATCTCCCTGTGTGATGGCCCACTTGAAGTGAAGTCTCAACAAGATATTGG 2357

2281 AGCTATCTCCCTGTGTGATGGCCCACTTGAAGTGAAGTCTCAACAAGATATTGG 2340
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2401 AAACCTCCAAATTTCTTAAATGATATGAGAGTCTGAAAGGAGATGCTCAATAGTCTGAC 2460
2478 AACAGCTTGCAGAAATTTGTTAGTCTTGGATCAAGCTGTGTTGGAGGATAGGAGGA 2537
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2718 AATATGTTCTCATTTATTTTGAATGATGAAATTTTACATGCTGAGTGTGTAATAGC 2777
2701 AATATGTTCTCATTTATTTTGAATGATGAAATTTTACATGCTGAGTGTGTAATAGC 2760
2778 TTTGAGTCAAGAGTCAAGAAAGTGAATGAATATGACGCTTATTAAGAAATGA 2832
2761 TTTGAGTCAAGAGTCAAGAAAGTGAATGAATATGACGCTTATTAAGAAATGA 2815

RESULT 8
US-09-863-818A-9
Sequence 9, Application US/09863818A
Publication No. US20030092881A1
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01170K
CURRENT APPLICATION NUMBER: US/09/863,818A
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,862
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 2786
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (70)..(2283)
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: (118)..()
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (8)..(8)
OTHER INFORMATION: unknown amino
NAME/KEY: misc_feature
LOCATION: (144)..(144)
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NAME/KEY: misc_feature
LOCATION: (170)..(170)
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NAME/KEY: misc_feature
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NAME/KEY: misc feature
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LOCATION: (519) ..(519)
OTHER INFORMATION: unknown amino
US-09-863-818A-9

Query Match 87.5%; Score 2696.6; DB 3; Length 2786;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2718; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

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QY 61 GTCAAGCGCTGCTTCAAGCGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB GTCAAGCGCTGCTTCAAGCGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 168
QY 121 TGGGCGGTGAGCACTGCTGCTGAGGGGAGTGGGGCGAGCGAGCAAGAACTGAGGCTG 180
DB CAGGGCGCGAGCACTGCTGCTGAGGGGAGTGGGGCGAGCGAGCAAGAACTGAGGCTG 228
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RESULT 9

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US-10-749-144-9
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; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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Query Match      87.5%; Score 2696.6; DB 8; Length 2786;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2718; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

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Db      1306 GAGTCCAGATTCATATGTTGTTTGTCCAAAGGATGAGATGATCTTTGGACATGAAG 1365
Qy      1321 AACTACAAACAAAGAGAGGTGCGAGGCTCGGAGAAAGAGAGAGCTCTTCTGTGAGG 1380
Db      1366 AACTACAAACAAAGAGAGGTGCGAGGCTCGGAGAAAGAGAGAGCTCTTCTGTGAGG 1425
Qy      1381 GTGTGAGCAATGTCGCAAAAGCTCCGCGAGGCGACAGAGATTCGTCCGCGGCTCAGC 1440
Db      1426 GTGTGAGCAATGTCGCAAAAGCTCCGCGAGGCGACAGAGATTCGTCCGCGGCTCAGC 1485
Qy      1441 AAGTTATGCGCGTCACTTTGATTAATTCCTGCGAGGAGAGAGCTCCCGGTATCCTAGAC 1500
Db      1486 AAGTTATGCGCGTCACTTTGATTAATTCCTGCGAGGAGAGAGCTCCCGGTATCCTAGAC 1545
Qy      1501 CTGAGTACCAAGTACAGACTGACATGACAAATCTCTCAGCTGTCTCCACCTGCACCTCC 1560
Db      1546 CTGAGTACCAAGTACAGACTGACATGACAAATCTCTCAGCTGTCTCCACCTGCACCTCC 1605
Qy      1561 CGAGACCAAGGCTCCAGAGAGCCGAGGCGAGCAACGCGACAGGCGAGCAAGAAAGAACTAC 1620
Db      1606 CGAGACCAAGGCTCCAGAGAGCCGAGGCGAGCAACGCGACAGGCGAGCAAGAAAGAACTAC 1665
Qy      1621 TTCGGAGAGAGTCAAGGCGGCTCTTAAGTGTGCGCAATTTGCAACATGCAACGTTTAT 1680
Db      1666 TTCGGAGAGAGTCAAGGCGGCTCTTAAGTGTGCGCAATTTGCAACATGCAACGTTTAT 1725
Qy      1681 GAGCAGAGAGCCGCACTGCTGTGAAAGAGTTCCTTCCCTTCCACTGCGC 1740
Db      1726 GAGCAGAGAGCCGCACTGCTGTGAAAGAGTTCCTTCCCTTCCACTGCGC 1785
Qy      1741 TACCGGAGCCAGCTTTGAGAAATTTGATTCGAGCTTTGTTTAAATGATCATGTGC 1800
Db      1786 TACCGGAGCCAGCTTTGAGAAATTTGATTCGAGCTTTGTTTAAATGATCATGTGC 1845
Qy      1801 AAACCAAGGCGCTGAGAGTCACTTCTGCTTAAGAGTGAAGGCGCTGTTTGGGGCAACC 1860
Db      1846 AAACCAAGGCGCTGAGAGTCACTTCTGCTTAAGAGTGAAGGCGCTGTTTGGGGCAACC 1905
Qy      1861 GAGCAGAGAGCTCCAGAGAGAGTCAAGCATGAGGAGGCGCTGGAACCAAGCGGGAGGCC 1920
Db      1906 GAGCAGAGAGCTCCAGAGAGAGTCAAGCATGAGGAGGCGCTGGAACCAAGCGGGAGGCC 1965
Qy      1921 CGGCTGCTGCTGACGCTGAGCGCGCGCTGCAACCCCTGCTGCAACGCTGAAAGCGCGC 1980
Db      1966 CGGCTGCTGCTGAGCGCTGAGCGCGCGCTGCAACCCCTGCTGCAACGCTGAAAGCGCGC 2025
Qy      1981 AGCCCTCGAGACATGCGCGGAGCTAGAGCATTTATGACTGCTGTGCTGCTCATCCGAG 2040
Db      2026 AGCCCTCGAGACATGCGCGGAGCTAGAGCATTTATGACTGCTGTGCTGCTCATCCGAG 2085
Qy      2041 CTGTCTCTGCACTGATGAGAGAGCTCTGAGGAGCAACAGAGAAAGCTTCTCCAGAG 2100
Db      2086 CTGTCTCTGCACTGATGAGAGAGCTCTGAGGAGCAACAGAGAAAGCTTCTCCAGAG 2145
Qy      2101 GAGAGGCTGCTCTCTCTTCAAGGCTGTGTGAGAGAAAGCTTCTGCTTCTTCCAG 2160
Db      2146 GAGAGGCTGCTCTCTCTTCAAGGCTGTGTGAGAGAAAGCTTCTGCTTCTTCCAG 2205
Qy      2161 CTCTCTCTTCTTGGGTGATGAGAAAGATCTTGTGTTCCGCGAGCTACATGTAAGCTC 2220
Db      2206 CTCTCTCTTCTTGGGTGATGAGAAAGATCTTGTGTTCCGCGAGCTACATGTAAGCTC 2265
Qy      2221 CAGCGGAGTGGCGCTTGTGAAGAAAGAAAGATCTTGAAGCAATTTGCACTTTAGCTGCTG 2280
Db      2266 CAGCGGAGTGGCGCTTGTGAAGAAAGAAAGATCTTGAAGCAATTTAGCTGCTG 2325

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Qy      2281 CCTCCTCTGATTTCCCAAGCTGATCTCCCTGGTTGAGAGGCCCACTTGAAGCTGAGGTCT 2340
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Qy      2341 CATACAGAGATATTTGAGTGAATGCTGGCAGTACTGTTCTCCCTTGGCCCAACCT 2400
Db      2386 CATACAGAGATATTTGAGTGAATGCTGGCAGTACTGTTCTCCCTTGGCCCAACCT 2445
Qy      2401 TTACCGGATATCTTGAACAACTCTCCAAATTTCTAAATATGATGAGCTCTGAAGGCA 2460
Db      2446 TTACCGGATATCTTGAACAACTCTCCAAATTTCTAAATATGATGAGCTCTGAAGGCA 2505
Qy      2461 TGTCCATAGGTCTGACACACCTTGGCAAAATTTGTTAGTCTTGGATCAGAGCCTGTT 2520
Db      2506 TGTCCATAGGTCTGACACACCTTGGCAAAATTTGTTAGTCTTGGATCAGAGCCTGTT 2565
Qy      2521 GTGGAGGTAGGAGAGAAATATGTAAGAAAGAAACAGAGAGATPACTGCACTAATCTCA 2580
Db      2566 GTGGAGGTAGGAGAGAAATATGTAAGAAAGAAACAGAGAGATPACTGCACTAATCTCA 2625
Qy      2581 GACTTCATTGAGCTGCAAACTTGGCTGTTGCTATTGCTACTGATTTGAATATG 2640
Db      2626 GACTTCATTGAGCTGCAAACTTGGCTGTTGCTATTGCTACTGATTTGAATATG 2685
Qy      2641 TTTTGAAAAAAGGCACTTTTAACTATGACCAAGAAATCAAGTCCAGTATCTG 2700
Db      2686 TTTTGAAAAAAGGCACTTTTAACTATGACCAAGAAATCAAGTCCAGTATCTG 2745
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Db      2746 AATCCATGTTGATGACATATATGTTCAATTAATTTTG 2786

RESULT 11
US-10-608-449-3
; Sequence 3, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Telinghua Universtiy
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: 12003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 4508
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-608-449-3

Query Match      87.1%; Score 2684.6; DB 8; Length 4508;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2690; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB
533 GTAGCTTCAAAAAGATGGAATGGAATCTCAACCTTCCGAAATAGAAATTTGAACGG 592
OY
494 ATTATTTCTGTAAGGTGTCTCCCTTTCTTCCATTAATAAAGCAATTAACACCTT 553
DB
593 ATTATTTCTGTAAGGTGTCTCCCTTTCTTCCATTAATAAAGCAATTAACACCTT 652
OY
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DB
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DB
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2453 TTGAGAGTGAATGCTGGCGCAGATCTTGTCTCCCTTGCCTTCAACCTTTACCGGATTC 2512
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2513 TGAACAACTCTCAATTTTCTAAATGATATGAGCTCTGAAGGAGATGCTCATTAAGT 2572
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DB
2633 AGGAATATGTAAAGAAAACGAGAAATCTGTGACCTTAATCTTCAACTTCACTTGAAC 2692
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Oy	2594	CTGCAAACTTGGCTGTTTGCTATGGCTACCTGATTGAAAACCTTTGGAAAAAG	2655
Db	2693	TCGCAAACTTGGCTGTTTGCTATGGCTACCTGATTGAAAACCTTTGGAAAAAG	2755
Oy	2654	GCACTTTTAAACATCATAAGCCAAGAAATCAAGTGGCACTTATCGAATCCATGGTGA	2713
Db	2753	GCACTTTTAAACATCATAAGCCAAGAAATCAAGTGGCACTTATCGAATCCATGGTGA	2812
Oy	2714	TTGCAGATTAATGTTCTCATTTATTTTGAATGAATTAACATTGCCATGGCTGTTAAAT	2773
Db	2813	TTGCAGATTAATGTTCTCATTTATTTTGAATGAATTAACATTGCCATGGCTGTTAAAT	2872
Oy	2774	AAGCTTTAGCTCAAAAGTCAAGAAAGTAGATCGAATATACAGTCACTTTATGAAATGA	2832
Db	2873	AAGCTTTAGCTCAAAAGTCAAGAAAGTAGATCGAATATACAGTCACTTTATGAAATGA	2931

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RESULT 12 04-047-1429
US-10-104-047-1429
Sequence 1429, Application US//10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104, 047
CURRENT FILING DATE: 2002-03-25
PRIORITY APPLICATION NUMBER:
PRIORITY FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1429
LENGTH: 2894
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-1429

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Query Match	Similarity	86.9%	Score 2678.6	DB 6	Length 2894
Best Local	Similarity	99.7%	Pred. No. 0		
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					Gaps
					0
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Db	202	CCTGGCCCTTGGCAAGGAGTGGGGGCCAGCCACAGAAACAGTGGGCTGTACAACTACCT	261		
QY	194	TCAATATATGACAAATTGTATCCACTTGAATCCAGTGGGGAGAGATGTGATGGTGAAC	253		
Db	262	TCAATATATGACAAATTGTATCCACTTGAATCCAGTGGGGAGAGATGTGATGGTGAAC	321		
QY	254	CCGAAATATCACCATTCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCACTCTTT	313		
Db	322	CCGAAATATCACCATTCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCACTCTTT	381		
QY	314	GGTCCCGCAGGGGGCCCTGGGCATTCGAATTCCTGAAAGATTTTGGTATATCTGAGGAGC	373		
Db	382	GGTCCCGCAGGGGGCCCTGGGCATTCGAATTCCTGAAAGATTTTGGTATATCTGAGGAGC	441		
QY	374	TGAAGTGGAGGGAAGACAGTGCACCAACTGATTTCTAAGGATCCGAAGCAGCTCAACA	433		
Db	442	TGAAGTGGAGGGAAGACAGTGCACCAACTGATTTCTAAGGATCCGAAGCAGCTCAACA	501		
QY	434	GTACCTTCAAAAGAACTGGGAATGGAAATCTCAACCTTTCCTGAAATGAAATTTGAAAGG	493		
Db	502	GTACCTTCAAAAGAACTGGGAATGGGAATCTCAACCTTTCCTGAAATGAAATTTGAAAGG	561		
QY	494	ATTATTTGCTAAAGGTGTGCCCTTTTCTTCCATTAATAAAGAAAGCAATTAACACCTT	553		
Db	562	ATTATTTGCTAAAGGTGTGCCCTTTTCTTCCATTAATAAAGAAAGCAATTAACACCTT	621		
QY	554	TCTTCTTTAGAACCCGAGCCTGTGACCTGTGTTACAGCCCGACCAATCTAGCTTTAAAC	613		
Db	622	TCTTCTTTAGAACCCGAGCCTGTGACCTGTGTTACAGCCCGACCAATCTAGCTTTAAAC	681		

QY	614	CTTTCTGGAAGCCCTGGAAAGCTGAAACATCAAGCCAGCATGCTCTGGACAATGCAAGGTGCTCT	673
Db	682	CTTTCTGGAAAGCCCTGGAAAGCTGAAACATCAAGCCAGCATGCTCTGGACAATGCAAGGTGCTCT	741
QY	674	TCGACCAAGCAGCCCAACAATTCGGCTTCGGCTTTCTTATCTTCACTTACATCAAGCTCAAGC	733
Db	742	TCGACCAAGCAGCCCAACAATTCGGCTTCGGCTTTCTTATCTTCACTTACATCAAGCTCAAGC	801
QY	734	ACGAAGACCTTTCAAGGAAAAGCTGTGAAGCAGAGCAAACTTACAGAGACGACAGCT	793
Db	802	ACGAAGACCTTTCAAGGAAAAGCTGTGAAGCAGAGCAAACTTACAGAGATGACAGCT	861
QY	794	GCCCTCTTCAAAAAGTTTCTCCAGGGATTAATATATTGAGCTGTGGAATGACCTAAACA	853
Db	862	GCCCTCTTCAAAAAGTTTCTCCAGGGATTAATATATTGAGCTGTGGAATGACCTAAACA	921
QY	854	CAACAAGAAAAGTATGATCATTTATCTTAAAGCAGTGACCTCCCGGTGGCCGGGCCCA	913
Db	922	CAACAAGAAAAGTATGATCATTTATCTTAAAGCAGTGACCTCCCGGTGGCCGGGCCCA	981
QY	914	TCAGAGCCATGCGCATCAAGTGTCCACTGTGATCATATCGGCAATTCGCGAGCTCTTCA	973
Db	982	TCAGAGCCATGCGCATCAAGTGTCCACTGTGATCATATCGGCAATTCGCGAGCTCTTCA	1041
QY	974	CTGAGATGTGCGCGAAGAACAAACAAATAATATATTCATCTTGAATGAAGAGCT	1033
Db	1042	CTGAGATGTGCGCGAAGAACAAACAAATAATATATTCATCTTGAATGAAGAGCT	1101
QY	1034	CTGAGCTCTTCCAATACATGACAGCAGCATCCCAAGAGAGAGGCTCCGGCCGGCCGCGAAG	1093
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QY	1094	TCCTTCTCTGCTATTCAGATTAAGATGAGCCAGAAATCAATGAATGTGCTTCAGTGTTCG	1153
Db	1162	TCCTTCTCTGCTATTCAGATTAAGATGAGCCAGAAATCAATGAATGTGCTTCAGTGTTCG	1222
QY	1154	CTTACTTCTTCAGGAATTCGTGTGGCTGTGAAGGTGGCTCTGAGCTCTGTGGAGAACCTTCA	1211
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QY	1214	GCCCTCTGTAAGAAAGGCGAAGAAATGGGTCATCCGAAATCAACGAGTCCCAATTC	1272
Db	1282	GCCCTCTGTAAGAAAGGCGAAGAAATGGGTCATCCGAAATCAACGAGTCCCAATTC	1341
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Db	1342	TCATTGTGTGTTGTTCCAAAGGTATGAAGTACTTTGTGGAACAAGAACTTACAAACACA	1401
QY	1334	AAGAGGTGTGCGCAGAGCTCGGCGAAAGAGAGCTCTTCTGTGTGGCGGTGTCAAGCATTG	1393
Db	1402	AAGAGGTGTGCGCAGAGCTCGGCGAAAGAGAGCTCTTCTGTGTGGCGGTGTCAAGCATTG	1461
QY	1394	CCGAAAAGCTTCGCGCAAGCCCAAGCAGAGTTCGTCCGGGGCGCTCAAGCAAGTTTATCCGCG	1455
Db	1462	CCGAAAAGCTTCGCGCAAGCCCAAGCAGAGTTCGTCCGGGGCGCTCAAGCAAGTTTATCCGCG	1521
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Db	1522	TCCTACTTTGAATTATTCCTGCGAGGGAGAACGTCGCCGGATCTGTGACCTGTAGTACCAAGT	1581
QY	1514	ACAGACTCATGACCAATCTTCTCAAGCTCTTGTCCCACTGTGACCTCCCGAGACCAAGGCT	1573
Db	1582	ACAGACTCATGACCAATCTTCTCAAGCTCTTGTCCCACTGTGACCTCCCGAGACCAAGGCT	1641
QY	1574	TCACAGAGCCCGGGCAGACAACGCGACAAGGCGACAGAGAACTTACTTCGAGACCAAGT	1633
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QY	1634	CAGGCGGCTCCCTATATAGTGTGCAATTTGCAACATGACCAAGTTATTTGACGAGGAGGCGG	1693
Db	1702	CAGGCGGCTCCCTATATAGTGTGCAATTTGCAACATGACCAAGTTATTTGACGAGGAGGCGG	1761

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2002 ACCGTTAGCGCGCTGCAACCCCTGCTGCAACCGGTGAAGCGCGGACCGCTCGGACA 2061
1994 TGGCGGGGAGTCAAGGATCTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2053
2062 TGGCGGGGAGTCAAGGATCTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2121
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2122 TGATGAGAGAGTCTGCAACCGAGCAGACAGAAAGTCTTCTGAGCAGAGGCTGCTGCT 2181
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2182 CTTCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2241
2174 GGTTCAGCAAGAGAGTCTTGGTTCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2233
2242 GGTTCAGCAAGAGAGTCTTGGTTCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2301
2234 CTTTGTACAAAAGAGAGTCTTAAAGTCAATGTCATGTCATGTCATGTCATGTCATGTCAT 2293
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2294 CCCAGCTCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2353
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2474 TGACAAAGTCTCCAAATTTGTTAGTCTGTTGATGAGGCTGTTGTTGTTGTTGTTGTTGTT 2533
2542 TGACAAAGTCTCCAAATTTGTTAGTCTGTTGATGAGGCTGTTGTTGTTGTTGTTGTTGTT 2601
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2782 TTGCAATATATGTTCTCATTTATTTTGAATGATGATTTTGAATGATGATTTTGAATGAT 2841
2774 AAGCTTTGAGTCAAAAGTCAAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2826

Db 2842 AAGCTTTGAGTCAAAAGTCAAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2894
RESULT 13
US-10-477-714-42
; Sequence 42, Application US/10477714
; Publication No. US2005003018A1
GENERAL INFORMATION:
; APPLICANT: LAL, Preeti G.; WARREN, Bridget A.;
; APPLICANT: XU, Yuming; DUGAN, Brendan M.;
; APPLICANT: HONCHIELL, Cynthia D.; KALLICK, Deborah A.;
; APPLICANT: BAUGHN, Mariah R.; TANG, Y. Tom;
; APPLICANT: YUE, Henry; BANDMAN, Olga;
; APPLICANT: JONES, Karen Anne; BECHT, Shanya D.;
; APPLICANT: TRAN, Yuen K.; AU-YOUNG, Janice K.;
; APPLICANT: GRIFFIN, Jennifer A.; ZEBARADIAN, Yeganeh;
; APPLICANT: LEB, Ernestine A.; ELLIOTT, Vicki S.;
; APPLICANT: THANGAVELU, Kavitha; RAMKUMAR, Jayalaxmi;
; APPLICANT: LU, Yan; HAFALIA, April J.A.;
; APPLICANT: CHAMLA, Narinder K.; ISON, Craig H.;
; APPLICANT: THORNTON, Michael B.; SWARNAKAR, Anita;
; APPLICANT: YANG, Junming; RICHARDSON, Thomas W.;
; APPLICANT: EMERLING, Brooke M.; YAO, Monique G.;
; APPLICANT: COCKS, Benjamin G.; SANJANMALA, Bharati;
; APPLICANT: MASON, Patricia M.; GANDHI, Ameena R.;
; APPLICANT: LI, Joana X.; FORSYTHE, Ian J.;
; APPLICANT: GURUBAJAN, Rajagopal; GIETZEN, Kimberly J.
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0992 USN
; CURRENT APPLICATION NUMBER: US/10/477,714
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: PCT/US02/15899
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/292,197
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/297,012
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/300,582
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/300,495
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/301,992
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/340,542
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO: 42
; LENGTH: 4450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 6986529CB1
US-10-477-714-42
Query Match 85.1%; Score 2622.2; DB 8; Length 4450;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2624; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 206 ATTGTACCACTTCACTTGAATCAAGTGGGGAACATGTGTTGCTGACGCCAGAAATATCA 265
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Db 324 CCATGAGCCAGTATGCTTCCATGACCAAGTGGAGTCAATCTTTGTTCCCAAGGG 383
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Db 384 CCTTGGGCAATGCAATTTCTGAAAGATTTCCGCTAATCTGAGAGAGCTGAAAGTGGAGG 443

386 GAAGACAGTGCACCACTGATTTCTAAAGATCCGAGACGCTCAACAGTAGCTTCAAA 445
444 GAAGACAGTGCACCACTGATTTCTAAAGATCCGAGACGCTCAACAGTAGCTTCAAA 503
446 GAACTGAATGGAATCTCAACCTTTCTGAAATGAAATTGAAACGGATTAATTTGTA 505
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626 CTCGGAACCTGAACATCAGCCAGCATGCTCGGACATGCAAGTGTCTTTCGACAGCAG 685
684 CTCGGAACCTGAACATCAGCCAGCATGCTCGGACATGCAAGTGTCTTTCGACAGCAG 743
686 CCGACCACTTCGCGCTTCCTTTCTTCTATCTTCACTAACGCTCAAGCAGGAGACCTT 745
744 CCGACCACTTCGCGCTTCCTTTCTTCTATCTTCACTAACGCTCAAGCAGGAGACCTT 803
746 TCAAGGAAAGACCTGTAAAGCAGAGCAATCTACAGAGCAGCAGTGTCTCTTCA 805
804 TCAAGGAAAGACCTGTAAAGCAGAGCAATCTACAGAGCAGCAGTGTCTCTTCA 863
806 ATGTTTCTCAGGGGATTAATATTAATGAGCTGTGATGACACTTAAACAAAGAAAAG 865
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866 TGAATGATTAATGCTTAAAGCCAGTGCACCTCCGAGGAGCCGAGCCATCAGAGCCGTG 925
924 TGAATGATTAATGCTTAAAGCCAGTGCACCTCCGAGGAGCCGAGCCATCAGAGCCGTG 983
926 CCAATCAGTGCACCTGTAGTATCTGACATTCGAGCAGCTCTTCACTGTATGAGCC 985
984 CCAATCAGTGCACCTGTAGTATCTGACATTCGAGCAGCTCTTCACTGTATGAGCC 1043
986 GCMAAGAGCAACMAAGAAATATATATTCACATTTAATGAAAGAGCTGTGATCTTCCA 1045
1044 GCMAAGAGCAACMAAGAAATATATATTCACATTTAATGAAAGAGCTGTGATCTTCCA 1103
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1226 AAGGGCAGAGAGATGGGTCAATCCAGAGATCCAGAGTCCAGTTCACTATGTGGTTT 1285
1284 AAGGGCAGAGAGATGGGTCAATCCAGAGATCCAGAGTCCAGTTCACTATGTGGTTT 1343
1286 GTTCCAAAGGTATGAAGTACTTTGTGACAAAGAACTTCAAAACAAAGAGAGGTGGCC 1345
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1464 GCCAGGCCAAGCAGAGTTCGTCGCGCGCTCAGCAAGTTTATCGCGCTTACTTTGATT 1523
1466 ATTCTCGGAGGAGAGCTCCCGGTATCTTGAAGCTGAGTACCAAGTACAGACTATGG 1525

1524 ATTCTCGGAGGAGAGCTCCCGGTATCTTGAAGCTGTAGTACCAAGTACAGACTATGG 1583
1526 ACAATTTCTCTCAGCTCTGTTCACCTGACACTCCGAGACCAAGCGCTTCAGAGCCGG 1585
1584 ACAATTTCTCTCAGCTCTGTTCACCTGACACTCCGAGACCAAGCGCTTCAGAGCCGG 1643
1586 GCGAGCAGCAGGAGCAGGCGCAGAGAGCACTCTTCCGAGCAAGTCAAGGCGGCTCC 1645
1644 GCGAGCAGCAGGAGCAGGCGCAGAGAGCACTCTTCCGAGCAAGTCAAGGCGGCTCC 1703
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1704 TATACGTCGCCATTTGCAACATGCAACAGTTATTTGACAGAGAGCCGACTGTTGAAA 1763
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1764 AGCAGTTGCTTCCTTCCATCTCTCTCTCACTGCGCTACCGGAGACCAAGTCTTGAAGAA 1823
1766 TTGATTCGGGCTTGTGTTTAAATGATGATGCAATGCAACAGGAGCTGTAGAGTCTCT 1825
1824 TTGATTCGGGCTTGTGTTTAAATGATGATGCAATGCAACAGGAGCTGTAGAGTCTCT 1883
1826 GCTTAAAGGTAAAGGCGCTGTCTTGTGGGCAACCGGACCGGACTCCAGCAGAGA 1885
1884 GCTTAAAGGTAAAGGCGCTGTCTTGTGGGCAACCGGACCGGACTCCAGCAGAGA 1943
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1944 GTTCAAGATGGGGGCTTGAACCAAGAGGAGGCGCGCTGCTTGAAGTGGCGCG 2003
1946 CCTGCAACCTCTGCTGCAACAGGTGAAGCCGAGCCCTTCGACATGCGCGGAGCT 2005
2004 CCTGCAACCTCTGCTGCAACAGGTGAAGCCGAGCCCTTCGACATGCGCGGAGCT 2063
2006 CAGGCACTATGATCTGTGCTGCTCTGAGCTGCTCTGCACTGATGGAAGAGC 2065
2064 CAGGCACTATGATCTGTGCTGCTCTGAGCTGCTCTGCACTGATGGAAGAGC 2123
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2124 TCTCGACGAGCAGACAGAAAGCTTCTTCCGAGAGAGCGGTCTCTTTCAGGCGC 2183
2126 TGGGTGAAGAGAGACTTCTGCGCTTCTTCCAGCTCTCTTCTTGTGGGTCAAGAAAG 2185
2184 TGGGTGAAGAGAGACTTCTGCGCTTCTTCCAGCTCTCTTCTTGTGGGTCAAGAAAG 2243
2186 CAGATCTGTGTTGCGGAGCTTCACTGATGAATCTCAGCGGAGCGCCCTTGTGAACAA 2245
2244 CAGATCTGTGTTGCGGAGCTTCACTGATGAATCTCAGCGGAGCGCCCTTGTGAACAA 2303
2246 ACGAAAGAGCTTAAGCACTTGAAGCTTGAAGCTGCTCTCTGATTTCCAGCTCATC 2305
2304 ACGAAAGAGCTTAAGCACTTGAAGCTTGAAGCTGCTCTCTGATTTCCAGCTCATC 2363
2306 TCCCTGTGTCATGAGCGCCACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 2365
2364 TCCCTGTGTCATGAGCGCCACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 2423
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2426 CAATTTCTTAAATGATATGAGAGCTCTGAAGAGCAATGTCATTAAGTCTGACAGAGCTT 2485
2484 CAATTTCTTAAATGATATGAGAGCTCTGAAGAGCAATGTCATTAAGTCTGACAGAGCTT 2543
2486 GCCAAATTTGTTAGTCTTGTGATCAAGAGCTGTTGTGGAGAGTGAAGAGAAATATGTA 2545
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Qy 2726 TTTCTCATTTATTTTGTATGATGAAATTTTACATTCGCAATGGGTGTTAAATAGCTTTGATC 2785
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RESULT 14

US-10-302-172-125
; Sequence 125, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Dmanac, Radcoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids an
; FILE REFERENCE: 803_1CNP
; CURRENT APPLICATION NUMBER: US/10/302,172
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: PL_FU_genes Version 2.0
; SEQ ID NO 125
; LENGTH: 3948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (60)..(1844)
US-10-302-172-125

Query Match 78.7%; Score 2426.4; DB 7; Length 3948;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 397 CAACAATGATTTCTAAGATTCGAAAGCAAGCTCAAGTAGCTTCAAAAAGATCTGAATG 456
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Qy 457 GAATCTCAACCTTTCTGAAATATGAATTTGAAACGGAATTAATTTGTTAAAGTTGTCCT 516
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Qy 517 TTTCTCTCATTTAAAGCAAGAACTTACCACTTTTCTTTTGAACCGGAGCTGT 576
Db 123 TTTCTCTCATTTAAAGCAAGAACTTACCACTTTTCTTTTGAACCGGAGCTGT 182
Qy 577 GAAGCTGTGTTACGCGGACCAATCTAGCTTTGAAACCTTTCTGAAAGCTCTGGAACCTG 636
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Db 243 AAGATCAGCAGATGAGCTTCGACATGCAAGGTCTCTTGAACGACGACGCAACCTTC 302

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Db 363 ACCGTGAAGCAGAGCAAACTACAGAGACCAAGCTGCTCTCTCAAAATGTTTCTCA 422
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Qy 877 GCGTTAAAGCAGTCACTCCCGTGGGCGGGCCCATCAAGACCAATGCACTCAAGTG 936
Db 483 GCGTTAAAGCAGTCACTCCCGTGGGCGGGCCCATCAAGACCGTGGCCATCAAGTG 542
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Db 543 CCACTGTATGATATGCGCATTCGCGACGCTCTTCACTGTATGTCCGCAAGACAA 602
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Db 1083 GGAAGAGTCCCGGTATCTTGAAGCTTGAAGTACAGACTCATGAGCAATCTTCTCT 1142
Qy 1537 CAGCTCTGTTCACCTGCACTCCGAGACCAAGCTCTCAGAAACCGGGGAGAGACAG 1596
Db 1143 CAGCTCTGTTCACCTGCACTCCGAGACCAAGCTCTCAGAAACCGGGGAGAGACAG 1202
Qy 1597 CGACAGGCGACAGAAAGAACTACTTCCGAGCAAGTCAAGCGCGGTCTCTATACGTGCG 1656
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Qy 1777 TTGGTTTAAATGATGATGCAAAACAGGCGCTGAGAGTGAATCTTCTGCTAAAGTGA 1836


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Db 1383 TTGGTTTAAATATATGTCATATGTCACAAACAGGGCCCTGAGAGTACTTCTCCCTAAAGTA 1442
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Db 1443 GAGGCGGCTGTTCTTGGGGCAACCGGACAGCGGACTCCAGACGAGAGTCAAGATGAGTGG 1502
Qy 1897 GGGCTTGACCAAGACGGGAGGGCCGGCCCTTGAAGGTAGCCCGCCCTGCAACCC 1956
Db 1503 GGGCTTGACCAAGACGGGAGGGCCGGCCCTTGAAGGTAGCCCGCCCTGCAACCC 1562
Qy 1957 CTGCTGACACGGGTGAAGAGCGGACGCGCTCGGACATGCGCGGAGTCAAGCATCTAT 2016
Db 1563 CTGCTGACACGGGTGAAGAGCGGACGCGCTCGGACATGCGCGGAGTCAAGCATCTAT 1622
Qy 2017 GACTGCTGTCGCTTCATCCGAGTGTCTCTGCACTGATGGAAGAGTCTTGAAGAG 2076
Db 1623 GACTGCTGTCGCTTCATCCGAGTGTCTCTGCACTGATGGAAGAGTCTTGAAGAG 1682
Qy 2077 CAGACGAAACGCTTCTTCCCTGACGAGAGGCTGCTCTCTTCAAGGCTGGGTGAGAG 2136
Db 1683 CAGACGAAACGCTTCTTCCCTGACGAGAGGCTGCTCTCTTCAAGGCTGGGTGAGAG 1742
Qy 2137 GAACCTCTGCGCCCTTCTTCCAGGCTCTCTCTTCTGAGTCAAGAGAGATCTTGGT 2196
Db 1743 GAACCTCTGCGCCCTTCTTCCAGGCTCTCTCTTCTGAGTCAAGAGAGATCTTGGT 1802
Qy 2197 TGGCGAGCTACATGATGAACTCAAGCGGTGCGCCCTTGTGAACAAACGAAAGATC 2256
Db 1803 TGGCGAGCTACATGATGAACTCAAGCGGTGCGCCCTTGTGAACAAACGAAAGATC 1862
Qy 2257 TAAAGCATTCGCACTTAACTGCTGCTGCTCTCTGATTTCCAGCTCATCTCTGTTGC 2316
Db 1863 TAAAGCATTCGCACTTAACTGCTGCTGCTCTCTGATTTCCAGCTCATCTCTGTTGC 1922
Qy 2317 ATGGCCCACTGAGGCTGAGGCTCTCATPACAAAGATTTGGAGTGAAGTGGCCAGTA 2376
Db 1923 ATGGCCCACTGAGGCTGAGGCTCTCATPACAAAGATTTGGAGTGAAGTGGCCAGTA 1982
Qy 2377 CTGTTCTCCCTTCCCAACCCCTTAAACGAGATATCTTGAACAACTCTCAATTTCTAA 2436
Db 1983 CTGTTCTCCCTTCCCAACCCCTTAAACGAGATATCTTGAACAACTCTCAATTTCTAA 2042
Qy 2437 AATGATATGAGCTGTGAAGAGCATGTCATTAAGTCTGACAAACAGTTGCCAAATTTGG 2496
Db 2043 AATGATATGAGCTGTGAAGAGCATGTCATTAAGTCTGACAAACAGTTGCCAAATTTGG 2102
Qy 2497 TTAGTCTCTGATCAAGAGCTGTTGGGAGGTAGGAGAGAAATATGTAAAGAAACAG 2556
Db 2103 TTAGTCTCTGATCAAGAGCTGTTGGGAGGTAGGAGAGAAATATGTAAAGAAACAG 2162
Qy 2557 GAGATACCTGCACTATCATCTGAGCTTCACTTGAAGTCTGCAAACTTTGCTGTTGCT 2616
Db 2163 GAGATACCTGCACTATCATCTGAGCTTCACTTGAAGTCTGCAAACTTTGCTGTTGCT 2222
Qy 2617 ATTGGTACCTGATTTGAAATGCTTTGTAAGAAAGGCACTTTTAAATCATATAGCCACA 2676
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Db 2283 GAAATCAAGTCCAGTCTATCTGGAATCCATGTTGATTTGCAATATATGTTCAATTTAT 2342
Qy 2737 TTTTGAATGATTTTAACTTGCATGGGTGTTAAATAGCTTGAATCAAGTCAAGA 2796
Db 2343 TTTTGAATGATTTTAACTTGCATGGGTGTTAAATAGCTTGAATCAAGTCAAGA 2402
Qy 2797 AAGTGAATGATTTTAACTTGCATGGGTGTTAAATAGCTTGAATCAAGTCAAGA 2832
Db 2403 AAGTGAATGATTTTAACTTGCATGGGTGTTAAATAGCTTGAATCAAGTCAAGA 2438
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RESULT 15

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US-09-912-157-7
; Sequence 7, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86) ... (2302)
US-09-912-157-7

Query Match 73.5%; Score 2267.4; DB 3; Length 2341;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2271; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGGCTGGGCGAGCGCAGCGCCATGGCCCGTGGCTGCACTCTGCTCCGTTCTTTAGC 60
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Qy 61 GTCAACGCTGCTGCTCAAGCGGCTCGAGCTGTGTGGCGGCGGAGTGGCGGCGCGG 120
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Qy 121 TGGGCGCTGCAACCTGTGTGGCTGAGGGGAGTGGGCGCAGCGAGAAACAGTGGCTG 180
Db 185 CGGGGCGCGGACACTGTGTGGCTGAGGGGAGTGGGCGCAGCGAGAAACAGTGGCTG 244
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Db 425 ATACTGAGAGAGCTGAGTGTGAGGGAGAGAGTGGCAACATGATTTGTAAGATTCG 484
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Qy 541 AATTACACCCCTTCTTCTTGAACCCGAGGCTGTGACTGTGTGTAACGCGGACAT 600
Db 605 AATTACACCCCTTCTTCTTGAACCCGAGGCTGTGACTGTGTGTAACGCGGACAT 664
Qy 601 CTAGCTTGAACCCCTTCTGGAAGCTCGGAACCTGAACATAGACGAGATGGCTCGAC 660
Db 665 CTAGCTTGAACCCCTTCTGGAAGCTCGGAACCTGAACATAGACGAGATGGCTCGAC 724
Qy 661 ATGCAAGTGTCTTGGACAGCAGCAGCACTTGGCTTCCGTTCTTATCTTCAAC 720
Db 725 ATGCAAGTGTCTTGGACAGCAGCAGCACTTGGCTTCCGTTCTTATCTTCAAC 784
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Qy 721 TACAAGCTCAAGACGAGAGACCTTTCAAGCGAAAAGACTGTAAAGCAGAGCAAACTACA 780
Db 785 TACAAGCTCAAGACGAGAGACCTTTCAAGCGAAAAGACTGTAAAGCAGAGCAAACTACA 844
Qy 781 GAGACGACGAGCTGCTCTTCAAAATGTTTCTTCAGGAGATTAATATATTAAGCTGTG 840
Db 845 GAGACGACGAGCTGCTCTTCAAAATGTTTCTTCAGGAGATTAATATATTAAGCTGTG 904
Qy 841 GAGACGACGACGAGCTGCTCTTCAAAATGTTTCTTCAGGAGATTAATATATTAAGCTGTG 900
Db 905 GAGACGACGACGAGCTGCTCTTCAAAATGTTTCTTCAGGAGATTAATATATTAAGCTGTG 964
Qy 901 TGGAGCGGAGGCTTCAGAGGCTATGAGCATGAGTGCATGAGTGCATGAGTGCATG 960
Db 965 TGGAGCGGAGGCTTCAGAGGCTATGAGCATGAGTGCATGAGTGCATGAGTGCATG 1024
Qy 961 GCGACGCTCTTCACTGTGATGTGCGGAGAGCAAGAGCAAAATATATATTAATTA 1020
Db 1025 GCGACGCTCTTCACTGTGATGTGCGGAGAGCAAGAGCAAAATATATATTAATTA 1084
Qy 1021 GATGAAGAGAGCTCTGAGTCTTCACTATCACTGACAGTCTCCAGAGAGAGGCTCCG 1080
Db 1085 GATGAAGAGAGCTCTGAGTCTTCACTATCACTGACAGTCTCCAGAGAGAGGCTCCG 1144
Qy 1081 CCGCGGCGGAGAGGCTCTTCTCTGCTATTCAGTAAAGATGAGCGAGATCAATGAATGTC 1140
Db 1145 CCGCGGCGGAGAGGCTCTTCTCTGCTATTCAGTAAAGATGAGCGAGATCAATGAATGTC 1204
Qy 1141 GTCAGTGTGTCCTTCACTTCTTCAGAGCTTGTGAGTGTGAGGCTGTGAGCTG 1200
Db 1205 GTCAGTGTGTCCTTCACTTCTTCAGAGCTTGTGAGTGTGAGGCTGTGAGCTG 1264
Qy 1201 TGGAGAGACTTCAGGCTCTGTAGAGAGGCGAGAGAGATGAGTCTTCAGAGATCCAC 1260
Db 1265 TGGAGAGACTTCAGGCTCTGTAGAGAGGCGAGAGAGATGAGTCTTCAGAGATCCAC 1324
Qy 1261 GAGTCCAGTTCATCATTTGTGTTTTCAGAAAGTATGAAGTATGTCAGAGAG 1320
Db 1325 GAGTCCAGTTCATCATTTGTGTTTTCAGAAAGTATGAAGTATGTCAGAGAG 1384
Qy 1321 AACTACAAACAAAGAGAGGTGCGGAGGCTCGGAGAAAGAGAGCTCTTCTGTGCG 1380
Db 1385 AACTACAAACAAAGAGAGGTGCGGAGGCTCGGAGAAAGAGAGCTCTTCTGTGCG 1444
Qy 1381 GGTCTCAGGCTTTCGCGAAAGCTCCGCGAGGCGAGAGAGTTCGTCGCGGCGCTCAGC 1440
Db 1445 GGTCTCAGGCTTTCGCGAAAGCTCCGCGAGGCGAGAGAGTTCGTCGCGGCGCTCAGC 1504
Qy 1441 AAGTTTATCGCGCTACTTGAATTAATTCGCGAGAGGAGAGCGTCCCGGATCTTAGAC 1500
Db 1505 AAGTTTATCGCGCTACTTGAATTAATTCGCGAGAGGAGAGCGTCCCGGATCTTAGAC 1564
Qy 1501 CTGAGTACCAAGTACAGACTCATGAGCAATCTTCTCAAGCTGTTCCTCACTGCACTCC 1560
Db 1565 CTGAGTACCAAGTACAGACTCATGAGCAATCTTCTCAAGCTGTTCCTCACTGCACTCC 1624
Qy 1561 CGAGACCAAGGCTTCAGAGGCGGCGAGAGCAACGCGAGAGGCGAGAGAGAACTAC 1620
Db 1625 CGAGACCAAGGCTTCAGAGGCGGCGAGAGCAACGCGAGAGGCGAGAGAGAACTAC 1684
Qy 1621 TTCGAGAGCAAGTCAAGGCGGCTCTTAATAGTGCCATTGCAACATGACAGAGTTTAT 1680
Db 1685 TTCGAGAGCAAGTCAAGGCGGCTCTTAATAGTGCCATTGCAACATGACAGAGTTTAT 1744
Qy 1681 GACGAGAGGCGGAGTGTGAAAAGCAAGTGTCTTCTTCATCTCTCACTGCGC 1740
Db 1745 GACGAGAGGCGGAGTGTGAAAAGCAAGTGTCTTCTTCATCTCTCACTGCGC 1804
Qy 1741 TACCGGAGGCGAGTGTGAAAATTTGATTCGCGCTTGTTTAAATGATGATGTC 1800
Db 1805 TACCGGAGGCGAGTGTGAAAATTTGATTCGCGCTTGTTTAAATGATGATGTC 1864

Qy 1801 AAACAGGAGCTGAGAGTACTTCTGCTTAAAGTATGAGGCGCTGTTCTTGCGGCAAC 1860
Db 1865 AAACAGGAGCTGAGAGTACTTCTGCTTAAAGTATGAGGCGCTGTTCTTGCGGCAAC 1924
Qy 1861 GAGACGAGGAGTCTCCAGAGAGAGTCAAGATGAGGAGGCTGTGACCAAGACGAGAGGCG 1920
Db 1925 GAGACGAGGAGTCTCCAGAGAGAGTCAAGATGAGGAGGCTGTGACCAAGACGAGAGGCG 1984
Qy 1921 CGGCGTGCCTTGAAGGTAGCGCGCGCGCGCAACCTGCTGCAACAGGTGAAGCGGCG 1980
Db 1985 CGGCGTGCCTTGAAGGTAGCGCGCGCGCGCAACCTGCTGCAACAGGTGAAGCGGCG 2044
Qy 1981 AGGCGCTCGAGATGCGCGGAGCTCAGGCACTATGACTGCTGTGCTGCTCATTCGAG 2040
Db 2045 AGGCGCTCGAGATGCGCGGAGCTCAGGCACTATGACTGCTGTGCTGCTCATTCGAG 2104
Qy 2041 CTGTCTCTGCACTGATGAGAGGACTCTGACGAGACAGACAGAAACGTCTTCTGACG 2100
Db 2105 CTGTCTCTGCACTGATGAGAGGACTCTGACGAGACAGACAGAAACGTCTTCTGACG 2164
Qy 2101 GAGAGGTGCTCTCTCTTCAAGGCTGAGTGAAGAGAACTCTGCGCTTCTTCCAG 2160
Db 2165 GAGAGGTGCTCTCTCTTCAAGGCTGAGTGAAGAGAACTCTGCGCTTCTTCCAG 2224
Qy 2161 CTCTCTCTTCTGAGTCAATGCAAGAGATCTTGTGTCGCGAGCTACATGATGACTC 2220
Db 2225 CTCTCTCTTCTGAGTCAATGCAAGAGATCTTGTGTCGCGAGCTACATGATGACTC 2284
Qy 2221 CAGCGGTGCGCTCTTGTGAACAAACGAAAGAGTGAAGCAATGCACTTAACTG 2277
Db 2285 CAGCGGTGCGCTCTTGTGAACAAACGAAAGAGTGAAGCAATGCACTTAACTG 2341

Search completed: March 1, 2006, 07:50:41
Job time : 2382 secs

QY 134 CTTGGCTGAGAGGAGTGGGCGAGCGACAGAAAACAGTGGCTGTACAATCACT 193
| | | | |
Db 202 CTTGGCTTGGCAGAGGTGGGGCGAGCGACAGAAAACAGTGGCTGTACAATCACT 261
| | | | |
QY 194 TCAAAATGACAAATTTGACCACTTACTTGAATCCAGTGGGAAAGCATGTGATGCTGACG 253
| | | | |
Db 262 TCAAAATGACAAATTTGACCACTTACTTGAATCCAGTGGGAAAGCATGTGATGCTGACG 321
| | | | |
QY 254 CCCAGAAATATCAATCAGCAGATGCTGGCCATGACAAAGTGGCATCAATCTTT 313
| | | | |
Db 322 CCCAGAAATATCAATCAGCAGATGCTGGCCATGACAAAGTGGCATCAATCTTT 381
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QY 314 GGTCCCGAGGGGCTCGGAGCATGAAATCTGAAAGGATTCGGGTAAATCTGAGAGAGC 373
| | | | |
Db 382 GGTCCCGAGGGGCTCGGAGCATGAAATCTGAAAGGATTCGGGTAAATCTGAGAGAGC 441
| | | | |
QY 374 TGAAGTCGAGGAGAGACAGTGCACAACTGATTTAAAGATCCGAGCAGCTCAACA 433
| | | | |
Db 442 TGAAGTCGAGGAGAGACAGTGCACAACTGATTTAAAGATCCGAGCAGCTCAACA 501
| | | | |
QY 434 GTAGCTTCAAAAAGACAGGAAATGGAATCTCAACCTTCCGAAATGAAATTTGAAACGG 493
| | | | |
Db 502 GTAGCTTCAAAAAGACAGGAAATGGAATCTCAACCTTCCGAAATGAAATTTGAAACGG 561
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QY 494 ATTATTTCTGAAAGGTGTGCTCTTCTCTTCAATTAATAAGAAAGCAATTAACACCTT 553
| | | | |
Db 562 ATTATTTCTGAAAGGTGTGCTCTTCTCTTCAATTAATAAGAAAGCAATTAACACCTT 621
| | | | |
QY 554 TCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGACAAATCTAGCTTGAAC 613
| | | | |
Db 622 TCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGACAAATCTAGCTTGAAC 681
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QY 614 CCTTCTGGAAGCCTCGGAACCTGAACCTGACGACGATGGCTGGGACATGACAGTGTCT 673
| | | | |
Db 682 CCTTCTGGAAGCCTCGGAACCTGAACCTGACGACGATGGCTGGGACATGACAGTGTCT 741
| | | | |
QY 674 TCGACACGACCGCACAACTTGGGCTTCGTTCTTCTATCTTCACTAACACTCAAGC 733
| | | | |
Db 742 TCGACACGACCGCACAACTTGGGCTTCGTTCTTCTATCTTCACTAACACTCAAGC 801
| | | | |
QY 734 ACGAAGACCTTTCAAGCGAAAGACCTGTAAAGCAGAGCAAACTACAGAGCAGCAGCT 793
| | | | |
Db 802 ACGAAGACCTTTCAAGCGAAAGACCTGTAAAGCAGAGCAAACTACAGAGCAGCAGCT 861
| | | | |
QY 794 GCCTCCCTCAAAATGTTTCTCCAGGGGATTAATTAATGAGCTGTGAGAGACATAACA 853
| | | | |
Db 862 GCCTCCCTCAAAATGTTTCTCCAGGGGATTAATTAATGAGCTGTGAGAGACATAACA 921
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QY 854 CAACAAGAAAAGTATGATGATTAATGCTTAAAGCAGTGCATCCCGTGGGCGGGCCCA 913
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Db 922 CAACAAGAAAAGTATGATGATTAATGCTTAAAGCAGTGCATCCCGTGGGCGGGCCCA 981
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QY 914 TCAAGCCATGAGCATCACTGAGTGCACCTGGTATCATATCGGCAATTCGCGAGCTCTTCA 973
| | | | |
Db 982 TCAAGCCGAGTGCATCACTGAGTGCACCTGGTATCATATCGGCAATTCGCGAGCTCTTCA 1041
| | | | |
QY 974 CTGTGATGTCGCGCAAGAGCAACAAGAAAATATTAATTAACAATTAAAGTGAAGAGAGCT 1033
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Db 1042 CTGTGATGTCGCGCAAGAGCAACAAGAAAATATTAATTAACAATTAAAGTGAAGAGAGCT 1101
| | | | |
QY 1034 CTGAGCTTTCAGATCACTGACAGACTCCCAAGAGAGAGCTCCGGCGCGGCGCAAGG 1093
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Db 1102 CTGAGCTTTCAGATCACTGACAGACTCCCAAGAGAGAGCTCCGGCGCGGCGCAAGG 1161
| | | | |
QY 1094 TCTTTCTGTGCTATTCAGTAAAGATGAGCAGAAATCAATGAATGTCTGCACTGTTTG 1153
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Db 1162 TCTTTCTGTGCTATTCAGTAAAGATGAGCAGAAATCAATGAATGTCTGCACTGTTTG 1221
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QY 1154 CCTACTTCTCCAGAGACTCTGTGGGCTGTGAGAGTGGCTGTGAGCCTGTGGGAAAGACTTCA 1213
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Db 1222 CCTACTTCTCCAGAGACTCTGTGGGCTGTGAGAGTGGCTGTGAGCCTGTGGGAAAGACTTCA 1281
| | | | |
QY 1214 GCCTCTGTAGAGAGAGGACAGAAATGGGTCAATCCAGAAATCCAGAGTCCAGTTCA 1273
| | | | |

Db 1282 GCCTCTGTAGAGAGGACAGAGAAATGGGTCAATCCAGAAATCCAGAGTCCAGTTCA 1341
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QY 1274 TCAATTTGGTTGTTTCCAAAGGATATGAAATCTTTTGGACAAGAAAGACTACAAACACA 1333
| | | | |
Db 1342 TCAATTTGGTTGTTTCCAAAGGATATGAAATCTTTTGGACAAGAAAGACTACAAACACA 1401
| | | | |
QY 1334 AAGAGAGTGGCGAGGCTCGGGGAAAGAGAGCTCTCTGGTGGGCGGTGACGCCATTG 1393
| | | | |
Db 1402 AAGAGAGTGGCGAGGCTCGGGGAAAGAGAGCTCTCTGGTGGGCGGTGACGCCATTG 1461
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QY 1394 CCGAAAAGTCCGCGCAGGCGCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTATCGCG 1453
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Db 1462 CCGAAAAGTCCGCGCAGGCGCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTATCGCG 1521
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| | | | |
QY 1514 ACGAGCTCATGGAACAATCTTCCAGCTGTGTTCCCACTGCACTCCGAGACAAGGCC 1573
| | | | |
Db 1582 ACGAGCTCATGGAACAATCTTCCAGCTGTGTTCCCACTGCACTCCGAGACAAGGCC 1641
| | | | |
QY 1574 TCGAGAGCCGGGGCAGCACGCGACAGGGGACAGAAAGAACTAATTCCGAGCAAGT 1633
| | | | |
Db 1642 TCGAGAGCCGGGGCAGCACGCGACAGGGGACAGAAAGAACTAATTCCGAGCAAGT 1701
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QY 1634 CAGGCGGTCCTTATACGTGCGCAATTTGCAACATGACCAAGTTTATGACAGAGAGCCG 1693
| | | | |
Db 1702 CAGGCGGTCCTTATACGTGCGCAATTTGCAACATGACCAAGTTTATGACAGAGAGCCG 1761
| | | | |
QY 1694 ACTGGTTCGAAAAGCAGTTCGTTCCCTCATCTCTCACTGAGCTACCGGAGCCAG 1753
| | | | |
Db 1762 ACTGGTTCGAAAAGCAGTTCGTTCCCTCATCTCTCACTGAGCTACCGGAGCCAG 1821
| | | | |
QY 1754 TCTTGGAGAAATTTGATTTGAGGCTTGTTTAAATGATGTCAATGTGCAACAGGAGCCCTG 1813
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Db 1822 TCTTGGAGAAATTTGATTTGAGGCTTGTTTAAATGATGTCAATGTGCAACAGGAGCCCTG 1881
| | | | |
QY 1814 AGAGTGAATTTCTGCTTAAAGGATGAGAGCGCTGTTCTTGGGCAACCGGACCGAGACT 1873
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Db 1882 AGAGTGAATTTCTGCTTAAAGGATGAGAGCGCTGTTCTTGGGCAACCGGACCGAGACT 1941
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QY 1874 CCAGACGAGAGTACGACATGGGGGCTGGACCAAGAGGGGAGGCGGGCTGACCTTG 1933
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Db 1942 CCAGACGAGAGTACGACATGGGGGCTGGACCAAGAGGGGAGGCGGGCTGACCTTG 2001
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QY 1934 ACGGTAGCGCGCCCTGCAACCCCTGCTGCAACAGGTGAAGCCGAGCCCTCGAGCA 1993
| | | | |
Db 2002 ACGGTAGCGCGCCCTGCAACCCCTGCTGCAACAGGTGAAGCCGAGCCCTCGAGCA 2061
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QY 1994 TGCCTGGGAGCTCAGGCACTATATGACTGCTGTGTGCTCATCCGAGCTGTCTGCGCAC 2053
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Db 2062 TGCCTGGGAGCTCAGGCACTATATGACTGCTGTGTGCTCATCCGAGCTGTCTGCGCAC 2121
| | | | |
QY 2054 TGATGGAAGGACCTTCGACGAGCAAGAGAAACGTTCCCTGACGAGAGAGCGTGTCT 2113
| | | | |
Db 2122 TGATGGAAGGACCTTCGACGAGCAAGAGAAACGTTCCCTGACGAGAGAGCGTGTCT 2181
| | | | |
QY 2114 CCTCTTCAAGGCTGTGGTGAAGAGAACTCTGACCTTCTCTTCAAGCTCTCTTCTG 2173
| | | | |
Db 2182 CCTCTTCAAGGCTGTGGTGAAGAGAACTCTGACCTTCTCTTCAAGCTCTCTTCTG 2241
| | | | |
QY 2174 GGTCAATGCAAGCAAGATCTTGGTTGCGGAGCTTACATGATGAATCTCAAGGCTGCGCC 2233
| | | | |
Db 2242 GGTCAATGCAAGCAAGATCTTGGTTGCGGAGCTTACATGATGAATCTCAAGGCTGCGCC 2301
| | | | |
QY 2234 CTTTGTAAACAAAAGAAAGCTTAAGCAATTCSCACTTATGATGCTGCTCTCTGAT 2293
| | | | |
Db 2302 CTTTGTAAACAAAAGAAAGCTTAAGCAATTCSCACTTATGATGCTGCTCTCTGAT 2361
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QY 2294 CCCAGCTCATCTCCCTGGTTGCAATGAGCCCACTTGAAGCTGAGTCTCATACAAAGATAT 2353
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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: atcb cloning vector pCMVSPORTS.0
US-11-251-821-44
Query Match
Best Local Similarity 99.6%; Pred. No. 4,6e-37;
Matches 223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Length 4396;

2362 CCCAGCTGATCTCCGTGTTGATGAGCCGCACTTGAGCTGAGCTGCATACAGATAT 2421
2354 TTGAGTGAATGCTGCGCAGTACTGTTCTCCCTGCCCCAACCTTTACCGGATATCT 2413
2422 TTGAGTGAATGCTGCGCAGTACTGTTCTCCCTGCCCCAACCTTTACCGGATATCT 2481
2414 TGAACAACCTCCAAATTTCTTAAATGATATGAGCTGGAAGGAGTCCCAATAGCTC 2473
2482 TGAACAACCTCCAAATTTCTTAAATGATATGAGCTGGAAGGAGTCCCAATAGCTC 2541
2474 TGAACAACCTCCAAATTTCTTAAATGATATGAGCTGGAAGGAGTCCCAATAGCTC 2533
2542 TGAACAACCTCCAAATTTCTTAAATGATATGAGCTGGAAGGAGTCCCAATAGCTC 2601
2534 AGGAAATATGTAAAGAAAACAGAAAGATACCTGCACTAATTCATTCATTGAGC 2593
2602 AGGAAATATGTAAAGAAAACAGAAAGATACCTGCACTAATTCATTCATTGAGC 2661
2594 TCTGCAACCTTCCCTGTTGCTATGCTAGCTACCTTGAATTTGAATGCTTTGAAAAAG 2653
2662 TCTGCAACCTTCCCTGTTGCTATGCTAGCTACCTTGAATTTGAATGCTTTGAAAAAG 2721
2654 GCACCTTAAACATCATAGCAGCAAGAAATCAAGTGCAGCTATCTGGAATCCATGTTGA 2713
2722 GCACCTTAAACATCATAGCAGCAAGAAATCAAGTGCAGCTATCTGGAATCCATGTTGA 2781
2714 TTGCAATAATGTTCTCATTTATTTTGTATGATGAAATTTACATTCGCGATGGTTPAAT 2773
2782 TTGCAATAATGTTCTCATTTATTTTGTATGATGAAATTTACATTCGCGATGGTTPAAT 2841
2774 AAGCTTGAATCAAAAGTCAAGAAAGTGAATGATATACGATCACTTTTATG 2826
2842 AAGCTTGAATCAAAAGTCAAGAAAGTGAATGATATACGATCACTTTTATG 2894

RESULT 2
US-11-251-821-44/c
; Sequence 44, Application US/11251821
; Publication No. US20060035272A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120002
; CURRENT APPLICATION NUMBER: US/11/251,821
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 10/640,422
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/402,920
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/732,914
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 4396

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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: atcb cloning vector pCMVSPORTS.0
US-11-251-821-63
Query Match
Best Local Similarity 99.6%; Pred. No. 4,6e-37;
Matches 223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Length 4396;

2860 GGGGCGGCTCTAGATATCCCTCGAGGGCCCAAGCTTACGCGTACCGAGCTTTCTGT 2919
780 GGGGCGGCTCTAGATATCCCTCGAGGGCCCAAGCTTACGCGTACCGAGCTTTCTGT 721
2920 ACAAGTGTCTCTATGATGAGTCTGATATTAAGCTAGCACTGCGCTTTTCAAC 2979
720 ACAAGTGTCTCTATGATGAGTCTGATATTAAGCTAGCACTGCGCTTTTCAAC 661
2980 GTGCTGACCTGGGAAAACCTGCTAGCTTGGGATCTTTGTGAAGAACCTTCTGTGGTG 3039
660 GTGCTGACCTGGGAAAACCTGCTAGCTTGGGATCTTTGTGAAGAACCTTCTGTGGTG 601
3040 TGACATTAATTGACCAACTACTACAGAGATTTAAAGCTCTAAG 3083
600 TGACATTAATTGACCAACTACTACAGAGATTTAAAGCTCTAAG 557

RESULT 3
US-11-251-821-63
; Sequence 63, Application US/11251821
; Publication No. US20060035272A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120002
; CURRENT APPLICATION NUMBER: US/11/251,821
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 10/640,422
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/402,920
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/732,914
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: atcb cloning vector pCMVSPORTS.0
US-11-251-821-63
Query Match
Best Local Similarity 99.4%; Pred. No. 4,8e-23;
Length 405;

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Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2860 GGGGGCGCTCTAGATATCCCTCGAGGGCCCAAGTTACGGTACCCAGCTTTCTTGT 2919
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DB 250 GGGGGCGCTCTAGATATCCCTCGAGGGCCCAAGTTACGGTACCCAGCTTTCTTGT 309
QY 2920 ACAAATGGTCCCTATATAGTACGCTATTTAAGTACGACGACGCGCTTTTACAAC 2979
    |||
DB 310 ACAAATGGTCCCTATATAGTACGCTATTTAAGTACGACGACGCGCTTTTACAAC 369
QY 2980 GTCTGACTGGGAAACTGCTAGCTTGGATCTTTG 3015
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DB 370 GTCTGACTGGGAAACTGCTAGCTTGGATCTTTG 405
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RESULT 4

US-09-925-065A-50990
Sequence 50990, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 50990
LENGTH: 612
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-50990

Query Match
Best Local Similarity 97.5%; Score 153.8; DB 6; Length 612;
Matches 155; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DB 188 CCAAGTGTGAAGCCTCGAAGCTGAACATCAGCAGCATGCTCGAATGCGAGTGTCC 247
QY 673 TTGACACGACGACCGACAACTTGGCTTCGTTCTTATCTTCACTAACAAGCTCAAG 732
    |||
DB 248 TTGACACGACGACCGACAACTTGGCTTCGTTCTTATCTTCACTAACAAGCTCAAG 307
QY 733 CACGAAGACCTTTCAGGAAAGACTGTAAAGCAGAG 771
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DB 308 CACGAAGACCTTTCAGGAAAGACTGTAAAGCAGAGT 346
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RESULT 5

US-09-925-065A-50991
Sequence 50991, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 50991
LENGTH: 612
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-50991

PRIOR FILING DATE: 2000-10-24

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QY 2860 GGGGGCGCTCTAGATATCCCTCGAGGGCCCAAGTTACGGTACCCAGCTTTCTTGT 2919
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DB 250 GGGGGCGCTCTAGATATCCCTCGAGGGCCCAAGTTACGGTACCCAGCTTTCTTGT 309
QY 2920 ACAAATGGTCCCTATATAGTACGCTATTTAAGTACGACGACGCGCTTTTACAAC 2979
    |||
DB 310 ACAAATGGTCCCTATATAGTACGCTATTTAAGTACGACGACGCGCTTTTACAAC 369
QY 2980 GTCTGACTGGGAAACTGCTAGCTTGGATCTTTG 3015
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DB 370 GTCTGACTGGGAAACTGCTAGCTTGGATCTTTG 405
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US-09-925-065A-50991

Query Match
Best Local Similarity 97.5%; Score 152.6; DB 6; Length 612;
Matches 155; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 188 CCAAGTGTGAAGCCTCGAAGCTGAACATCAGCAGCATGCTCGAATGCGAGTGTCC 247
QY 673 TTGACACGACGACCGACAACTTGGCTTCGTTCTTATCTTCACTAACAAGCTCAAG 732
    |||
DB 248 TTGACACGACGACCGACAACTTGGCTTCGTTCTTATCTTCACTAACAAGCTCAAG 307
QY 733 CACGAAGACCTTTCAGGAAAGACTGTAAAGCAGAG 771
    |||
DB 308 CACGAAGACCTTTCAGGAAAGACTGTAAAGCAGAGT 346
```

RESULT 6

US-09-925-065A-672368
Sequence 672368, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 672368
LENGTH: 2387
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-672368

Query Match
Best Local Similarity 97.5%; Score 152.6; DB 6; Length 2387;
Matches 155; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 613 CCCTTGTGAAGCCTCGAAGCTGAACATCAGCAGCATGCTCGAATGCGAGTGTCC 672
    |||
DB 1963 CCAAGTGTGAAGCCTCGAAGCTGAACATCAGCAGCATGCTCGAATGCGAGTGTCC 2022
QY 673 TTGACACGACGACCGACAACTTGGCTTCGTTCTTATCTTCACTAACAAGCTCAAG 732
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Db 2023 TTGACCATGACACCGACAACCTTGGCTTCCTTCTTATCTGACATGACATCAAG 2082
 QY 733 CACGAGACCTTTCAAGGAAAGACCTTAACAGAG 771
 Db 2083 CACGAGACCTTTCAAGGAAAGACCTTAACAGAG 2121

RESULT 7
 US-11-102-026A-6

; Sequence 6, Application US/11102026A
 ; Publication No. US20060021087A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology LLC
 ; APPLICANT: Baum, James A
 ; APPLICANT: Gilbertson, Larry A
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: LaRosa, Thomas J
 ; APPLICANT: Lu, Maolong
 ; APPLICANT: Munyikwa, Tichifa R. I.
 ; APPLICANT: Roberts, James K
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Zhang, Bei
 ; TITLE OF INVENTION: Compositions and Methods for Control of Insect Infestations in Pl
 ; FILE REFERENCE: 38-21(53596)
 ; CURRENT APPLICATION NUMBER: US/11/102,026A
 ; CURRENT FILING DATE: 2005-04-08
 ; PRIOR APPLICATION NUMBER: 60560842
 ; PRIOR FILING DATE: 2004-04-09
 ; PRIOR APPLICATION NUMBER: 60565632
 ; PRIOR FILING DATE: 2004-04-27
 ; PRIOR APPLICATION NUMBER: 60579062
 ; PRIOR FILING DATE: 2004-06-11
 ; PRIOR APPLICATION NUMBER: 60603421
 ; PRIOR FILING DATE: 2004-08-20
 ; PRIOR APPLICATION NUMBER: 60617261
 ; PRIOR FILING DATE: 2004-10-11
 ; PRIOR APPLICATION NUMBER: 60669241
 ; PRIOR FILING DATE: 2005-04-07
 ; NUMBER OF SEQ ID NOS: 190
 ; SEQ ID NO 6
 ; LENGTH: 2656
 ; TYPE: DNA
 ; ORGANISM: Lygus hesperus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: n is a, c, g, or t
 US-11-102-026A-6

Query Match 3.9%; Score 118.8; DB 12; Length 2656;
 Best Local Similarity 61.1%; Pred. No. 2.8e-15;
 Matches 192; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 2770 AATAAGCTTGTGCAAAAGTCAAGAAAGTCAATTAATACGACCTTTTAAAGAA 2829
 Db 2083 AA 2142
 QY 2830 TGAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTAGATATCCCTCGAGGG 2889
 Db 2143 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTTAAATCCCGCGGG 2202
 QY 2890 CCCAGCTTACGCGTACCCAGCTTCTGTGCAAAAGTGTCTCTATAGTGAATTA 2949
 Db 2203 GCCCAATTTTCCGAGACCCCTTTTGTGAAAAAGGCGGCCCTTAAGGCGCTATTT 2262
 QY 2950 TAAGTAGGACAGCGCGCTGTTTCAACGCTGTAAGTGAAGAACTGCTACTTGGGA 3009
 Db 2263 AAAAGTAGGCGCGCGCGCTGTTTAAACGCGCGCGGGAATGTTAATTTGGGA 2322
 QY 3010 TCTTTGGAAGAACCTTCTCTGTGTGTGAATTAATTTGACAACTACCTACAGAG 3069
 Db 2323 TTTTGTGGAAGAACCTTTTGTGGGCGGGAATATTGGGAAAAATCCCAAAAA 2382

QY 3070 TTTAAGCTTAAG 3083
 Db 2383 TTTAAGCTTTAAG 2396

RESULT 8
 US-09-925-065A-829666

; Sequence 829666, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 829666
 ; LENGTH: 599
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-829666

Query Match 3.8%; Score 117.2; DB 6; Length 599;
 Best Local Similarity 97.5%; Pred. No. 3.8e-15;
 Matches 119; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 613 CCCTTGTGAGAGCTTGGAACTGAACATGACCGACATGCGTGGACATGCGGTGCC 672
 Db 478 CCACTGTGAGAGCTTGGAACTGAACATGACCGACATGCGTGGACATGCGGTGCC 537
 QY 673 TTGACCATGACACCGACAACCTTGGCTTCCTTCTTATCTGACATGACATCAAG 732
 Db 538 TTGACCATGACACCGACAACCTTGGCTTCCTTCTTATCTGACATGACATCAAG 597
 QY 733 CA 734
 Db 598 CA 599

RESULT 9
 US-10-991-285-284

; Sequence 284, Application US/10991285
 ; Publication No. US20060041962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
 ; TITLE OF INVENTION: GENES AND USES THEREOF TO MODULATE SECONDARY METABOLITE BIOSYNTHESIS
 ; FILE REFERENCE: DIN/SEM/V116
 ; CURRENT APPLICATION NUMBER: US/10/991,285
 ; CURRENT FILING DATE: 2004-11-16
 ; PRIOR APPLICATION NUMBER: EP02076973.3
 ; PRIOR FILING DATE: 2002-05-17
 ; NUMBER OF SEQ ID NOS: 901
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 284
 ; LENGTH: 1434
 ; TYPE: DNA
 ; ORGANISM: Nicotiana tabacum
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: MAP2
 US-10-991-285-284

QY	2830	TGAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCCGCTAGAGTATCCCTGAGGGG	2889
Db	800	AAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGCTTTTAAATTTCCCGGGGGG	741
QY	2890	CCCAAGCTTACGCGTACCACGCTTTCTTGTACAAAGTGTCCTTAATAGTGGATTTA	2949
Db	740	GGCCAATTTTTTGGGGCCCCCTTTTTTTTTTAAAAAGGGGGCCCCCAAGGGGGGGTTT	681
QY	2950	TAAGCTAGGCACTGGCCGTCGTTTTACAAGTCGAGATGGGAAACCTGTAAGTTGGGA	3009
Db	680	AAAAAAAAAGGGGGGGGGGGGTTTTTAAACCGGGGGGGGAAAAATTTTTTTGGCT	621
QY	3010	TCCTTGTGAAGAACTTACTTCCTGTGTGTGACATAATTTGACAAACTACTACAGAGA	3068
Db	620	TTTTTTTGGAAAAACACTTTTTTTTGGGGGGGGGTTTTTGGAAAAACCCCCCCAGAAA	561
QY	3070	TTTAAAGCTC	3080
Db	560	ATTTAGGCTT	550

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RESULT 13
US-11-193-750-1/c
; Sequence 1, Application US/11193750
; Publication No. US20050273873A1
; GENERAL INFORMATION:
; APPLICANT: Avigenics, Inc
; TITLE OF INVENTION: MODIFICATION OF THE GENOME BY INTRODUCTION OF LARGE NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: AVI-025CIP4
; CURRENT APPLICATION NUMBER: US/11/193,750
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/11/068,155
; PRIOR FILING DATE: 2005-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pCMV-31int
US-11-193-750-1

Query Match          2.8%; Score 86; DB 12; Length 6230;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2998  GCTAGCTTGGGATCTTTGTGGAAGAACCTTACTTCTGTGTTGTTGACATTAATTGGACAAC 3057
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DB      641   GCTAGCTTGGGATCTTTGTGGAAGAACCTTACTTCTGTGTTGTTGACATTAATTGGACAAC 582

QY      3058  TACCTACAGAGATTTAAAGCTCTAAG 3083
          |||||||
DB      581  TACCTACAGAGATTTAAAGCTCTAAG 556

RESULT 14
US-11-096-622-20/c
; Sequence 20, Application US/11096622
; Publication No. US20050260643A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: DAY, CHI-PING
; APPLICANT: RAU, KUN-MING
; APPLICANT: XIE, XIAOMING
; APPLICANT: LI, ZHENG
; TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS
; FILE REFERENCE: UTSC:845US
; CURRENT APPLICATION NUMBER: US/11/096,622
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/559,111
; PRIOR FILING DATE: 2004-04-02

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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 8512
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-096-622-20

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Query March 2.7%; Score 83; DB 12; Length 8512;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	3001	AGCTTGGATCTTGTGTAAGGAACCTTACTTCTGTGTGATGACATTAATTGGACAAACTAC	3066
DB	470	AGCTTGGATCTTGTGTAAAGGAACCTTACTTCTGTGTGATGACATTAATTGGACAAACTAC	411
QY	3061	CTACAGAGATTTAAGCTTAAG	3083
DB	410	CTACAGAGATTTAAGCTTAAG	388

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RESULT 15
US-11-096-622--21/c
: Sequence 21, Application US/11096622
: Publication No. US20050260643A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: DAY, CHI-PING
APPLICANT: RAO, KUN-MING
APPLICANT: XIE, XIAOMING
APPLICANT: LI, ZHENG
TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS
FILE REFERENCE: UTSC:845US
CURRENT APPLICATION NUMBER: US/11/096,622
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: 60/559,111
PRIOR FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 8565
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-096-622-21

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	Query Match	2.7%	Score 83;	DB 12;	Length 8565;
	Best Local Similarity	100.0%;	Pred. No.	1.4e-07;	
	Matches	83;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Oy	3001	AGCTGGGATCTTGTGAAGAACCCTACTCTGTGTGTGCATATAATTGACCAAACTAC			3060
Dd	567	AGCTGGGATCTTGTGAAGAACCCTACTCTGTGTGTGCATATAATTGACCAAACTAC			508
Oy	3061	CTACAGAGATTAAAGCTTAAG			3083
Dd	507	CTACAGAGATTAAAGCTTAAG			485

Search completed: March 1, 2006, 11:15:43
Job time : 3282 secs

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1	2678.6	86.9	2894	3	US-10-104-047-1429	Sequence 1429, App
2	2426.4	78.7	3948	3	US-09-799-651-125	Sequence 125, App
3	2075.6	67.3	2319	3	US-09-747-259-17	Sequence 17, App
4	194.6	6.3	2334	3	US-09-504-615-15	Sequence 15, App
5	194.6	6.3	2334	3	US-10-054-938-15	Sequence 15, App
6	178.6	5.8	2799	3	US-09-181-399-2	Sequence 2, App
7	113	3.7	2243	3	US-09-620-312D-12	Sequence 12, App
8	111.8	3.6	1277	3	US-09-620-312D-968	Sequence 968, App
9	108.4	3.5	2265	3	US-09-620-312D-108	Sequence 108, App
10	108.4	3.5	2349	3	US-09-620-312D-109	Sequence 109, App
11	106.8	3.5	1476	3	US-09-620-312D-964	Sequence 964, App
12	90.8	2.9	4062	3	US-09-620-312D-348	Sequence 348, App
13	89.8	2.9	1912	3	US-09-620-312D-742	Sequence 742, App
14	89.4	2.9	2275	3	US-09-620-312D-100	Sequence 100, App
15	89.4	2.9	2817	3	US-09-620-312D-101	Sequence 101, App
16	87	2.8	2817	3	US-09-620-312D-101	Sequence 101, App
17	86	2.8	1717	3	US-09-153-927-11	Sequence 11, App
18	86	2.8	1717	3	US-10-082-260-1	Sequence 1, App
19	86	2.8	1717	3	US-08-815-783-1	Sequence 1, App
20	86	2.8	1717	3	US-09-879-919-1	Sequence 1, App
21	86	2.8	6674	3	US-09-620-312D-110	Sequence 110, App
22	85.8	2.8	828	3	US-09-620-312D-103	Sequence 103, App
23	85.8	2.8	8225	3	US-08-793-618-1	Sequence 1, App
24	85.8	2.8	8225	3	US-09-794-431-1	Sequence 1, App

25	85	5030	2	US-08-588-201-14	Sequence 14, Appl
26	85	5030	2	US-09-169-605-11	Sequence 14, Appl
27	85	5030	3	US-08-893-337-14	Sequence 14, Appl
28	84.8	7731	3	US-09-301-553-29	Sequence 29, Appl
29	84.8	7731	3	US-09-301-553-42	Sequence 42, Appl
30	84.8	7892	2	US-07-916-038A-40	Sequence 40, Appl
31	83.4	6674	3	US-07-620-312D-110	Sequence 110, Appl
32	81.8	3251	2	US-09-410-132-1	Sequence 12, Appl
33	79.2	6151	6	PCR-US91-02954-12	Sequence 12, Appl
34	79	4059	6	US-08-564-313-2	Sequence 2, Appl
35	79	4059	6	PCR-US94-06069-2	Sequence 2, Appl
36	78.8	1606	3	US-09-620-312D-99	Sequence 99, Appl
37	78.6	10728	3	US-09-376-774-5	Sequence 5, Appl
38	78	3318	3	US-08-169-613A-1	Sequence 1, Appl
39	77.6	5516	3	US-09-826-630-9	Sequence 9, Appl
40	77.6	5178	2	US-08-474-169-2	Sequence 2, Appl
41	77.4	6206	2	US-08-474-169-3	Sequence 3, Appl
42	77.4	6601	2	US-08-233-463-15	Sequence 15, Appl
43	77.2	77318	2	US-08-233-463-14	Sequence 14, Appl
44	77.2	9690	2	US-08-233-463-18	Sequence 18, Appl
45	77.2	9916	2	US-08-233-463-17	Sequence 17, Appl

ALIGNMENTS

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RESULT 1
US-10-104-047-1429
; Sequence 1429, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cdnna
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1429
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1429

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Query Match	86.9%	Score 2678.6;	DB 3;	Length 2894;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 2684; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0

Qy	134	CCGTGGCTGAGAGGGGAGTGGGGGCCAGGCAGGAGAGAAACAGTGGCTGTACAACTCACT	193
Db	202	CCGTGGCTTGGCAGGGGAGTGGGGCCAGGCAGGAGAAAACATGGGCTGTACAACTCACT	261
Qy	194	TCAAAATATGACAAATGTATACACCTTCTTGAAATCCAGTGGGGAGACATGTATTTGCTGACG	253
Db	262	TCAAAATATGACAAATGTATACACCTTCTTGAAATCCAGTGGGGAGACATGTATTTGCTGACG	321
Qy	254	CCGAGATATCAACCATCAGCCAGTATGGCTTCCATGACCAAGTGGCAGTCACTCTTT	313
Db	322	CCGAGATATCAACCATCAGCCAGTATGGCTTCCATGACCAAGTGGCAGTCACTCTTT	381
Qy	314	GGTCCCAAGGGGCCCTCCGCATCCGAATTCCTGAAAGGATTTCCGGTAACTCTGAGGAGC	373
Db	382	GGTCCCAAGGGGCCCTCCGCATCCGAATTCCTGAAAGGATTTCCGGTAACTCTGAGGAGC	441
Qy	374	TGAAGTCGAGGGGAGAGACAGTGCACCAACACTGATTTCTAAAGATCCGAGCAGCTCAACA	433
Db	442	TGAAGTCGAGGGGAGAGACAGTGCACCAACACTGATTTCTAAAGATCCGAGCAGCTCAACA	501
Qy	434	GTAGCTTCAAAAGAACTGGAATGGAATTCACAACCTTTCTGAAATATGAAATTTGAAACGG	493
Db	502	GTAGCTTCAAAAGAACTGGAATGGAATTCACAACCTTTCTGAAATATGAAATTTGAAACGG	561

QY	494	TTATATTTCTGTAAGTGTGCTCTTTTCTCTTCAATTAAAGAAAGCAATTACACCCCT	553
Db	562	ATATATTTCTGTAAGGTGTGCTCTTTTCTCTCAATTAAAGAAAGCAATTACACCCCT	621
QY	554	TCCTCTTTAGAACCCGAGCTGTGACCTGTGTGTTACAGCCGGACCAATCTAGCTTTAAAC	613
Db	622	TCCTCTTTAGAACCCGAGCTGTGACCTGTGTGTTACAGCCGGACCAATCTAGCTTTAAAC	681
QY	614	CCTTCTGGAAAGCTTCGGAACTGAAACATCAGCCAGCATGCTCGGACATGCAAGTGTCTCT	673
Db	682	CCTTCTGGAAAGCTTCGGAAAGCTGAAACATCAGCCAGCATGCTCGGACATGCAAGTGTCTCT	741
QY	674	TCGACCAAGCCGCGCAACATTCCTGGCTTCGCTTTCTTATCTTCACTACACAAAGCTCAAGC	733
Db	742	TCGACCAAGCCGCGCAACATTCCTGGCTTCGCTTTCTTATCTTCACTACAGCTCAAGC	801
QY	734	ACGAAAGACCTTTCAAGCCGAAAGACCTGTAAAGCAGAGCAAACTACAGAGACGACAGCT	793
Db	802	ACGAAAGACCTTTCAAGCCGAAAGACCTGTAAAGCAGAGCAAACTACAGAGTACACAGCT	861
QY	794	GGCTTCCTTCAAAATGTTTCTTCAAGGGATTTATATTAATTGACCTGGTGGATGACCTAAAC	853
Db	862	GGCTTCCTTCAAAATGTTTCTTCAAGGGATTTATATTAATTGACCTGGTGGATGACCTAAAC	921
QY	854	CAACAAAGAAAGTATGATGATTTATGCTTTAAAGCCAGTGCACCTCCCGTGGCCGCGGCCCA	913
Db	922	CAACAAAGAAAGTATGATGATTTATGCTTTAAAGCCAGTGCACCTCCCGTGGCCGCGGCCCA	981
QY	914	TCAGAGCCATGCGCATCAACAGTGCACCTGTGATGTCATATCGGCATTTGCCACGCTCTTCA	973
Db	982	TCAGAGCCGATGCGCATCAACAGTGCACCTGTGATGTCATATCGGCATTTGCCACGCTCTTCA	1041
QY	974	CTGTGATGTGCGCGCAAGAAAGCAACAAGAAATATATATTTCACATTTAATAGAAAGAGCT	1033
Db	1042	CTGTGATGTGCGCGCAAGAAAGCAACAAGAAATATATATTTCACATTTAATAGAAAGAGCT	1101
QY	1034	CTGAGCTTTCACATPACACTGACAGCACTCCCAAGAGAGAGGCTCCGCGCGCGCCGAAGG	1093
Db	1102	CTGAGCTTTCACATPACACTGACAGCACTCCCAAGAGAGAGGCTCCGCGCGCGCCGAAGG	1161
QY	1094	TCCTTCTCTGTATTTCCAGTAAAGATGGCCAGAAATCAATGAATGTGCTCCAGATTTTGG	1155
Db	1162	TCCTTCTCTGTATTTCCAGTAAAGATGGCCAGAAATCAATGAATGTGCTCCAGATTTTGG	1221
QY	1154	CCTAATTCCTTCAGAGACTTCTGTGGCTGTGAGTGAGTGGCTCTGAGACCTGTGTGGAAAGCTTCA	1213
Db	1222	CCTAATTCCTTCAGAGACTTCTGTGGCTGTGAGTGAGTGGCTCTGAGACCTGTGTGGAAAGCTTCA	1281
QY	1214	GCCCTCTGTAGAAAGGGCGAGAGAAATGGGTTCATCCAAAGATCCACAGTCCCAAGTTCAC	1273
Db	1282	GCCCTCTGTAGAAAGGGCGAGAGAAATGGGTTCATCCAAAGATCCACAGTCCCAAGTTCAC	1341
QY	1274	TCATTGTGTGTTGTTCTCAAAAGGTATGAAGTACTTTGTGTGACAAAGAAAGCACTACAAACACA	1333
Db	1342	TCATTGTGTGTTGTTCTCAAAAGGTATGAAGTACTTTGTGTGACAAAGAAAGCACTACAAACACA	1401
QY	1334	AAGAGGTGCGCGAGGCTCGGCGAAAGAGAGCTTCTCTGTGTGCGGTGTCAAGCATTTG	1393
Db	1402	AAGAGGTGCGCGAGGCTCGGCGAAAGAGAGAGCTTCTCTGTGTGCGGTGTCAAGCATTTG	1461
QY	1394	CCGAAAGAGCTCCGCGAAGCCGCAAGCAAGATTCGTCCGCGCGCTCAGCAAGTTTATCCGCG	1455
Db	1462	CCGAAAGAGCTCCGCGAAGCCGCAAGCAAGATTCGTCCGCGCGCTCAGCAAGTTTATCCGCG	1521
QY	1454	TCCTACTTTGATTTATTCCTGTGCGAGGAGAGAGTCCCGGATATCTTGAAGCTCTGATACCAAGT	1513
Db	1522	TCCTACTTTGATTTATTCCTGTGCGAGGAGAGAGTCCCGGATATCTTGAAGCTCTGATACCAAGT	1581
QY	1514	ACAGAGCTCATGGAACAAATTTCTCTCAAGCTCTGTGTTCCCACTGTGCACTGCCGAGACCAAGGCC	1573
Db	1582	ACAGAGCTCATGGAACAAATTTCTCTCAAGCTCTGTGTTCCCACTGTGCACTGCCGAGACCAAGGCC	1641

QY	1574	TCGAGGAGCCGGGGCAGCACACCGGACAGGGGACAGAAACTACTTCGCGAGCAAGT	1633
Db	1642	TCGAGGAGCCGGGGCAGCACACCGGACAGGGGACAGAAAGAACTACTTCGCGAGCAAGT	1701
QY	1634	CAGGCCCGGTCCCTATAGTGCACATTGTCGAAACAATGCACAGTTATATGACGAGAGCCCG	1693
Db	1702	CAGGCCCGGTCCCTATAGTGCACATTGTCGAAACAATGCACAGTTATATGACGAGAGAGCCCG	1761
QY	1694	ACTGGTTTGAAAAGCAGATTGTTCCCTTCATCTCTCCATCTGCGTACCTGGAGCCAG	1753
Db	1762	ACTGGTTTGAAAAGCAGATTGTTCCCTTCATCTCTCCATCTGCGTACCTGGAGAGCCAG	1821
QY	1754	TCCTTGAGAAATTTGATTTCGGGCTTGGTTTTAAATGATATGATCATATGTGAAAACAGAGGCTG	1813
Db	1822	TCCTTGAGAAATTTGATTTCGGGCTTGGTTTTAAATGATATGATCATATGTGAAAACAGAGGCTG	1881
QY	1814	AGAGTGACTTCTGCGCTTAAGGTAAGAGGCGCTGTCTTGTGGGGCAACCGGACACAGCCGACT	1873
Db	1882	AGAGTGACTTCTGCGCTTAAAGGTAGAGGCGGCTGTCTTGTGGGGCAACCGGACACAGCCGACT	1941
QY	1874	CCGACGACAGAGATCAGCATGGGGGCTTGACACAGACGCGGAGGCCCGGCTGCTTG	1933
Db	1942	CCGACGACAGAGAGTCAACATGGGGGCTTGACACAGACGCGGAGGCCCGGCTGCTTG	2001
QY	1934	ACGGTACCGCGCGCTTGCACAACCTCTGCTGCACACAGTGAAAGCCGCGACGCCCTCTCGGACA	1993
Db	2002	ACGGTACCGCGCGCTTGCACAACCCCTGTGACACAGGTGAAAGCCGCGACGCCCTCTCGGACA	2061
QY	1994	TGCGCGGGAGACTCAGGAGATCTATGACTCGTCTGAGCCCTATCCAGGACCTGTCTCTGCAAC	2053
Db	2062	TGCGCGGGAGACTCAGGAGATCTATGACTCGTCTGAGCCCTATCCAGGACCTGTCTCTGCAAC	2121
QY	2054	TGATGGAAGGACTTCGACGGAACGACACAGAAAAGTCTTCCCTGACGAGAGCGTGTCT	2113
Db	2122	TGATGGAAGGACTTCGACCGGACGACACAGAAAAGTCTTCCCTGACGAGAGCGTGTCT	2181
QY	2114	CCTCTTCAAGGCTTGGGTGAGAGGAAGACTCTGCGCTTCTCTTCCAGCTCTCTCTTCTG	2173
Db	2182	CCTCTTCAAGGCTTGGGTGAGAGGAAGACTCTGCGCTTCTCTTCCAGCTCTCTCTTCTG	2241
QY	2174	GGTATGCAAGAGCAGATCTTGGTTGGCGGAGCTTACACTGATGAACTCACGCGGTGCGCC	2233
Db	2242	GGTATGCAAGAGCAGATCTTGGTTGGCGGAGCTTACACTGATGAACTCACGCGGTGCGCC	2301
QY	2234	CTTGTGTAACAAAACGAAAGAGTCTTACAGCTTGGCATTGTCAGTCTGCTCCCTCTGATTT	2293
Db	2302	CTTGTGTAACAAAACGAAAGAGTCTTACAGCTTGGCATTGTCAGTCTGCTCCCTCTGATTT	2361
QY	2294	CCCCAGCTCATCTCCCTGTGTCATGGCCCATCTTGAAGCTGAGAGTCTCATACAAAGATAT	2353
Db	2362	CCCCAGCTCATCTCCCTGTGTCATGGCCCATCTTGAAGCTGAGAGTCTCATACAAAGATAT	2421
QY	2354	TTTGAGAGGAATGTGGCGCAGTACTTGTCTCCCTGGCCCAACCCCTTACCCGGAATATCT	2413
Db	2422	TTTGAGAGGAATGTGGCGCAGTACTTGTCTCCCTGGCCCAACCCCTTACCCGGAATATCT	2481
QY	2414	TGACAAACTCTCCAAATTTTCTTAAATATATATGAGCTCTGAAAGGCATGTCCATTAAGTCT	2473
Db	2482	TGACAAACTCTCCAAATTTTCTTAAATATATATGAGCTCTGAAAGGCATGTCCATTAAGTCT	2541
QY	2474	TGACAAACAGCTTGCACAAATTTGGTTAGTCTTGGATCAGAGCCGTGTTGGGAGAGTAAAGG	2533
Db	2542	TGACAAACAGCTTGCACAAATTTGGTTAGTCTTGGATCAGAGCCGTGTTGGGAGAGTAAAGG	2601
QY	2534	AGGAAATATGTGTAAGAAACAAAGAAATATACCTGCATATATCATTTGACATTTAGAGC	2593
Db	2602	AGGAAATATGTGTAAGAAACAAAGAAATATACCTGCATATATCATTTGACATTTAGAGC	2661
QY	2594	TCGCAAACTTTGGCTGTGTGCTATATTTGGCTACCTGTGATTTGAAATGCTTTGTGAAAAAG	2653
Db	2662	TCGCAAACTTTGGCTGTGTGCTATATTTGGCTACCTGTGATTTGAAATGCTTTGTGAAAAAG	2721
QY	2654	GCACTTTTAACTATCATGACACAGAAATCAAGTGCAGTCTATCTGGAATCATGTTGTA	2713

Accession	Sequence	Position
D8	2722 GCACCTTTAACTCATCATACGACAGAAATCAAGTGGCACTCATCTCGAATCCATCTGTGA	2781
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D8	2782 TTGCAGATTAAGTCTCATTTATTTTGAATGATGAATTTACATTCGCAATGGGTGTTAAT	2841
Q7	2774 AAGCTTTAGTCAAAAGTCAGAAGAGTACATGAATATACAGACACCTTTTATG	2826
D8	2842 AAGCTTTAGTCAAAAGTCAGAAGAGTACATGAATATACAGACACCTTTTATG	2894

RESULT 2
US-09-799-451-125
; Sequence 125, Application US/09799451

```

APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aiding J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yungqing
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhimei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Keena
APPLICANT: Dmanac, Radjoe T.
TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/07/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 125
LENGTH: 3948
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS (1844)
LOCATION: (60)..(1844)
OS-09-799-451-125

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Query Match	78.7%;	Score 2426.4;	DB 3;	Length 3948;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 2430; Conservative	0;	Mismatches	6;	Indels 0; Gaps 0;

QY	397	CAACACACGATTCCTAAAGATCCGAAGACGTCACACAGTAGCTTCATAAAGACATGAATG	456
Db	3	CCACAACATCGATTCCTAAAGATCCGAAGACGTCACACAGTAGCTTCATAAAGACATGAATG	62
QY	457	GAATCTCAACCTTCTCTGAATATGAAATTGGAATCGAATTTATTCCTGAAGGTTGTCCT	516
Db	63	GAAATCTCAACCTTCTCTGAATATGAAATTGGAATCGAATTTATTCCTGAAGGTTGTCCT	122
QY	517	TTTCTCTCATTTAAAAAGAAAGCAATTACCAACCTTTCTTCTTTAGAACCCGACCTGT	576
Db	123	TTTCTCTCATTTAAAAAGAAAGCAATTACCAACCTTTCTTCTTTAGAACCCGACCTGT	182
QY	577	GACCGTGTGTAAACGCGGAGCAACTAGCTGTAAACCTTCGTGAAGCGCTCGAAGCTG	636
Db	183	GACCTGTGTGTAAACGCGGAGCAACTAGCTGTGTAAACCTTCGTGAAGCGCTCGAAGCTG	242
QY	637	AACATCAGCCAGCATGCTCGGACATGCAAGGTGTCTTCAGACAGCAACCGGACAACTTC	696

Db	243	AACATCAAGCCAGCAATGGCTGGACATGCAAGGTGCTTTCGACCAAGCAACGCCACAATTC	302
OY	697	GGCTTCGGTTTCTTCTATCTTCACTACAAGTCAAGCAACGAAGACCTTTCAACGGAAG	756
Db	303	GGCTTCGGTTTCTTCTATCTTCACTACAAGTCAAGCAACGAAGACCTTTCAACGGAAG	362
OY	757	ACCTGTAAAGCAGGAGCAAACTCAAGAGACGACAGTGGCTTCCTCAAAATGTTTCTTCCA	816
Db	363	ACCTGTAAAGCAGGAGCAAACTCAAGAGATGACAGTGGCTTCCTCAAAATGTTTCTTCCA	422
OY	817	GGGATTAATAATATTGAGCTGTGTGATGACACTAAACAACAAGAAAAGTATCATTTAT	876
Db	423	GGGATTAATAATATTGAGCTGTGTGATGACACTAAACAACAAGAAAAGTATCATTTAT	482
OY	877	GCTTTAAAGCCAGTGACACTCCCGGTGGCCGCGGACCATGAGGCAATGGCCATCAAGTG	936
Db	483	GCTTTAAAGCCAGTGACACTCCCGGTGGCCGCGGACCATGAGGCAATGGCCATCAAGTG	542
OY	937	CCACTGTGATGATCATATGGGCAATTCGGCAGCTCTTCACTGATGATGTCGGCAAGAA	996
Db	543	CCACTGTGATGATCATATGGGCAATTCGGCAGCTCTTCACTGATGATGTCGGCAAGAA	602
OY	997	CAAGAAAATATATATTTCACTTTGATGATGAAGAGAGCTCTGAGTCTTCCACATACCTGCA	1056
Db	603	CAAGAAAATATATATTTCACTTTGATGATGAAGAGAGCTCTGAGTCTTCCACATACCTGCA	662
OY	1057	GCACTCCCAAGAGAGAGGCTCCCGGCGCGGCGGAAGGCTTTCTCTGCTATTCAGTAA	1116
Db	663	GCACTCCCAAGAGAGAGGCTCCCGGCGCGGCGGAAGGCTTTCTCTGCTATTCAGTAA	722
OY	1117	GATGGCCAGATTCATCATGATGTGTCTCAGTGTTCGCTTACTTCTTCAGAGATTTCTGT	1176
Db	723	GATGGCCAGATTCATCATGATGTGTCTCAGTGTTCGCTTACTTCTTCAGAGATTTCTGT	782
OY	1177	GGCTGTGAGGCTGCTCGAGACTGTGTGGAAAGACTTCAGCCTCTGTAGGAAGGCGAGAGA	1236
Db	783	GGCTGTGAGGCTGCTCGAGACTGTGTGGAAAGACTTCAGCCTCTGTAGGAAGGCGAGAGA	842
OY	1237	GAATGGGTCAATCCAGAAAGATCCAGAGTCCCAATTCAATGTGTGTTTCTTCAAAAGT	1296
Db	843	GAATGGGTCAATCCAGAAAGATCCAGAGTCCCAATTCAATGTGTGTTTCTTCAAAAGT	902
OY	1297	ATGAAGTACTTTGTGTGAACAAGAGAACTTCAAAACAACAAGAGGTTGGCCGAGGCTCGGG	1356
Db	903	ATGAAGTACTTTGTGTGAACAAGAGAACTTCAAAACAACAAGAGGTTGGCCGAGGCTCGGG	962
OY	1357	AAAGGAGAGCTCTTCTCTGTGTGGCGGTCTCAGCCATTGCCAAAGGCTCCGCAAGGCAAG	1416
Db	963	AAAGGAGAGCTCTTCTCTGTGTGGCGGTCTCAGCCATTGCCAAAGGCTCCGCAAGGCAAG	1022
OY	1417	CAGAGTTCTGTCCGCGGGCGGCTCAGCAAGTTTATCGCCGCTTACTTTGATTTTCTTGGAG	1476
Db	1023	CAGAGTTCTGTCCGCGGGCGGCTCAGCAAGTTTATCGCCGCTTACTTTGATTTTCTTGGAG	1082
OY	1477	GGAGAGCTCCCCGGTATCTTGAACCTGAGTCAACAAGTACAGACTCATGGAACAATCTTCT	1536
Db	1083	GGAGAGCTCCCCGGTATCTTGAACCTGAGTCAACAAGTACAGACTCATGGAACAATCTTCT	1142
OY	1537	CAGCTCTGTTCCTCAGCTGTGCACTCCCGAGACCAAGGCTCTCAAGAGCGGGGAGACACAAG	1596
Db	1143	CAGCTCTGTTCCTCAGCTGTGCACTCCCGAGACCAAGGCTCTCAAGAGCGGGGAGACACAAG	1202
OY	1597	CGACAGGGGAGCAAGAAAGAACTATTCGCGAGCAAGTCAAGGCGGGTCCCTATAGTGGCC	1656
Db	1203	CGACAGGGGAGCAAGAAAGAACTATTCGCGAGCAAGTCAAGGCGGGTCCCTATAGTGGCC	1262
OY	1657	ATTGTGAACATGACCAAGTTTATTGAGAGAGGCCGCACTGGTTGAAAAGCAATTCGTT	1716
Db	1263	ATTGTGAACATGACCAAGTTTATTGAGAGAGGCCGCACTGGTTGAAAAGCAATTCGTT	1322
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Db	1323	CCCTTTCATCTCTCTCACTGTGCGTATCCGGGAGCCAGTCTTGAGAAATTTGATTTGGGC	1382

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1897 GAGGCGGCTGTTCTTGGGGCAACCGGAGCGGCTGAGAGTGAAGGCGGCGGCGGCAACC 1956
1503 GAGGCGGCTGTTCTTGGGGCAACCGGAGCGGCTGAGAGTGAAGGCGGCGGCGGCAACC 1562
1957 CTGTGTCACACGGGTGAAGACCGGACCGCTCGGACATGCGCGGAGCTCAGGACATCTAT 2016
1563 CTGTGTCACACGGGTGAAGACCGGACCGCTCGGACATGCGCGGAGCTCAGGACATCTAT 1622
2017 GACTGCTGTGTCCTCATCTCCAGCTGTCTCTGCACTGATGGAAGAACTCTTGACGAGAC 2076
1623 GACTGCTGTGTCCTCATCTCCAGCTGTCTCTGCACTGATGGAAGAACTCTTGACGAGAC 1682
2077 CAGACAGAAACGTTCTTCCCTGACGAGAGCTGTCTCTCTTCAAGGCTTGAGTGAAGAG 2136
1683 CAGACAGAAACGTTCTTCCCTGACGAGAGCTGTCTCTCTTCAAGGCTTGAGTGAAGAG 1742
2137 GAACCTCTGCGCTTCTTCAAGCTCTCTCTTGGGTCATGCAAGCAGATCTTGGT 2196
1743 GAACCTCTGCGCTTCTTCAAGCTCTCTCTTGGGTCATGCAAGCAGATCTTGGT 1802
2197 TGCCGAGCTACACGTATGAACTCCACGCGGTGCGCTTGGTGAACAAACGAAAGAGTC 2256
1803 TGCCGAGCTACACGTATGAACTCCACGCGGTGCGCTTGGTGAACAAACGAAAGAGTC 1862
2257 TTAAGCATTTGGCCTTTAGCTGCTGCTCTCTGATTTCCCGAGCTATCTCCCTGTTGC 2316
1863 TTAAGCATTTGGCCTTTAGCTGCTGCTCTCTGATTTCCCGAGCTATCTCCCTGTTGC 1922
2317 ATGGCCCACTTGAAGCTGAGTCTCATACAGGAATTGAGTGAATGTCGACGATA 2376
1923 ATGGCCCACTTGAAGCTGAGTCTCATACAGGAATTGAGTGAATGTCGACGATA 1982
2377 CTGTGTTCTGCTTGGCCCAACCTTTACCGGATATCTTGAACAACTCTCAATTTCTAA 2436
1983 CTGTGTTCTGCTTGGCCCAACCTTTACCGGATATCTTGAACAACTCTCAATTTCTAA 2042
2437 AATGATATGAGACTCTGAAAGGCAATCCATAAGTCTGACAAACAGCTTGCCAAATTTGG 2496
2043 AATGATATGAGACTCTGAAAGGCAATCCATAAGTCTGACAAACAGCTTGCCAAATTTGG 2102
2497 TTAGTCTCTGATCAGAGCTGTGTGGAGGTGAGGAGGAAATATGTAAAGAAAAACAG 2556
2103 TTAGTCTCTGATCAGAGCTGTGTGGAGGTGAGGAGGAAATATGTAAAGAAAAACAG 2162
2557 GAAAGTACCTGACCTATCATCTTCAAGCTTCTGCAACCTTTGCTGCTTGTGCT 2616
2163 GAAAGTACCTGACCTATCATCTTCAAGCTTCTGCAACCTTTGCTGCTTGTGCT 2222
2617 AATGGCTACCTGATTTGAAAGCTTTGGAAGAAAAAGCACTTTAACTCATAGCAAA 2676
2223 AATGGCTACCTGATTTGAAAGCTTTGGAAGAAAAAGCACTTTAACTCATAGCAAA 2282
2677 GAAATCAAGTGCAGCTATCTGCAATCCATGTTGATGAGATTAATGTTCTCATTTAT 2736
2283 GAAATCAAGTGCAGCTATCTGCAATCCATGTTGATGAGATTAATGTTCTCATTTAT 2342
2737 TTTTGTATGATGATTTTACATTCGCAATGGTGTAAATTAAGCTTTGAGTCAAAAGTCAGA 2796
2343 TTTTGTATGATGATTTTACATTCGCAATGGTGTAAATTAAGCTTTGAGTCAAAAGTCAGA 2402
2797 AAGTACTGAATATACAGTCACTTTTAAATGA 2832
2403 AAGTACTGAATATACAGTCACTTTTAAATGA 2438

RESULT 3
US-09-747-259-17
Sequence 17, Application US/09747259
Patent No. 6569645
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P1 (US)
CURRENT APPLICATION NUMBER: US/09/747,259
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US 60/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 09/644,848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 17
LENGTH: 2319
TYPE: DNA
ORGANISM: Homo Sapien
US-09-747-259-17

Query Match 67.3%; Score 2075.6; DB 3; Length 2319;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 2130; Conservative 0; Mismatches 9; Indels 39; Gaps 1;
DB 135 CTGTGCTGAGAGGAGTGGGGCCAGCCAGAGAAACAGTGGGCTGTACACATCACTCTT 194
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Db 171 CAATATGACATTTGACCACTTGAATCCAGTGGGGAAGCATGATGCTGACGC 230
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QY 435 TACCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGA 494
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QY 495 TTAATTTGTAAGGTTGTCTCTTTTCTTCCATTTAAAGGAAAGCAATTAACACCTTT 554
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QY 615 CTTCCTGGAAGCTCTCGAAGCTGGAACATCAGCCAGCATGCTC----- 656
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Db 591 CTTCCTGGAAGCTCTCGAAGCTGGAACATCAGCCAGCATGCTC----- 650
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Db 831 AGGGGATTAATTAATTAAGCTGTGATGACACTTAAACAACAAGAAAGTATGACTTA 890
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QY 876 TGCCTTAAGCCAGTGCATCTCCGCTGGGCGGCGCCATCAAGAGCCATGACAGT 935
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Db 891 TGCCTTAAGCCAGTGCATCTCCGCTGGGCGGCGCCATCAAGAGCCATGACAGT 950
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QY 936 GGCACGTGTGATATTCGACATTCGCGAGCTCTTCACTGTATGATGAGCGGCAAGAGCA 995
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Db 951 GGCACGTGTGATATTCGACATTCGCGAGCTCTTCACTGTATGATGAGCGGCAAGAGCA 1010
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QY 996 ACAAGAAATATTAATTAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1055
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Db 1011 ACAAGAAATATTAATTAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
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QY 1296 TATGAATCTTTGTGAGCAAG 1355
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Db 1311 TATGAATCTTTGTGAGCAAG 1370
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QY 1356 GAAAGAGAGCTTTCTGTGTGGGCTGTGACGATTTGCCGAAAGAGAGAGAGAGAGAGAGAG 1415
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Db 1491 GGGAGAGCTCCCGGATATCTTAGACCTGAGTACAGATCAAGCTATGCAATCTTCC 1550
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QY 1536 TCACTCTGTCTCCACTGCTGACCTCCGAGACAGCGGCTTCAGAGAGCCGGGAGAGACAC 1595
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Db 1551 TCACTCTGTCTCCACTGCTGACCTCCGAGACAGCGGCTTCAGAGAGCCGGGAGAGACAC 1610
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QY 1596 GGGAGAGGAG 1655
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Db 1611 GGGAGAGGAG 1670
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QY 1656 CATTTGCAACATGACAGATTTATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1715
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Db 1671 CATTTGCAACATGACAGATTTATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1730
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Db 1731 TCCCTTCATCTCTCTGACCTGCGCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1790
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QY 1776 CTTCGTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1835
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Db 1791 CTTCGTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1850
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QY 1836 AGAGGCGCTGTTCTTGGGAG 1895
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Db 1851 AGAGGCGCTGTTCTTGGGAG 1910
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QY 1896 GGGCTGTGACCAAG 1955
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Db 1911 GGGCTGTGACCAAG 1970
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QY 1956 CCGCTGTGACAG 2015
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Db 1971 CCGCTGTGACAG 2030
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QY 2016 TGACTGTGTGAGCTCTTCCAGAGCTGTCTGACAGTATGAGAGAGAGAGAGAGAGAGAGAG 2075
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Db 2031 TGACTGTGTGAGCTCTTCCAGAGCTGTCTGACAGTATGAGAGAGAGAGAGAGAGAGAGAG 2090
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QY 2076 CCAG 2135
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Db 2091 CCAG 2150
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Db 2151 GGAAGCTCTGCGCTCTTCCAGAGCTCTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 2210
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QY 2196 TTGCGCAGACTACATGATGAG 2255
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Db 2211 TTGCGCAGACTACATGATGAG 2270
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QY 2256 CTAAAGCATTTGCACTTTA 2273
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Db 2271 CTAAAGCATTTGCACTTTA 2288
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RESULT 4
US-09-904-615-15
Sequence 15, Application US/09904615
Patent No. 6566325
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 2334
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2278)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (2290)
OTHER INFORMATION: n equals a,t,g, or c
US-09-904-615-15

Query Match
Best Local Similarity 89.2%; Score 194.6; DB 3; Length 2334;
Matches 222; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY	2835	AAAAAAAAAAAAAAAAAGGCGCGCGCTCTAGATATCCCTGAGGGGCCCA	2894
DB	1696	ACATGAGAAAAAAGGCGCGCGCTCTAGAGATCCCTGAGGGGCCCA	1755
QY	2895	GCTTACGCGTACCCAGCTTTCTGTACAAGTGTCCCTATAGTGTATTAAGC	2954
DB	1756	GCTTACGCGTGC--ATGCGAGCTCATACCTCTCTCCATAGTGTATTAAGC	1812
QY	2955	TAGGCACTGCGCGCTTTTACACGTCGTGATGGGAAAGCTAGCTTGGGATCTTT	3014
DB	1813	TAGGCACTGCGCGCTTTTACACGTCGTGATGGGAAAGCTAGCTTGGGATCTTT	1872
QY	3015	GTGAAGAACTTACTTCTGTGTGTGACATTAATGACAACTACTACAGATTTAA	3074
DB	1873	GTGAAGAACTTACTTCTGTGTGTGACATTAATGACAACTACTACAGATTTAA	1932
QY	3075	AGCTCTAAG 3083	
DB	1933	AGCTCTAAG 1941	

RESULT 5
US-10-054-988-15
Sequence 15, Application US/10054988
Patent No. 6953667
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/10/054,988
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 09/904,615
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634

PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 2334
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2278)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (2290)
OTHER INFORMATION: n equals a,t,g, or c
US-10-054-988-15

Query Match
Best Local Similarity 89.2%; Score 194.6; DB 3; Length 2334;
Matches 222; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY	2835	AAAAAAAAAAAAAAAAAGGCGCGCGCTCTAGATATCCCTGAGGGGCCCA	2894
DB	1696	ACATGAGAAAAAAGGCGCGCGCTCTAGAGATCCCTGAGGGGCCCA	1755
QY	2895	GCTTACGCGTACCCAGCTTTCTGTACAAGTGTCCCTATAGTGTATTAAGC	2954
DB	1756	GCTTACGCGTGC--ATGCGAGCTCATACCTCTCTCCATAGTGTATTAAGC	1812
QY	2955	TAGGCACTGCGCGCTTTTACACGTCGTGATGGGAAAGCTAGCTTGGGATCTTT	3014
DB	1813	TAGGCACTGCGCGCTTTTACACGTCGTGATGGGAAAGCTAGCTTGGGATCTTT	1872
QY	3015	GTGAAGAACTTACTTCTGTGTGTGACATTAATGACAACTACTACAGATTTAA	3074
DB	1873	GTGAAGAACTTACTTCTGTGTGTGACATTAATGACAACTACTACAGATTTAA	1932
QY	3075	AGCTCTAAG 3083	
DB	1933	AGCTCTAAG 1941	

RESULT 6
US-09-181-339-2
Sequence 2, Application US/09181339
Patent No. 6610827
GENERAL INFORMATION:
APPLICANT: Forsayeth, John R.
APPLICANT: Zhao, Byron
TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
FILE REFERENCE: 5865-0033.30
CURRENT APPLICATION NUMBER: US/09/181,339
CURRENT FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 60/063,450
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2799
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (154) ... (1647)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1) ... (2799)
OTHER INFORMATION: n = A,T,C or G
US-09-181-339-2

Query Match
Best Local Similarity 89.0%; Score 178.6; DB 3; Length 2799;
Matches 222; Conservative 0; Mismatches 24; Indels 3; Gaps 1;


```

/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunding
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghaast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 656962el Nucleic Acids and
/ FILE REFERENCE: Polypeptides
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc_FL_genes Version 1.0
/ SEQ ID NO 108
/ LENGTH: 2265
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79)..(1614)
US-09-620-312D-108

```

```

Query Match          3.5%; Score 108.4; DB 3; Length 2265;
Best Local Similarity 98.4%; Pred. No. 1.6e-17;
Matches 120; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

QY 2841 AAAAAAAAAAAAAAAAAAGGGGCGGCTTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2900
DB 2116 AAAAAAAAAAAAAAAAAAGGGGCGGCTTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2175
QY 2901 GCGTACCCAGCTTCTTGTACAAAGTGTCCTATAGTAGTCGTATTATTAAGCTAGGCA 2960
DB 2176 GCGTACCCAGCTTCTTGTACAAAGTGTCCTATAGTAGTCGTATTATTAAGCTAGGCA 2234
QY 2961 CT 2962
DB 2235 GT 2236

RESULT 10
US-09-620-312D-109
/ Sequence 109, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunding
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghaast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 656962el Nucleic Acids and

```

```

/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 784CIP2B
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc_FL_genes Version 1.0
/ SEQ ID NO 109
/ LENGTH: 2349
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79)..(1698)
US-09-620-312D-109

```

```

Query Match          3.5%; Score 108.4; DB 3; Length 2349;
Best Local Similarity 98.4%; Pred. No. 1.6e-17;
Matches 120; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

QY 2841 AAAAAAAAAAAAAAAAAAGGGGCGGCTTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2900
DB 2200 AAAAAAAAAAAAAAAAAAGGGGCGGCTTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2259
QY 2901 GCGTACCCAGCTTCTTGTACAAAGTGTCCTATAGTAGTCGTATTATTAAGCTAGGCA 2960
DB 2260 GCGTACCCAGCTTCTTGTACAAAGTGTCCTATAGTAGTCGTATTATTAAGCTAGGCA 2318
QY 2961 CT 2962
DB 2319 GT 2320

```

```

RESULT 11
US-09-620-312D-964
/ Sequence 964, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunding
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghaast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 656962el Nucleic Acids and
/ FILE REFERENCE: 784CIP2B
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc_FL_genes Version 1.0
/ SEQ ID NO 964
/ LENGTH: 1476
/ TYPE: DNA
/ ORGANISM: Homo sapiens

```

FEATURE:
NAME/KEY: CDS
LOCATION: (149) .. (778)
US-09-620-312D-964

Query Match 3.5%; Score 106.8; DB 3; Length 1476;
Best Local Similarity 90.5%; Pred. No. 3,2e-17;
Matches 114; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2822 TATGAAATGAAAAAAGGCGCGCTCTAGAGTATCCC 2881
DB 1311 TATGAAATGCTTAATCTCAACAAAGGCGCGCTCTAGAGTATCCC 1370
QY 2882 TCGAGGGCCCAAGCTTACCCGCTTCTTGTACAAAGTGTCTCTATAGTAC 2941
DB 1371 TCGAGGGCCCAAGCTTACCCGCTTCTTGTACAAAGTGTCTCTATAGTAC 1430
QY 2942 TCGTAT 2947
DB 1431 TCGTAT 1436

RESULT 12
US-09-620-312D-348
Sequence 348, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Auudi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_FL_genes Version 1.0
SEQ ID NO 348
LENGTH: 4062
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (25) .. (2976)
US-09-620-312D-348

Query Match 2.9%; Score 90.8; DB 3; Length 4062;
Best Local Similarity 93.1%; Pred. No. 7.6e-13;
Matches 95; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2827 AATGAAAAAAGGCGCGCTCTAGAGTATCCCTCGAG 2886
DB 3961 AATGAAATTACAGATTAAGAAAAAAGGCGCGCTCTAGAGTATCCCTCGAG 4020
QY 2887 GGGCCCAAGCTTACCGCTTCTTGTACAAAGTGG 2928

DB 4021 GGGCCCAAGCTTACCGCTTCTTGTACAAAGTGG 4062

RESULT 13
US-09-620-312D-742
Sequence 742, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Auudi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_FL_genes Version 1.0
SEQ ID NO 742
LENGTH: 1912
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (340) .. (1176)
US-09-620-312D-742

Query Match 2.9%; Score 89.8; DB 3; Length 1912;
Best Local Similarity 97.8%; Pred. No. 9.5e-13;
Matches 91; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2836 AAAAAAAGGCGCGCTCTAGAGTATCCCTCGAGGCGCCAG 2895
DB 1820 ACATAAAAAAGGCGCGCTCTAGAGTATCCCTCGAGGCGCCAG 1879
QY 2896 CTTACCGCTTACCGCTTCTTGTACAAAGTGG 2928
DB 1880 CTTACCGCTTACCGCTTCTTGTACAAAGTGG 1912

RESULT 14
US-09-620-312D-100/C
Sequence 100, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Auudi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.

```
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunging
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghaast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
/ FILE REFERENCE: 784CIP28
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc_fl_genes Version 1.0
/ SEQ ID NO 100
/ LENGTH: 2275
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (770)..(2230)
US-09-620-312D-100
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```
Query Match 2.9%; Score 89.4; DB 3; Length 2275;
Best Local Similarity 98.9%; Pred. No. 1.3e-12;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2838 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 2897
DB 91 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 32
QY 2898 TAGCGTACCCAGCTTCTTGTAACAAGTGG 2928
DB 31 TAGCGTACCCAGCTTCTTGTAACAAGTGG 1
```

```
RESULT 15
US-09-620-312D-101/c
/ Sequence 101, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Xue, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunging
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghaast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
/ FILE REFERENCE: 784CIP28
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
```

```
/ SOFTWARE: pc_fl_genes Version 1.0
/ SEQ ID NO 101
/ LENGTH: 2817
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (770)..(2359)
US-09-620-312D-101
```

```
Query Match 2.9%; Score 89.4; DB 3; Length 2817;
Best Local Similarity 98.9%; Pred. No. 1.5e-12;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2838 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 2897
DB 91 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 32
QY 2898 TAGCGTACCCAGCTTCTTGTAACAAGTGG 2928
DB 31 TAGCGTACCCAGCTTCTTGTAACAAGTGG 1
```

```
Search completed: March 1, 2006, 09:01:00
Job time : 535 secs
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Db      1561 CGAGACCAAGGCTCCAGAGAGCGGGGCAACACGAGACAGGGGCAAGAGAACTAC 1620
Qy      1621 TTCGGAGAGCAAGTCAAGGCGGGTCCCTATACGTGCCATTGGCAACATGACCAAGTTATT 1680
Db      1621 TTCGGAGAGCAAGTCAAGGCGGGTCCCTATACGTGCCATTGGCAACATGACCAAGTTATT 1680
Qy      1681 GAGGAGAGGCGGAGCTGTGGTGGAAAGCAATGGTCCCTTCCATCCTCTCCATGCGC 1740
Db      1681 GAGGAGAGGCGGAGCTGTGGTGGAAAGCAATGGTCCCTTCCATCCTCTCCATGCGC 1740
Qy      1741 TACCGGAGAGCAAGTCTTGAGAAATTTGATTGGGCTTTTAAATGATCATGTGC 1800
Db      1741 TACCGGAGAGCAAGTCTTGAGAAATTTGATTGGGCTTTTAAATGATCATGTGC 1800
Qy      1801 AAACCAAGGCTGAGAGTGAATTCTGCTAAAGGTAGAGGCGCTGTCTTGGGGCAAC 1860
Db      1801 AAACCAAGGCTGAGAGTGAATTCTGCTAAAGGTAGAGGCGCTGTCTTGGGGCAAC 1860
Qy      1861 GAGCAAGCCGACTCCAGACAGAGTCAAGATGAGGAGGCTTGGACCAAGCGGGAGGCC 1920
Db      1861 GAGCAAGCCGACTCCAGACAGAGTCAAGATGAGGAGGCTTGGACCAAGCGGGAGGCC 1920
Qy      1921 CGGCTGAGGCTTGAAGGCTGAGCGGCGCTGCAACCCCTGCTGCAACGAGTGAAGCGGC 1980
Db      1921 CGGCTGAGGCTTGAAGGCTGAGCGGCGCTGCAACCCCTGCTGCAACGAGTGAAGCGGC 1980
Qy      1981 AGCCCTCGAGACATGCGCGGGAATCAAGGATATGACTGCTGTGCTCATCGAG 2040
Db      1981 AGCCCTCGAGACATGCGCGGGAATCAAGGATATGACTGCTGTGCTCATCGAG 2040
Qy      2041 CTGTCTCTGCAATGATGAAAGATCTTCGACCGAACCAAGAAAGTCTTCCCTGACG 2100
Db      2041 CTGTCTCTGCAATGATGAAAGATCTTCGACCGAACCAAGAAAGTCTTCCCTGACG 2100
Qy      2101 GAGAGGCTGCTCTCTCTTCAAGGCTGAGTGAAGGAACTCTGCGCTTCTTCCAAAG 2160
Db      2101 GAGAGGCTGCTCTCTCTTCAAGGCTGAGTGAAGGAACTCTGCGCTTCTTCCAAAG 2160
Qy      2161 CTCTCTCTCTCTGAGGCTATGCAAGAGATCTTGTGTCGAGCACTACATGATGAACTC 2220
Db      2161 CTCTCTCTCTCTGAGGCTATGCAAGAGATCTTGTGTCGAGCACTACATGATGAACTC 2220
Qy      2221 CAGCGGCTGCGGCTTTGTAACAAAGAAAGTCTAAGCATTTGCCATTTAGCTGCTG 2280
Db      2221 CAGCGGCTGCGGCTTTGTAACAAAGAAAGTCTAAGCATTTGCCATTTAGCTGCTG 2280
Qy      2281 CCTCCCTCTGATCCCAAGCTCATCTCCGCTGATGCAATGAGCCCACTTGAAGTCTG 2340
Db      2281 CCTCCCTCTGATCCCAAGCTCATCTCCGCTGATGCAATGAGCCCACTTGAAGTCTG 2340
Qy      2341 CATACAGATATTTGAGAGTGAATGCTGAGCACTTGTCTCCCTTGGCCCAACCT 2400
Db      2341 CATACAGATATTTGAGAGTGAATGCTGAGCACTTGTCTCCCTTGGCCCAACCT 2400
Qy      2401 TTACCGGATATCTTGACAACTCTCAATTTCTAAATGATATGAGCTTGAAGGCA 2460
Db      2401 TTACCGGATATCTTGACAACTCTCAATTTCTAAATGATATGAGCTTGAAGGCA 2460
Qy      2461 TGTCCATTAAGGCTGCAACAGCTTGCMAATTTGTTAGTCCCTTGGATAGAGCTGTT 2520
Db      2461 TGTCCATTAAGGCTGCAACAGCTTGCMAATTTGTTAGTCCCTTGGATAGAGCTGTT 2520
Qy      2521 GTGGAGAGTATGAGAGAAATATATTAAGAAACAGAGATACCTGCACTAATCTCA 2580
Db      2521 GTGGAGAGTATGAGAGAAATATATTAAGAAACAGAGATACCTGCACTAATCTCA 2580
Qy      2581 GACTTCAATGAGCTCTGCAAACTTTGCTGTTGCTATTTGCTAATCTTGAATGCT 2640
Db      2581 GACTTCAATGAGCTCTGCAAACTTTGCTGTTGCTATTTGCTAATCTTGAATGCT 2640
Qy      2641 TTGTGAAAAAGCACTTTAATCATATGCAAGAAATCAAGTCCAGTCTATCTGG 2700

```

```

Db      2641 TTGTGAAAAAGCACTTTAATCATATGCAAGAAATCAAGTCCAGTCTATCTGG 2700
Qy      2701 AATCCATGTTGATATGCAATATGTTCTCATTTATTTTGTATGATTAATTACATTTGCC 2760
Db      2701 AATCCATGTTGATATGCAATATGTTCTCATTTATTTTGTATGATTAATTACATTTGCC 2760
Qy      2761 ATGGGTTTAAATTAAGCTTTGAGTCAAAAGTCAAGAGTGAATGATATACAGTCACT 2820
Db      2761 ATGGGTTTAAATTAAGCTTTGAGTCAAAAGTGAAGTGAATATACAGTCACT 2820
Qy      2821 TTATGAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2880
Db      2821 TTATGAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2880
Qy      2881 CTGAGAGGCGCCAGCTTACGGTACCGAGCTTTCTTGTACAAAGTGTCCCTATATGTA 2940
Db      2881 CTGAGAGGCGCCAGCTTACGGTACCGAGCTTTCTTGTACAAAGTGTCCCTATATGTA 2940
Qy      2941 GTGTATTTAAGCTATGAGCACTGGCGGCTTTTACAAAGTGTGACTGGAAAACTGCT 3000
Db      2941 GTGTATTTAAGCTATGAGCACTGGCGGCTTTTACAAAGTGTGACTGGAAAACTGCT 3000
Qy      3001 AGCTTGGATCTTTGTAAGAACTTACTCTGTGTGTGACATATTTGACAAACTAC 3060
Db      3001 AGCTTGGATCTTTGTAAGAACTTACTCTGTGTGTGACATATTTGACAAACTAC 3060
Qy      3061 CTACAGAGATTTAAGCTCTTAAG 3083
Db      3061 CTACAGAGATTTAAGCTCTTAAG 3083

```

```

RESULT 2
ADU69243
ID ADU69243 standard; DNA; 3083 BP.
XX
AC ADU69243;
XX
DT 10-FEB-2005 (first entry)
DE
XX Human SEF gene variant SEQ ID NO:3.
XX
XX db: fibroblast growth factor; SEF; similar expression of FGF genes;
XX cytostatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
XX vasotrophic; hypotensive; nephrotrophic; gene therapy; diagnosis;
XX prognosis; proliferative disorders; cardiovascular disorders;
XX renal disease; glomerular disease; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 22..2241
FT /tag= a
FT /product= "SEF"
XX
PN US2004235104-A1.
XX
XX 25-NOV-2004.
PD
XX
XX 07-MAY-2004; 2004US-00842006.
PF
XX
XX 08-MAY-2003; 2003US-0469522P.
PR
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Yang R;
PI
XX WPI; 2004-821320/81.
XX P-PSDB; ADU69244.
DR
XX
XX New isolated SEF nucleic acid and polypeptide, useful for monitoring,
XX treating, or diagnosing proliferative and/or differentiative disorders,
XX e.g. ovarian cancer, breast cancer, or cardiovascular disorder including
XX arteriosclerosis.

```


QY 1741 TACCGGAGCCAGCTTTGGAGAAATTGATCGGGCTTGTTTAAATGATGATGTC 1800
 DB 1741 TACCGGAGCCAGCTTTGGAGAAATTGATCGGGCTTGTTTAAATGATGATGTC 1800
 QY 1801 AAACCAAGGCTTGAAGAGTCTTCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGGCAAC 1860
 DB 1801 AAACCAAGGCTTGAAGAGTCTTCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGGCAAC 1860
 QY 1861 GGAACGAGCCGACTCCAGACAGAGATGACATGGGGGCTTGACCAAGACGGGAGGCC 1920
 DB 1861 GGAACGAGCCGACTCCAGACAGAGATGACATGGGGGCTTGACCAAGACGGGAGGCC 1920
 QY 1921 CGGCTGCTCTTGAAGAGTACGCGCGCTGTCACACCCCTGTCACACGCGTAAAGCCGCG 1980
 DB 1921 CGGCTGCTCTTGAAGAGTACGCGCGCTGTCACACCCCTGTCACACGCGTAAAGCCGCG 1980
 QY 1981 AGCCCTCGGACATGCGCGGAGCTAGGCACTATGACTCGTCTGCTGCTCATCGAG 2040
 DB 1981 AGCCCTCGGACATGCGCGGAGCTAGGCACTATGACTCGTCTGCTGCTCATCGAG 2040
 QY 2041 CTGCTCTGCACTGATGAGAGAGCTCTGACGAGACAGACAGAAAGTCTTCCCTGACG 2100
 DB 2041 CTGCTCTGCACTGATGAGAGAGCTCTGACGAGACAGACAGAAAGTCTTCCCTGACG 2100
 QY 2101 GAGAGCGTGTCTCTCTCTTCAAGGCTGGGTGAGAGAGAACCTCTGCGCTTCTTCCAG 2160
 DB 2101 GAGAGCGTGTCTCTCTCTTCAAGGCTGGGTGAGAGAGAACCTCTGCGCTTCTTCCAG 2160
 QY 2161 CTCCTCTCTTCTGAGTATGCAAGAGAGATCTTGTGTCGCGAGCTTACACTGATGAACTC 2220
 DB 2161 CTCCTCTCTTCTGAGTATGCAAGAGAGATCTTGTGTCGCGAGCTTACACTGATGAACTC 2220
 QY 2221 CAGCGCGTGGCCCTTCTTGTAAACAAAAGAAAGTCTAAGCATTTGACCTTGTCTG 2280
 DB 2221 CAGCGCGTGGCCCTTCTTGTAAACAAAAGAAAGTCTAAGCATTTGACCTTGTCTG 2280
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 DB 2281 CCTCCTCTGANTCCCGAGCTCATCTCCTGTTGCAATGCGCCACTTGAAGTCTG 2340
 QY 2341 CATACAGAGATTTTGAAGTGAATGCTGCGCAGTACTTGTCTCCTTCCCTGCGCAACCT 2400
 DB 2341 CATACAGAGATTTTGAAGTGAATGCTGCGCAGTACTTGTCTCCTTCCCTGCGCAACCT 2400
 QY 2401 TTAACCGATATCTTGAACAACTCTCCAAATTTCTAAATGATATGAGCTTGAAGGCA 2460
 DB 2401 TTAACCGATATCTTGAACAACTCTCCAAATTTCTAAATGATATGAGCTTGAAGGCA 2460
 QY 2461 TGTCCATTAAGTCTGACAAAGCTTGGCCAAATTTGTTAGTCTTGGATCAGAGCTGTT 2520
 DB 2461 TGTCCATTAAGTCTGACAAAGCTTGGCCAAATTTGTTAGTCTTGGATCAGAGCTGTT 2520
 QY 2521 GTGGGAGTGAAGGAGAAATATGTAAGAAACAGAGAGATGCTGCACTATATCTCA 2580
 DB 2521 GTGGGAGTGAAGGAGAAATATGTAAGAAACAGAGAGATGCTGCACTATATCTCA 2580
 QY 2581 GACTTATTTAGCTTGAACAACTTTCCTGTTGCTATTTGCTATGCTTGAATGCAATGC 2640
 DB 2581 GACTTATTTAGCTTGAACAACTTTCCTGTTGCTATTTGCTATGCTTGAATGCAATGC 2640
 QY 2641 TTTGTGAAAAAGGCACTTTTAAATCATATGACACAGAAATCAAGTCCAGTCTAATCTGG 2700
 DB 2641 TTTGTGAAAAAGGCACTTTTAAATCATATGACACAGAAATCAAGTCCAGTCTAATCTGG 2700
 QY 2701 AATCCATGTTGTTTGAAGTGAATATGTTCTATTTTGAATGATGAAATTTTCAATGCC 2760
 DB 2701 AATCCATGTTGTTTGAAGTGAATATGTTCTATTTTGAATGATGAAATTTTCAATGCC 2760
 QY 2761 ATGGGTTTAAATGAGTTTGAATGCAAAAGTCAAGAAAGTCAATATATACAGTCACT 2820
 DB 2761 ATGGGTTTAAATGAGTTTGAATGCAAAAGTCAAGAAAGTCAATATATACAGTCACT 2820

QY 2821 TTTATGAATGAAAAAAGGCGCGCTCTAGAGTATCC 2880
 DB 2821 TTTATGAATGAAAAAAGGCGCGCTCTAGAGTATCC 2880
 QY 2881 CTCGAGGCGCCCAAGCTTACGCGTACCCAGCTTCTTGTACAAAGTGTCCCTATAGTA 2940
 DB 2881 CTCGAGGCGCCCAAGCTTACGCGTACCCAGCTTCTTGTACAAAGTGTCCCTATAGTA 2940
 QY 2941 GTGCTATTATTAAGCTTACGCGTGTCTTTTACAAAGTGTCTGACCTGGAAAACTGCT 3000
 DB 2941 GTGCTATTATTAAGCTTACGCGTGTCTTTTACAAAGTGTCTGACCTGGAAAACTGCT 3000
 QY 3001 AGCTTGGAGTCTTGTGAAGAACCTTACTCTGCTGCTGTAATTAATGCAAACTAC 3060
 DB 3001 AGCTTGGAGTCTTGTGAAGAACCTTACTCTGCTGCTGTAATTAATGCAAACTAC 3060
 QY 3061 CTACAGAGATTTAAAGCTCTAAG 3083
 DB 3061 CTACAGAGATTTAAAGCTCTAAG 3083

RESULT 3
 ADU69241
 ID ADU69241 standard; DNA; 4477 BP.
 XX
 AC ADU69241;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human SRF gene SEQ ID NO:1.
 XX
 KW db; gene; fibroblast growth factor; SRF; similar expression of FGF genes;
 KW cytosolic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
 KW vasotrophic; hypotensive; nephrotropic; gene therapy; diagnosis;
 KW prognosis; proliferative disorders; cardiovascular disorders;
 KW renal disease; glomerular disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 90..2309
 FT /tag= a
 FT /product= "SRF"
 XX
 PN US200423104-A1.
 XX
 PD 25-NOV-2004.
 XX
 PP 07-MAY-2004; 2004US-00842006.
 XX
 PR 08-MAY-2003; 2003US-0469522P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Yang R;
 XX
 DR WPI; 2004-821320/81.
 XX
 DR P-PSDB; ADU69242.
 XX
 PT New isolated SRF nucleic acid and polypeptide, useful for monitoring,
 PT treating, or diagnosing proliferative and/or differentiative disorders,
 PT e.g. ovarian cancer, breast cancer, or cardiovascular disorder including
 PT arteriosclerosis.
 XX
 PS Claim 1; SEQ ID NO 1; 46bp; English.
 XX
 CC The invention relates to a novel isolated SRF (similar expression of FGF
 CC genes) nucleic acid molecule (1). An SRF of the invention has cytosolic,
 CC cardiovascular-gen., antiarteriosclerotic, cardiant, vasotropic,
 CC hypotensive, and nephrotropic activity, and may have a use in gene
 CC therapy. The SRF nucleic acids and polypeptides can be used for
 CC diagnostic assays, prognostic assays, and monitoring clinical trials.
 CC They can also be used for treating a subject at risk of or susceptible to

CC a disorder or having a disorder associated with aberrant or unwanted SER
CC expression or activity. The SER molecules can also be used for
CC monitoring, treating, or diagnosing proliferative and/or differentiative
CC disorders, e.g. ovarian cancer, breast cancer, colon cancer, prostatic
CC cancer, RGE related disorder, cardiovascular disorder including
CC arteriosclerosis, coronary artery disease, ischemia, reperfusion injury,
CC restenosis, arterial inflammation, hypertension, endothelial disorders,
CC and a kidney disorder, e.g. glomerulonephritis, vascular nephropathy,
CC renal failure, or glomerular disease. The SER molecules can also be used
CC as markers of disorders or disease states, as markers for precursors of
CC disease states, as markers for predisposition of disease states, as
CC markers of drug activity, or as markers of the pharmacogenomic profile of
CC a subject. The present sequence represents the SER nucleic acid molecule
CC of the invention.

XX
SQ Sequence 4477 BP; 1133 A; 1086 C; 1141 G; 1117 T; 0 U; 0 Other;

Query Match 91.5%; Score 2822.4; DB 13; Length 4477;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2826; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 TGGCTGGGAGGAGGCAACGGCCATGCGCCCTGGCTGCAAGTCTGCTCCGTTCTTTAG 60
DB 69 TGGCTGGGAGGAGGCAACGGCCATGCGCCCTGGCTGCAAGTCTGCTCCGTTCTTTAG 128
QY 61 GTCAACGCGCTGCTCAACGGGCTGCAAGTGGCTGCGGCTGGCGGCTGGCGCGCG 120
DB 129 GTCAACGCGCTGCTCAACGGGCTGCAAGTGGCTGCGGCTGGCGGCTGGCGCGCG 188
QY 121 TGGGCGGTGCAACCTGTGGCTGGAGGGAGTGGGGCCAGCCAGCAAAACAGTGGGCTG 180
DB 189 CGGGGCGCGCAACCTGTGGCTGGAGGGAGTGGGGCCAGCCAGCAAAACAGTGGGCTG 248
QY 181 TACAAATACCTCTTAAATATGCAATTTGACCACTTAAATGCAAGTGGGAGCAT 240
DB 249 TACAAATACCTCTTAAATATGCAATTTGACCACTTAAATGCAAGTGGGAGCAT 308
QY 241 TGAATGCTGAGCGCCAGAAATATCAACATGAGCTGATGCTGGATGCAAGTGGCA 300
DB 309 GTGATGCTGAGCGCCAGAAATATCAACATGAGCTGATGCTGGATGCAAGTGGCA 368
QY 301 GTCAACCATCTTCTTGTGCTCCAGGGGCTGCGGATGCAATCTGAAAGGATTTGGGTA 360
DB 369 GTCAACCATCTTCTTGTGCTCCAGGGGCTGCGGATGCAATCTGAAAGGATTTGGGTA 428
QY 361 ATACTGAGAGAGCTGAAGTGGAGGAGAACAGTGGCAACATGATTTGAAAGATTCG 420
DB 429 ATACTGAGAGAGCTGAAGTGGAGGAGAACAGTGGCAACATGATTTGAAAGATTCG 488
QY 421 AAGCAGCTCAACAGTAGCTTCAAAAGAACTGAAATGGAATCTCAACCTTCTGAAATATG 480
DB 489 AAGCAGCTCAACAGTAGCTTCAAAAGAACTGAAATGGAATCTCAACCTTCTGAAATATG 548
QY 481 AAATTTGAAACGAGATTATTTGTAAGGTTGTCCTTTCTTCAATTAAGAAACGAAAC 540
DB 549 AAATTTGAAACGAGATTATTTGTAAGGTTGTCCTTTCTTCAATTAAGAAACGAAAC 608
QY 541 AATTACACCTCTTCTTCTTGAAGCCGAGCTGAGCTGTTGTTTACAGCGGCAAT 600
DB 609 AATTACACCTCTTCTTCTTGAAGCCGAGCTGAGCTGTTGTTTACAGCGGCAAT 668
QY 601 CTAGCTTGAACCCCTTCTGAAAGCTGGAACCTGAACATCAAGCAGAGATGGCTGGAG 660
DB 669 CTAGCTTGAACCCCTTCTGAAAGCTGGAACCTGAACATCAAGCAGAGATGGCTGGAG 728
QY 661 ATGCAAGTGTCTTTCAGACACGCAACCACTTGGCTTCCGTTCTTCAATCTTCAAC 720
DB 729 ATGCAAGTGTCTTTCAGACACGCAACCACTTGGCTTCCGTTCTTCAATCTTCAAC 788
QY 721 TACAACTACAGACGAAAGACCTTTCAAGCGAAAGACCTGTAAGACGAGCAATCAAC 780
DB 789 TACAACTACAGACGAAAGACCTTTCAAGCGAAAGACCTGTAAGACGAGCAATCAAC 848
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QY 781 GAGACGACGAGCTGCTCTCTTCAAAATGTTCTCAAGGGATTAATATGAGCTGTG 840
DB 849 GAGATGACGAGCTGCTCTCTTCAAAATGTTCTCAAGGGATTAATATGAGCTGTG 908
QY 841 GATGACACTAACAAACAAAGAAAGTATGATTTATGCTTTAAAGCAGTGCATCCCG 900
DB 909 GATGACACTAACAAACAAAGAAAGTATGATTTATGCTTTAAAGCAGTGCATCCCG 968
QY 901 TGGGCGGGGCGCATGAGAGCCATGAGCATCAAGGCGCATGATGCTATCCGATTC 960
DB 969 TGGGCGGGGCGCATGAGAGCCATGAGCATCAAGGCGCATGATGCTATCCGATTC 1028
QY 961 GCGAGCTCTTCACTGTGATGTCGCGCAAGAGCAACAAAGAAATATATATTCATTTA 1020
DB 1029 GCGAGCTCTTCACTGTGATGTCGCGCAAGAGCAACAAAGAAATATATATTCATTTA 1088
QY 1021 GATGAAAGAGCTGTGATGTTCTTCAATTCATCTGACACTTCCCAAGAGAGGCTCCG 1080
DB 1089 GATGAAAGAGCTGTGATGTTCTTCAATTCATCTGACACTTCCCAAGAGAGGCTCCG 1148
QY 1081 CGCGGCGGAGAGTCTTCTGCTAATTCAGTAAAGATGCGCAATTCATGAAATGTC 1140
DB 1149 CGCGGCGGAGAGTCTTCTGCTAATTCAGTAAAGATGCGCAATTCATGAAATGTC 1208
QY 1141 GTCAAGTGTGCTTCTCTTCAAGAGCTTCTGTGCTGTGAGTGGCTTGAACCTG 1200
DB 1209 GTCAAGTGTGCTTCTCTTCAAGAGCTTCTGTGCTGTGAGTGGCTTGAACCTG 1268
QY 1201 TGGGAAAGTTCAGCTCTGTGAGAGGAGAGAGAAATGGGTATCCAAAGTCCAC 1260
DB 1269 TGGGAAAGTTCAGCTCTGTGAGAGGAGAGAGAAATGGGTATCCAAAGTCCAC 1328
QY 1261 GAGTCCAGTTCATGATGTTGTTGTTTCCAAAGATGAAATGATCTTGTGCAAGAG 1320
DB 1329 GAGTCCAGTTCATGATGTTGTTGTTTCCAAAGATGAAATGATCTTGTGCAAGAG 1388
QY 1321 AACTCAAAACAAAGAGAGTGGCCAGAGCTTGGGAAAGAGAGAGCTCTTCTGTGGG 1380
DB 1389 AACTCAAAACAAAGAGAGTGGCCAGAGCTTGGGAAAGAGAGAGCTCTTCTGTGGG 1448
QY 1381 GTGTGAGCATTTGCGGAAAGTCCGCGCAGGCGCAAGAGTTCGTCGCGCGCTCAGC 1440
DB 1449 GTGTGAGCATTTGCGGAAAGTCCGCGCAGGCGCAAGAGTTCGTCGCGCGCTCAGC 1508
QY 1441 AAGTTATCGCGGTCTACTTTGATTTATTCGCGAGGAGAGTCCCGGTATCCAGAC 1500
DB 1509 AAGTTATCGCGGTCTACTTTGATTTATTCGCGAGGAGAGTCCCGGTATCCAGAC 1568
QY 1501 CTGAGTACCAAGTACAGACTCAATGAGCAATCTTCTCAGCTCTGTTCCACCTGCACTCC 1560
DB 1569 CTGAGTACCAAGTACAGACTCAATGAGCAATCTTCTCAGCTCTGTTCCACCTGCACTCC 1628
QY 1561 CGAGACACAGGCTTCAAGAGCTCGGGGAGCAGCAGCGCAGGGGAGCAAGAACTAC 1620
DB 1629 CGAGACACAGGCTTCAAGAGCTCGGGGAGCAGCAGCGCAGGGGAGCAAGAACTAC 1688
QY 1621 TTCCGAGAGAGTCAAGGCGGCTCTTATACGTCGCAATTTGCAATGACCAAGTTAT 1680
DB 1689 TTCCGAGAGAGTCAAGGCGGCTCTTATACGTCGCAATTTGCAATGACCAAGTTAT 1748
QY 1681 GACGAGAGGCGGAGCTGTTGAGAAAGAGTTCGTTCCCTTCATCTCTCAGTGGGC 1740
DB 1749 GACGAGAGGCGGAGCTGTTGAGAAAGAGTTCGTTCCCTTCATCTCTCAGTGGGC 1808
QY 1741 TACGAGAGGCGGAGCTTGGAGAAATTTGAGCTTGGCTTTAAATGATGTCATGTC 1800
DB 1809 TACGAGAGGCGGAGCTTGGAGAAATTTGAGCTTGGCTTTAAATGATGTCATGTC 1868
QY 1801 AAAACAGAGGCTGAGAGGACTTCTGCTTAAAGGATGAGAGGCGCTCTTGGGGCAAC 1860
DB 1869 AAAACAGAGGCTGAGAGGACTTCTGCTTAAAGGATGAGAGGCGCTCTTGGGGCAAC 1928
QY 1861 GGACGAGGCACTCCAGACAGAGAGTCAAGTGGGGGCTTGGACCAAGACGGGGAGGCC 1920
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D	1929	GGACCAAGCCCACTCCACGACGAGAGTACATGGGGGCTTGACACAAAGACGGGAGGCC	1988
Q	1921	CGGCTTGCCCTTGAACGGTAGCGCGCCCTGCAACCCCTGTGCACACGGTGAAGCCGGC	1980
D	1989	CGGCTTGCCCTTGAACGGTAGCGCGCCCTGCAACCCCTGTGCACACGGTGAAGCCGGC	2048
Q	1981	AGCCCTTCGACATGCGCGGGGACCTCAGGGACCTATATGCTGTGTGGCCCTCAATCCGAG	2040
D	2049	AGCCCTTCGACATGCGCGGGGACCTCAGGGACCTATATGCTGTGTGGCCCTCAATCCGAG	2108
Q	2041	CTGTCTCTGCCACTGATGGAAGACTCTTCGACGACACAGAAACGCTCTTCCCTGACG	2100
D	2109	CTGTCTCTGCCACTGATGGAAGACTCTTCGACGACACAGAAACGCTCTTCCCTGACG	2168
Q	2101	GAGAGCGGTGCTCTCTTTCAGGGCTGGGTGAGAGGAACCTCTGCGCTTCTTCCAG	2160
D	2169	GAGAGCGGTGCTCTCTTTCAGGGCTGGGTGAGAGGAACCTCTGCGCTTCTTCCAG	2228
Q	2161	CTCTCTCTTTCGAGGTCAATGCAAGACAGATCTTGATGTCGCGACATACATGATGAATC	2220
D	2229	CTCTCTCTTTCGAGGTCAATGCAAGACAGATCTTGATGTCGCGACATACATGATGAATC	2288
Q	2221	CAGCGCGGTGCGCCCTTGTGAACAAACGAAAGACTTAAAGATTGCCACTTTAGCTGCTG	2280
D	2289	CAGCGCGGTGCGCCCTTGTGAACAAACGAAAGACTTAAAGATTGCCACTTTAGCTGCTG	2348
Q	2281	CGTCCCTCTGATGCCCAAGCTCATCTCCGTGGTGAATGGGCCACTTGGACATGAGGCT	2340
D	2349	CGTCCCTCTGATGCCCAAGCTCATCTCCGTGGTGAATGGGCCACTTGGACATGAGGCT	2408
Q	2341	CATACAAAGATATTGAGTGAAGTGAATGCTGGCAGTACTTGTCTCCCTTGCCCAACCT	2400
D	2409	CATACAAAGATATTGAGTGAAGTGAATGCTGGCAGTACTTGTCTCCCTTGCCCAACCT	2468
Q	2401	TTAACCGATATCTTGAACAAACTCTCCCAATTTCTTAAATGATATAGAGCTCTGAAGGCA	2460
D	2469	TTAACCGATATCTTGAACAAACTCTCCCAATTTCTTAAATGATATAGAGCTCTGAAGGCA	2528
Q	2461	TGTCATTAAGTCTGACAAACAGTTCGCAATTTGGTTAGTCTTGGATCGAGCCTGTT	2520
D	2529	TGTCATTAAGTCTGACAAACAGTTCGCAATTTGGTTAGTCTTGGATCGAGCCTGTT	2588
Q	2521	GTGGGAGGTGAGGAGAAATATGTAAAGAAAACAGAAAGTATCTGCACTAATCATTC	2580
D	2589	GTGGGAGGTGAGGAGAAATATGTAAAGAAAACAGAAAGTATCTGCACTAATCATTC	2648
Q	2581	GACTTCATTAAGCTCTGCAAACTTGGCTGTGGTCTATGGCTACCTTGATTTGAATG	2640
D	2649	GACTTCATTAAGCTCTGCAAACTTGGCTGTGGTCTATGGCTACCTTGATTTGAATG	2708
Q	2641	TTTGTGAAAAAAGGCACTTTTAAACATCATATAGCCACAGAAATCAAGTGCAGTCTATG	2700
D	2709	TTTGTGAAAAAAGGCACTTTTAAACATCATATAGCCACAGAAATCAAGTGCAGTCTATG	2768
Q	2701	AATTCATGTTGATATGCAGATTAATGTTCTCAATTAATTTTGAATGATTAATTAATG	2760
D	2769	AATTCATGTTGATATGCAGATTAATGTTCTCAATTAATTTTGAATGATTAATTAATG	2828
Q	2761	ATGGGTGTTAAATTAAGCTTGAATCAAAAGTCAAGAAAGTACATGAATATACATGCACT	2820
D	2829	ATGGGTGTTAAATTAAGCTTGAATCAAAAGTCAAGAAAGTACATGAATATACATGCACT	2888
Q	2821	TTTATGAATGA 2832	
D	2889	TTTATGAATGA 2900	

RESULT 4	
ADW23599	
ID	ADW23599 standard; DNA; 4477 BP.
XX	
AC	ADW23599;

[illegible]

Db 369 GTCAACATTCCTTGTGATCCCCAGGGGCGCTCGGCATCGAAATTCCTGAAGAGATTTCCGGGA 428
Qy 361 ATACTGAGAGAGCTGAAGTCGAGGGAGACAGTGCACAACCTGATTTCTAAAGATCCG 420
Db 429 ATACTGAGAGAGCTGAAGTCGAGGGAGACAGTGCACAACCTGATTTCTAAAGATCCG 488
Qy 421 AAGCAGCTCAACAGTAGCTTCAAAAGACTGGAATGGAATCTCAACCTTTCTGAATATG 480
Db 489 AAGCAGCTCAACAGTAGCTTCAAAAGACTGGAATGGAATCTCAACCTTTCTGAATATG 548
Qy 481 AATTTGAAACGGATATATTTCTGTAAGGTGTGCTTTCTCTTCCATTTAAAAAGAAAGC 540
Db 549 AATTTGAAACGGATATATTTCTGTAAGGTGTGCTTTCTCTTCCATTTAAAAAGAAAGC 608
Qy 541 AATTTACACCCCTTCTTCTTTAGAACCCGAGCCTGTGACCTGTGTTTACAGCCGGACAAT 600
Db 609 AATTTACACCCCTTCTTCTTTAGAACCCGAGCCTGTGACCTGTGTTTACAGCCGGACAAT 668
Qy 601 CTAGCTTGTAAACCTTCTGTGAAGCCTCGGAACCTGAAACATCAGCCAGCATGGCTCGAC 660
Db 669 CTAGCTTGTAAACCTTCTGTGAAGCCTCGGAACCTGAAACATCAGCCAGCATGGCTCGAC 728
Qy 661 ATGCAAGGTGCTCTTGCACACGCAACGCGACACTTGGGCTTCCGTTTCTTATCTTCAAC 720
Db 729 ATGCAAGGTGCTCTTGCACACGCAACGCGACACTTGGGCTTCCGTTTCTTATCTTCAAC 788
Qy 721 TACAACTCAAGACGAAAGGACCTTTCAAGCGAAAGACTGTAAAGACGAGACAACTACA 780
Db 789 TACAACTCAAGACGAAAGGACCTTTCAAGCGAAAGACTGTAAAGACGAGACAACTACA 848
Qy 781 GAGACGACGAGCTGCTCTTCAAAATGTTTCTCAAGGGATTTATTAATGAGCTGTG 840
Db 849 GAGATGACGAGCTGCTCTTCAAAATGTTTCTCAAGGGATTTATTAATGAGCTGTG 908
Qy 841 GATGACACTTAACCAACAAAGAAAGTATGATTAATGCTTAAAGCACTGACCTCCCG 900
Db 909 GATGACACTTAACCAACAAAGAAAGTATGATTAATGCTTAAAGCACTGACCTCCCG 968
Qy 901 TGGGCGGGGCGCATGAGGCAATGGCATCAGTAGGCACTGGTAGTCAATATGGGCAATTC 960
Db 969 TGGGCGGGGCGCATGAGGCAATGGCATCAGTAGGCACTGGTAGTCAATATGGGCAATTC 1028
Qy 961 GCGACGCTCTTCACTGTGATGTGCGCAAGAACCAACAAAGAAATATATTTACATTTTA 1020
Db 1029 GCGACGCTCTTCACTGTGATGTGCGCAAGAACCAACAAAGAAATATATTTACATTTTA 1088
Qy 1021 GATGAAGAGAGCTCTGATGCTTCAACATACATGACGACTCCCAAGAGAGAGCTCCGG 1080
Db 1089 GATGAAGAGAGCTCTGATGCTTCAACATACATGACGACTCCCAAGAGAGAGCTCCGG 1148
Qy 1081 CCGCGGCGGAAGTCTTCTGTGCTATTCAGTAAAGATGGCCAGAAATCATGAATGTTC 1140
Db 1149 CCGCGGCGGAAGTCTTCTGTGCTATTCAGTAAAGATGGCCAGAAATCATGAATGTTC 1208
Qy 1141 GTTCAAGTGTTCGCTACTTCTCAAGAACTTCTGTGCTGTGAGGTGCTTGAACCTG 1200
Db 1209 GTTCAAGTGTTCGCTACTTCTCAAGAACTTCTGTGCTGTGAGGTGCTTGAACCTG 1268
Qy 1201 TGGGAAGACTTACGCTCTGTAGAGAAAGGCGAGAGAAATGGGTCAATCCAGAAATCCAC 1260
Db 1269 TGGGAAGACTTACGCTCTGTAGAGAAAGGCGAGAGAAATGGGTCAATCCAGAAATCCAC 1328
Qy 1261 GAGTCCAGTTCATCATTTGTGTTTCTCAAGAGTATGAAGTATCTTTGTGCAAGAAAG 1320
Db 1329 GAGTCCAGTTCATCATTTGTGTTTCTCAAGAGTATGAAGTATCTTTGTGCAAGAAAG 1388
Qy 1321 AACTACAAACAAAGAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTTCTGTGTGGC 1380
Db 1389 AACTACAAACAAAGAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTTCTGTGTGGC 1448
Qy 1381 GTGTCAAGCATTTGCGGAAAGCTCGGCGAAGGCGCAAGCAAGATTCGTTCGGCGGCGCTCAGC 1440
Db 1449 GTGTCAAGCATTTGCGGAAAGCTCGGCGAAGGCGCAAGCAAGATTCGTTCGGCGGCGCTCAGC 1508

Qy 1441 AAGTTATGCGCGTCACTTGTGATTAATTCCTGCGAGGAGAGAGTCCCGGTATCCTAGAC 1500
Db 1509 AAGTTATGCGCGTCACTTGTGATTAATTCCTGCGAGGAGAGAGTCCCGGTATCCTAGAC 1568
Qy 1501 CTGAGTACCAAGTACAGACTACATGCAATCTTCTCAAGCTGTGTTCCACTGCACTCC 1560
Db 1569 CTGAGTACCAAGTACAGACTACATGCAATCTTCTCAAGCTGTGTTCCACTGCACTCC 1628
Qy 1561 CGAGACACAGGCTCGAGAGCGGGGAGCAGCGGACAGGGGAGAGAGAACTAC 1620
Db 1629 CGAGACACAGGCTCGAGAGCGGGGAGCAGCGGACAGGGGAGAGAGAACTAC 1688
Qy 1621 TTCGGAGCAAGTACAGCGCGGTCCCTATACGTGCGCAATTTGCAACATGACCAAGTTAT 1680
Db 1689 TTCGGAGCAAGTACAGCGCGGTCCCTATACGTGCGCAATTTGCAACATGACCAAGTTAT 1748
Qy 1681 GACGAGAGAGCCGCACTGTGTAAGAAAGCATGTTGCTTCCCTCAATCTCTCACTGCGC 1740
Db 1749 GACGAGAGAGCCGCACTGTGTAAGAAAGCATGTTGCTTCCCTCAATCTCTCACTGCGC 1808
Qy 1741 TACCGGAGGCGAGCTGTGAGAAATTTGATTCGGGCTTGTTTAAATGATGATGTC 1800
Db 1809 TACCGGAGGCGAGCTGTGAGAAATTTGATTCGGGCTTGTTTAAATGATGATGTC 1868
Qy 1801 AAACCAAGGCTGAGAGTGACTTGTGCTTAAAGTAAAGAGCGCTGTTCTTGCGGCAAC 1860
Db 1869 AAACCAAGGCTGAGAGTGACTTGTGCTTAAAGTAAAGAGCGGCTGTTCTTGCGGCAAC 1928
Qy 1861 GGAACGAGGCACTCCGACGACAGAGTCACTGAGGAGCTGAGACCAAGAGCGGAGGCGC 1920
Db 1929 GGAACGAGGCACTCCGACGACAGAGTCACTGAGGAGCTGAGACCAAGAGCGGAGGCGC 1988
Qy 1921 GGGCTGCGCTGAGAGGTAGGCGCGCGCTGCAACCCCTGTGCAACAGCGGTGAAGCGGCGC 1980
Db 1989 GGGCTGCGCTGAGAGGTAGGCGCGCGCTGCAACCCCTGTGCAACAGCGGTGAAGCGGCGC 2048
Qy 1981 AGCCCTCGGACATGCGCGGAGCTCAAGCATCTATGACTGCTGTGCTCATTCGAG 2040
Db 2049 AGCCCTCGGACATGCGCGGAGCTCAAGCATCTATGACTGCTGTGCTCATTCGAG 2108
Qy 2041 CTGTCTCTGCACTGATGGAAGAACTTCTGACGAGACAGAAACGCTTCCCTGACG 2100
Db 2109 CTGTCTCTGCACTGATGGAAGAACTTCTGACGAGACAGAAACGCTTCCCTGACG 2168
Qy 2101 GAGAGGTGTCTCTCTTCAAGGCTGTGAGAGAACTCTGCGCTTCTTCCAG 2160
Db 2169 GAGAGGTGTCTCTCTTCAAGGCTGTGAGAGAACTCTGCGCTTCTTCCAG 2228
Qy 2161 CTCTCTCTTCTGAGTCAATGCAAGCAAGATCTTGGTTGCGGAGCTACATGATGATC 2220
Db 2229 CTCTCTCTTCTGAGTCAATGCAAGCAAGATCTTGGTTGCGGAGCTACATGATGATC 2288
Qy 2221 CAGCGGTGTGCGGCTTGTGAACAAACGAAAGACTTAAGCATTTGCACTTACTGCTG 2280
Db 2289 CAGCGGTGTGCGGCTTGTGAACAAACGAAAGACTTAAGCATTTGCACTTACTGCTG 2348
Qy 2281 CCTCTCTGATTTCCCGAGCTCATCTCGGTGCAATGAGGCGCACTGAGAGCTGAGTCT 2340
Db 2349 CCTCTCTGATTTCCCGAGCTCATCTCGGTGCAATGAGGCGCACTGAGAGCTGAGTCT 2408
Qy 2341 CATACAAAGATTTTGAAGTAAATGCTGAGCAATGTTCTCCCTTGCCCAACCT 2400
Db 2409 CATACAAAGATTTTGAAGTAAATGCTGAGCAATGTTCTCCCTTGCCCAACCT 2468
Qy 2401 TTACGGATATCTTGACAAACTCTCAATTTTCTAAATGATAGAGCTTGAAAGCA 2460
Db 2469 TTACGGATATCTTGACAAACTCTCAATTTTCTAAATGATAGAGCTTGAAAGCA 2528
Qy 2461 TGTCCATTAAGGTCTGACAAAGACTTGCAGAAATTTGGTTAGTCTTGGATCAGAGCTGTT 2520
Db 2529 TGTCCATTAAGGTCTGACAAAGACTTGCAGAAATTTGGTTAGTCTTGGATCAGAGCTGTT 2588

Db 661 GACCGCACACTCGGCTTCGGTTCCTTCTATCTTCACTAACAGCTCAAGACGAGGA 720
Qy 742 CCTTCAAGGAAAGACTGTAAAGCAGAGCAAACTACAGAGACGACGCTGCTCTT 801
Db 721 CCTTCAAGGAAAGACTGTAAAGCAGAGCAAACTACAGAGACGACGCTGCTCTT 780
Qy 802 CAAAATGTTTCTTCAGGGGATTAATATTAATTGAGCTGTGTGATGACATTAACACAAAGA 861
Db 781 CAAAATGTTTCTTCAGGGGATTAATATTAATTGAGCTGTGTGATGACATTAACACAAAGA 840
Qy 862 AAGTATGATTAATAGCTTTAAAGCAGAGCACTCCCGGTGGGCGGGCCATCAAGGCC 921
Db 841 AAGTATGATTAATAGCTTTAAAGCAGAGCACTCCCGGTGGGCGGGCCATCAAGGCC 900
Qy 922 ATGGCATCACTAGTGCACCTGATGATCATATCGGCAATTCGCGACGCTTCACTGTATG 981
Db 901 GTGGCATCACTAGTGCACCTGATGATCATATCGGCAATTCGCGACGCTTCACTGTATG 960
Qy 982 TGGCGAAGAGCAACAGAAATATATATTAATTAATTAATTAATTAATTAATTAATTAAT 1041
Db 961 TGGCGAAGAGCAACAGAAATATATATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
Qy 1042 TCACATTAACCTGACAGCACTCCCAAGAGAGGCTCCGGCCGGCGAAAGTCTTCTC 1101
Db 1021 TCACATTAACCTGACAGCACTCCCAAGAGAGGCTCCGGCCGGCGAAAGTCTTCTC 1080
Qy 1102 TGGTATTCAGTAAAGATGGCGAATCACTAGATGTGTCCAGTTCGCTTCCGCTACTTC 1161
Db 1081 TGGTATTCAGTAAAGATGGCGAATCACTAGATGTGTCCAGTTCGCTTCCGCTACTTC 1140
Qy 1162 CTCACAGACTTCTGTGGCTGTGAGTGGCTCTGGAACCTGTGGAGAACCTTCAAGCTCTG 1221
Db 1141 CTCACAGACTTCTGTGGCTGTGAGTGGCTCTGGAACCTGTGGAGAACCTTCAAGCTCTG 1200
Qy 1222 AAGAAAGGCGAGAGAAATGGGTCACTCCAGAGATCCAGAGATCCAGATTCATCATTTG 1281
Db 1201 AAGAAAGGCGAGAGAAATGGGTCACTCCAGAGATCCAGAGATCCAGATTCATCATTTG 1260
Qy 1282 GTTGTTCCAAAGGTATGAAGTACTTGTGGAACAAGAACTAACAAACAAGAGGT 1341
Db 1261 GTTGTTCCAAAGGTATGAAGTACTTGTGGAACAAGAACTAACAAACAAGAGGT 1320
Qy 1342 GGCAGAGCTCGGGGAAAGAGAGCTCTTCTGTGGCGGTCTCAAGCTTGGCCGAAAG 1401
Db 1321 GGCAGAGCTCGGGGAAAGAGAGCTCTTCTGTGGCGGTCTCAAGCTTGGCCGAAAG 1380
Qy 1402 CTCGCCAGGCCAGAGAGTTCCTCGCGGCGCTCAGCAAGTTATCGCCGCTTACTT 1461
Db 1381 CTCGCCAGGCCAGAGAGTTCCTCGCGGCGCTCAGCAAGTTATCGCCGCTTACTT 1440
Qy 1462 GATTATTCCTGGAGGGAACGTCGCCGATTCCTAGACTGATGATCCAAAGTACAGACTC 1521
Db 1441 GATTATTCCTGGAGGGAACGTCGCCGATTCCTAGACTGATGATCCAAAGTACAGACTC 1500
Qy 1522 ATGACAAATC-TTCTCAGCTCTGTTCCAC-CTGACCTCCGAGACCAAGGCTCTCAG 1579
Db 1501 ATGACAAATCCTTCTCAGCTCTGTTCCACCTGACCTCCGAGACCAAGGCTCTCAG 1560
Qy 1580 AGCCGGGGGCA-GCACAGCGGACAGGCA-GCAGAAAGAACTACTTCGAGGACAGTCA 1637
Db 1561 AGCCGGGGGCACTACACAGCGGACAGGCAAGGAAAGAACTACTTCGAGGACAGTCA 1620
Qy 1638 CGGATCCCTAATAGTCGCAATTTGCAATGCAATGCAATGTTATTTAGAGAGACCCGAC 1697
Db 1621 CGGATCCCTAATAGTCGCAATTTGCAATGCAATGCAATGTTATTTAGAGAGACCCGAC 1680
Qy 1698 GTTCAAAAAGCAGTTCCTTCCCTTCCATCTCTCCATGCGCTACCGGAGACAGTCTT 1757
Db 1681 GTTCAAAAAGCAGTTCCTTCCCTTCCATCTCTCCATGCGCTACCGGAGACAGTCTT 1740
Qy 1758 GGAGAAATTTGATTCGGGCTTGTTTAAATGATGATGATGATGATGATGATGATGATG 1817
Db 1741 GGAGAAATTTGATTCGGGCTTGTTTAAATGATGATGATGATGATGATGATGATGATG 1800

Qy 1818 TGACTTCTGCTTAAAGGTAGAGGCGCTGTCTTGGGGCAACCGGACAGCCGACTCCCA 1877
Db 1801 TGACTTCTGCTTAAAGGTAGAGGCGCTGTCTTGGGGCAACCGGACAGCCGACTCCCA 1860
Qy 1878 GCAAGAGTCAAGCATGGGGGCTTGGACCAAGACGGGAGGCGCGGCTTGGACGG 1937
Db 1861 GCAAGAGTCAAGCATGGGGGCTTGGACCAAGACGGGAGGCGCGGCTTGGACGG 1920
Qy 1938 TAGCGCGCGCTGCAACCCCTGCTGCAACGCTGGAAGCGGGCAAGCCCTCCGACATG 1997
Db 1921 TAGCGCGCGCTGCAACCCCTGCTGCAACGCTGGAAGCGGGCAAGCCCTCCGACATG 1980
Qy 1998 GCGGACCTCAGGCACTATGACTGCTGTGCTGCTCATCCGAGCTGTCTCTCCACTGAT 2057
Db 1981 GCGGACCTCAGGCACTATGACTGCTGTGCTGCTCATCCGAGCTGTCTCTCCACTGAT 2040
Qy 2058 GGAAGGACTCTGACGAGCAGACAGAAACGTCCTTCCCTGACGAGAGGCTGCTCTC 2117
Db 2041 GGAAGGACTCTGACGAGCAGACAGAAACGTCCTTCCCTGACGAGAGGCTGCTCTC 2100
Qy 2118 TTCAAGCTTGGGTGAGAGAACTCTGCTCTTCTTCCAAAGCTCTCTTCTGCGT 2177
Db 2101 TTCAAGCTTGGGTGAGAGAACTCTGCTCTTCTTCCAAAGCTCTCTTCTGCGT 2160
Qy 2178 ATGCAAGAGATCTTGGTTCGCGAGCTACATGATGAATCCAGCGGTGCGCCCTT 2237
Db 2161 ATGCAAGAGATCTTGGTTCGCGAGCTACATGATGAATCCAGCGGTGCGCCCTT 2220
Qy 2238 GTAAACAAACGAAAGATCTTAAGATTCGACCTTAACTGCTGCTCTCTGATTCCTC 2297
Db 2221 GTAAACAAACGAAAGATCTTAAGATTCGACCTTAACTGCTGCTCTCTGATTCCTC 2280
Qy 2298 AGCTCATCTCCCTGGGTGATGAGCCCACTTGGAGCTGAGGCTCATCAAGATATTGG 2357
Db 2281 AGCTCATCTCCCTGGGTGATGAGCCCACTTGGAGCTGAGGCTCATCAAGATATTGG 2340
Qy 2358 AGTAAATGCTGGCCAGTACTTGTCTCCCTTGCACCACCTTAAACGATATCTTGA 2417
Db 2341 AGTAAATGCTGGCCAGTACTTGTCTCCCTTGCACCACCTTAAACGATATCTTGA 2400
Qy 2418 AAACCTCTCAATTTCTAAATGATATGAGAGCTCTGAAGGATGCTAATAGTCTGAC 2477
Db 2401 AAACCTCTCAATTTCTAAATGATATGAGAGCTCTGAAGGATGCTAATAGTCTGAC 2460
Qy 2478 AAACCTTGCCTAATTTGGTTAGTCTTGGATCAGAGCTGTGTGGAGGTAAGGAG 2537
Db 2461 AAACCTTGCCTAATTTGGTTAGTCTTGGATCAGAGCTGTGTGGAGGTAAGGAG 2520
Qy 2538 AATATGTAAGAAACAGAAAGATACCTGACATTAATCAATCAAGCTTCAATGAGCTG 2597
Db 2521 AATATGTAAGAAACAGAAAGATACCTGACATTAATCAATCAAGCTTCAATGAGCTG 2580
Qy 2598 CAAACTTTCCTGTTTGGCTAATTTGGCTACTGATTTGGAATGCTTTGAAAAAGGAC 2657
Db 2581 CAAACTTTCCTGTTTGGCTAATTTGGCTACTGATTTGGAATGCTTTGAAAAAGGAC 2640
Qy 2658 TTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGGAATCAATGTTGATTGC 2717
Db 2641 TTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGGAATCAATGTTGATTGC 2700
Qy 2718 AGATTAATGTTCTAATTTATTTTGAATGAAATTTAATCAATTCAGTGTGTAATAGC 2777
Db 2701 AGATTAATGTTCTAATTTATTTTGAATGAAATTTAATTCATTCAGTGTGTAATAGC 2760
Qy 2778 TTTGAGTCAAAAAGTCAAGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2832
Db 2761 TTTGAGTCAAAAAGTCAAGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2815

RESULT 6
AAS18134
ID AAS18134 standard; cDNA; 2786 BP.


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OY 1321 AACTACAAACAAAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGG 1380
DB 1366 AACTACAAACAAAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGG 1425
OY 1381 GTGTCAAGCAATGGCCGAAAAGCTCCGCGACAGGCAAGAGATTGTCGCGGCGCTCAGC 1440
DB 1426 GTGTCAAGCAATGGCCGAAAAGCTCCGCGACAGGCAAGAGATTGTCGCGGCGCTCAGC 1485
OY 1441 AAGTTATATGCGGCTACTTTGATTAATTCCTGCGAGGAGAGAGTCCCGGTAATCTAGAC 1500
DB 1486 AAGTTATATGCGGCTACTTTGATTAATTCCTGCGAGGAGAGAGTCCCGGTAATCTAGAC 1545
OY 1501 CTGAGTACCAAGTACAGACTACATGACAAATCTTCTCAAGCTGTTCACACTGCACTCC 1560
DB 1546 CTGAGTACCAAGTACAGACTACATGACAAATCTTCTCAAGCTGTTCACACTGCACTCC 1605
OY 1561 CGAGACCAAGGCTCTCAGAGAGCCGGGGCAGACACGCGACAGGGCAGCAGAGAACTAC 1620
DB 1606 CGAGACCAAGGCTCTCAGAGAGCCGGGGCAGACACGCGACAGGGCAGCAGAGAACTAC 1665
OY 1621 TTCCGGAGCAAGTCAAGCCGGTCCCTATAGTCCGCAATTTGCAACATGACCAAGTTATT 1680
DB 1666 TTCCGGAGCAAGTCAAGCCGGTCCCTATAGTCCGCAATTTGCAACATGACCAAGTTATT 1725
OY 1681 GACGAGAGCCCGCACTGTTCGAAAAGCAATTGCTTCCCTTCATCTCTCCACTGCGC 1740
DB 1726 GACGAGAGCCCGCACTGTTCGAAAAGCAATTGCTTCCCTTCATCTCTCCACTGCGC 1785
OY 1741 TACCGGAGCCCAAGTCTTGAGAAATTTGATTGCGGCTTGTTTAAATGATCATGTGC 1800
DB 1786 TACCGGAGCCCAAGTCTTGAGAAATTTGATTGCGGCTTGTTTAAATGATCATGTGC 1845
OY 1801 AAACCAAGGCTGAGAGTGAATCTTGCCTTAAAGTGAAGGCGCTGTTCTGCGGGAAC 1860
DB 1846 AAACCAAGGCTGAGAGTGAATCTTGCCTTAAAGTGAAGGCGCTGTTCTGCGGGAAC 1905
OY 1861 GGACCAAGCCGACTCCGACAGACAGAGTCAAGTGAAGGCGCTGACCAAGACGCGGAGGC 1920
DB 1906 GGACCAAGCCGACTCCGACAGACAGAGTCAAGTGAAGGCGCTGACCAAGACGCGGAGGC 1965
OY 1921 CGAGCTGCTTGACGATGACGCGCGCTGCAACCCCTGCTGCAACGCGTGAAGCGGC 1980
DB 1966 CGAGCTGCTTGACGATGACGCGCGCTGCAACCCCTGCTGCAACGCGTGAAGCGGC 2025
OY 1981 AACCCCTCGGACATGCGCGGAGCATGAGGCACTTATGACTCGCTGTCATCCGAG 2040
DB 2026 AACCCCTCGGACATGCGCGGAGCATGAGGCACTTATGACTCGCTGTCATCCGAG 2085
OY 2041 CTGTCTCTGCACTGATGAGAGCACTCTGACGAGCAGACAGAAAGTCTTCTCCGAGC 2100
DB 2086 CTGTCTCTGCACTGATGAGAGCACTCTGACGAGCAGACAGAAAGTCTTCTCCGAGC 2145
OY 2101 GAGAGCTGTCTCTCTTCAAGGCTGGGTGAGAGAGAACTCTGCGCTTCTCTCAAG 2160
DB 2146 GAGAGCTGTCTCTCTTCAAGGCTGGGTGAGAGAGAACTCTGCGCTTCTCTCAAG 2205
OY 2161 CTCCTCTCTTCTGGGTCAGCAAGAGAGATCTTGTGTCGAGGTCATGATGAACTC 2220
DB 2206 CTCCTCTCTTCTGGGTCAGCAAGAGAGATCTTGTGTCGAGGTCATGATGAACTC 2265
OY 2221 CAGCGGTCGCGCTTGTGTAACAAAGAGAGTCTAAGCATTTGAGCTGAGCTG 2280
DB 2266 CAGCGGTCGCGCTTGTGTAACAAAGAGAGTCTAAGCATTTGAGCTGAGCTG 2325
OY 2281 CCTCCCTCTGATTTCCCACTCATCTCTGTTGATGGCCCACTTGAAGCTGAGCT 2340
DB 2326 CCTCCCTCTGATTTCCCACTCATCTCTGTTGATGGCCCACTTGAAGCTGAGCT 2385
OY 2341 CATACAGAGATTTTGAAGTGAAGTGTGGCCAGTACTTGTTCCTCTTGGCCCACT 2400
DB 2386 CATACAGAGATTTTGAAGTGAAGTGTGGCCAGTACTTGTTCCTCTTGGCCCACT 2445
OY 2401 TTACGGATATCTGACAAACTCTCAATTTTCTAATAATGATGAGCTGTGAAGGCA 2460

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DB 2446 TTACGGATATCTTGACAAACTCTCAATTTTCTAATAATGATGAGCTGTGAAGGCA 2505
OY 2461 TGTCCATTAAGTCTGACAAACAGCTTGCCAAATTTGTAGTCTCTGATCAAGACCTGTT 2520
DB 2506 TGTCCATTAAGTCTGACAAACAGCTTGCCAAATTTGTAGTCTCTGATCAAGACCTGTT 2565
OY 2521 GTGGAGGTAGGAGGAAATATGTAAGAAAAAGAGAGATACCTGCACTAATCACTCA 2580
DB 2566 GTGGAGGTAGGAGGAAATATGTAAGAAAAAGAGAGATACCTGCACTAATCACTCA 2625
OY 2581 GACTTCATTTAGCTCTGCAAACTTTGCTGTTGCTATTGCTACCTGATTTGAATGC 2640
DB 2626 GACTTCATTTAGCTCTGCAAACTTTGCTGTTGCTATTGCTACCTGATTTGAATGC 2685
OY 2641 TTTTGAAAAAAGGCACTTTTAACTATACCAACAGAAATTAAGTCCAGTCTATCTGG 2700
DB 2686 TTTTGAAAAAAGGCACTTTTAACTATACCAACAGAAATTAAGTCCAGTCTATCTGG 2745
OY 2701 AATTCATGTTGTATTCAGATATATGTTCTCATTTATTTTGG 2741
DB 2746 AATTCATGTTGTATTCAGATATATGTTCTCATTTATTTTGG 2786

RESULT 7
AB55653
ID AB55653 brandard; cDNA; 2786 BP.
XX AC AB55653;
XX XX
XX XX
XX 22-SBP-2005 (first entry)
XX XX
DE Human DCSR8 polypeptide encoding cDNA.
XX KW Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
KW DCSR8; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
KW interstitial lung disorder; asthma; allergy; atherosclerosis;
KW gastrointestinal-gen.; antiinflammatory; antiaesthetic; antiallergic;
KW antipsoriatic; antiarteriosclerotic; respiratory-gen.; immunosuppressive;
KW antitumor; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;
KW IL-17C agonist; human; DCSR8; gene; ss; antisense therapy; RNAi therapy.
XX KW
XX Homo sapiens.
XX XX
XX Key Location/Qualifiers
FH 70..2286
FT CDS
FT FT
FT /product= "DCSR8"
FT /transl_except= (pos: 169..171, aa: Xaa)
FT /transl_except= (pos: 193..195, aa: Xaa)
FT /transl_except= (pos: 442..444, aa: Xaa)
FT /transl_except= (pos: 475..478, aa: Xaa)
FT /transl_except= (pos: 517..519, aa: Xaa)
FT /note= "Xaa = unknown"
FT sig_peptide 70..117
FT /*tag= a
FT mat_peptide 118..2283
FT /*tag= c
XX PN WO2005065711-A2.
XX PD 21-JUL-2005.
XX PF 22-DEC-2004; 2004WO-US042935.
XX PR 29-DEC-2003; 2003US-00749144.
XX PA (SCHE ) SCHERING CORP.
XX Gorman DM;
XX PI
XX WPI; 2005-506792/51.
XX DR P-PSDB; AB55654.

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XX Modulating activity of cell, involves contacting cell with an agonist or
 PT antagonist of DNA cytokine receptor subunit.
 XX

PS Example 5; SEQ ID NO 9, 130bp; English.

CC The invention relates to modulating (M) activity of cell, by contacting
 CC cell with an agonist or antagonist of DNA cytokine receptor subunit
 CC (DCRS9) or of interleukin (IL)-17C where the cell modulates psoriasis,
 CC inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or
 CC allergy, or atherosclerosis. Also provided are methods for treating (M2)
 CC the disorders which involves administration of the modulator and
 CC diagnosing (M3) a disorder as mentioned above that involves contacting a
 CC sample from a test subject with a binding composition that specifically
 CC binds to a polypeptide or nucleic acid of DCRS9 or IL-17C. (M1) is useful
 CC for modulating an activity of a cell. (M2) is useful for treating a
 CC subject suffering from a disorder such as psoriasis, IBD, interstitial
 CC lung disorder, asthma or allergy, or atherosclerosis, where the
 CC interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic
 CC granuloma, or hypersensitivity pneumonitis. The IBD is Crohn's disease or
 CC ulcerative colitis. The present sequence represents a human DCRS8
 CC polypeptide encoding cDNA.

XX Sequence 2786 BP; 673 A; 760 C; 709 G; 637 T; 0 U; 7 Other;

Query Match 87.5%; Score 2696.6; DB 14; Length 2786;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 2718; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

QY 1 TGGCTGGGCGAGCGACGCGATGCGCCGCTGAGCTGAGCTGCTCCGCTCTTTACG 60
 Db 49 TGGCTGGGCGAGCGACGCGATGCGCCGCTGAGCTGAGCTGCTCCGCTCTTTACG 108
 QY 61 GTCAACGCTGCTCTCAACGCGCTGCGAGCTGCTGCGCGCTGCGCGCTGCGCG 120
 Db 109 GTCAACGCTGCTCTCAACGCGCTGCGAGCTGCTGCGCGCTGCGCGCTGCGCG 168
 QY 121 TGGGCGGTGACACCTGTGCTGAGGAGGAGTGGGGCCAGCCAGCAAAACATGGGCTG 180
 Db 169 CNGGGGCGGACACCTGTGCTGAGGAGGAGTGGGGCCAGCCAGCAAAACATGGGCTG 228
 QY 181 TACAACATCACTTCAAAATATGACATTTGACCACTTGAATCAAGTGGGGAAGCAT 240
 Db 229 TACAACATCACTTCAAAATATGACATTTGACCACTTGAATCAAGTGGGGAAGCAT 288
 QY 241 GTGATTTGCTGAGCGCCAGAAATATCACATCAAGCAGTATGCTTGCATGACCAAGTGGCA 300
 Db 289 GTGATTTGCTGAGCGCCAGAAATATCACATCAAGCAGTATGCTTGCATGACCAAGTGGCA 348
 QY 301 GTCAACATTTCTTTGTGCTCCCAAGGGGCTCTGCGCATGGAATTTCTGAAAGATTTGGGCTA 360
 Db 349 GTCAACATTTCTTTGTGCTCCCAAGGGGCTCTGCGCATGGAATTTCTGAAAGATTTGGGCTA 408
 QY 361 ATACTGAGAGAGCTGAAGTCTGAGGAGAGACAGTGCACCAACTGATTTCTAAAGATTCG 420
 Db 409 ATACTGAGAGAGCTGAAGTCTGAGGAGAGACAGTGCACCAACTGATTTCTAAAGATTCG 468
 QY 421 AAGCAGCTCAACAGTATGCTTCAAAAGAACTGGAATGGAATCTCACTTCTGGAATATG 480
 Db 469 AAGCAGCTCAACAGTATGCTTCAAAAGAACTGGAATGGAATCTCACTTCTGGAATATG 528
 QY 481 AAATTTGAAACGAGTATTTCTGTAAGGTTGCTCTTTCTCTTCAATTAAGAAAGCAAGC 540
 Db 529 AAATTTGAAACGAGTATTTCTGTAAGGTTGCTCTTTCTCTTCAATTAAGAAAGCAAGC 585
 QY 541 AATTACCACTTTCTTTCTTTAGAACCGAGCTGAGCCTGTTGTTTACAGCGGCAAT 600
 Db 586 AATTACCACTTTCTTTCTTTAGAACCGAGCTGAGCCTGTTGTTTACAGCGGCAAT 645
 QY 601 CTAGCTTGTAAACCTTTCTGGAAGCTCGGAACCTGAACATCAAGCAGCATGGCTCGGAC 660
 Db 646 CTAGCTTGTAAACCTTTCTGGAAGCTCGGAACCTGAACATCAAGCAGCATGGCTCGGAC 705

QY 661 ATGACAGTGTGCTTTCAGCACGACCGCACAACTTGGGCTTCGTTCTTCAATCTTAC 720
 Db 706 ATGACAGTGTGCTTTCAGCACGACCGCACAACTTGGGCTTCGTTCTTCAATCTTAC 765
 QY 721 TACAACCTCAAGACGAGAGACCTTTCAAGCGAAGACCTGTAAAGCAGAGCAACTACA 780
 Db 766 TACAACCTCAAGACGAGAGACCTTTCAAGCGAAGACCTGTAAAGCAGAGCAACTACA 825
 QY 781 GAGACACCAAGCTGCTCTCTTCAAAATGTTTCTCCAGGGAGATTAATTAATGAGCTGG 840
 Db 826 GAGATACCAAGCTGCTCTCTTCAAAATGTTTCTCCAGGGAGATTAATTAATGAGCTGG 885
 QY 841 GATGACCTTAACCAAGAAAGATGATGATTAATGCTTAAGGACAGTGCCTCCG 900
 Db 886 GATGACCTTAACCAAGAAAGATGATGATTAATGCTTAAGGACAGTGCCTCCG 945
 QY 901 TGGGCGGGCCCATCAAGACATGAGCATCAAGTGCACCTGGTACTCATTCGCAATTC 960
 Db 946 TGGGCGGGCCCATCAAGACATGAGCATCAAGTGCACCTGGTACTCATTCGCAATTC 1005
 QY 961 GCGAGCTCTTCACTGTGATGTGCGGCAAGAACCAAGAAATATATATTCATCATTTA 1020
 Db 1006 GCGAGCTCTTCACTGTGATGTGCGGCAAGAACCAAGAAATATATATTCATCATTTA 1065
 QY 1021 GATGAAGAGAGCTGAGTCTTCCATACATACCTGACGACCTCCAGAGAGGCTCCG 1080
 Db 1066 GATGAAGAGAGCTGAGTCTTCCATACATACCTGACGACCTCCAGAGAGAGGCTCCG 1125
 QY 1081 CCGCGGCCAAGGCTTTTCTCTGCTATTCAGTAAAGATGCGCAAGATCAATGAATGTC 1140
 Db 1126 CCGCGGCCAAGGCTTTTCTCTGCTATTCAGTAAAGATGCGCAAGATCAATGAATGTC 1185
 QY 1141 GTCAAGTGTGCTTCTCTTCCAGACCTTGTGTGAGTGGCTGTGACCTG 1200
 Db 1186 GTCAAGTGTGCTTCTCTTCCAGACCTTGTGTGAGTGGCTGTGACCTG 1245
 QY 1201 TGGGAAGACCTTCAAGCTCTGTGAGAGAGGCGAGAGAAATGGGTCTATCCAGAAATCCAC 1260
 Db 1246 TGGGAAGACCTTCAAGCTCTGTGAGAGAGGCGAGAGAAATGGGTCTATCCAGAAATCCAC 1305
 QY 1261 GAGTCCCAATTCATCTTGTGTTGTTTCAAAAGTATGAATCTTTGTGCAAGAAAG 1320
 Db 1306 GAGTCCCAATTCATCTTGTGTTGTTTCAAAAGTATGAATCTTTGTGCAAGAAAG 1365
 QY 1321 AACTACAAACAAAGAGAGTGGCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGCG 1380
 Db 1366 AACTACAAACAAAGAGAGTGGCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGCG 1425
 QY 1381 GTGTACGCAATTCGGAAGAAAGCTCCGCGCAGGCGCAAGCAAGTTCCTCCGCGGCTCACG 1440
 Db 1426 GTGTACGCAATTCGGAAGAAAGCTCCGCGCAGGCGCAAGCAAGTTCCTCCGCGGCTCACG 1485
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 QY 1501 GTGAGTACCAAGTACAGACTACATGACAAATCTTCTGAGCTGTGTTCCACCTGACCTCC 1560
 Db 1546 GTGAGTACCAAGTACAGACTACATGACAAATCTTCTGAGCTGTGTTCCACCTGACCTCC 1605
 QY 1561 CGAGACCAAGGCTCTCAAGAGCGCGGGGAGACACCGGCAAGGGGAGGAAAGAACTAC 1620
 Db 1606 CGAGACCAAGGCTCTCAAGAGCGCGGGGAGACACCGGCAAGGGGAGGAAAGAACTAC 1665
 QY 1621 TTCGGAGCAAGTCAAGGCGGCTCCCTATATGCTGCAATTTGCAACATGACCAAGTTAT 1680
 Db 1666 TTCGGAGCAAGTCAAGGCGGCTCCCTATATGCTGCAATTTGCAACATGACCAAGTTAT 1725
 QY 1681 GACGAGAGCCCGACTGTGTGAAAGAGAGTGTTCCTTCATCTCTGACCTGCGC 1740
 Db 1726 GACGAGAGCCCGACTGTGTGAAAGAGAGTGTTCCTTCATCTCTGACCTGCGC 1785
 QY 1741 TACCGGAGCCAGTCTGTGAGAAATTTGATTTGGGCTGTGTTTAAATCATATCATGTGC 1800

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Db 1786 TACCGGAGCCAGTCTTGAGAGAAATTGATTGGGCTTGTTTAATGATGTCATGTGC 1845
Qy 1801 AAACCGAGGCGCTGAGAGTGACTTCTGCTTAAAGSTAGAGGCGCTCTTCTTGCGGCAACC 1860
Db 1846 AAACCGAGGCGCTGAGAGTGACTTCTGCTTAAAGSTAGAGGCGCTCTTCTTGCGGCAACC 1905
Qy 1861 GAGACGAGGCGACTCCAGAGCAGAGAGTCAAGCATGAGGAGGCGCTTGACCAAGACGAGGAGGCC 1920
Db 1906 GAGACGAGGCGACTCCAGAGCAGAGAGTCAAGCATGAGGAGGCGCTTGACCAAGACGAGGAGGCC 1965
Qy 1921 CGAGCTGCGCTTGAGCGGTAGCGCGCGCTTGCAACCCCTGCTGCAACGAGTGAAGCGCGGC 1980
Db 1966 CGAGCTGCGCTTGAGCGGTAGCGCGCGCTTGCAACCCCTGCTGCAACGAGTGAAGCGCGGC 2025
Qy 1981 AGCCCTCGGAGCAATGCGCGGCGGACTGAGGCACTTAATGATCTGCTGCTGCTCATCTCGAG 2040
Db 2026 AGCCCTCGGAGCAATGCGCGGCGGACTGAGGCACTTAATGATCTGCTGCTGCTCATCTCGAG 2085
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Db 2086 CTGCTCTGCACTGATGAGAGAGACTCTGCAAGGACAGACAGAAAGTCTTCCCTGACG 2145
Qy 2101 GAGAGCGTCTCTCTCTTCAAGGCTGAGTGAAGAGAACTTCTGCTGCTGCTTCCCTGCAAG 2160
Db 2146 GAGAGCGTCTCTCTCTTCAAGGCTGAGTGAAGAGAACTTCTGCTGCTGCTTCCCTGCAAG 2205
Qy 2161 CTCTCTCTCTTCTGAGTCAAGAGAGATCTTGGTTCGCGAGCTACATGATGAATCTC 2220
Db 2206 CTCTCTCTCTTCTGAGTCAAGAGAGATCTTGGTTCGCGAGCTACATGATGAATCTC 2265
Qy 2221 CAGCGGCTGCGCGCTTGTGAACAAAGAGAGTCTAAGCATTTGACATTTGAGTGTCTG 2280
Db 2266 CAGCGGCTGCGCGCTTGTGTGAACAAAGAGAGTCTAAGCATTTGAGTGTCTG 2325
Qy 2281 CCTCTCTGATTTCCCGAGCTCATCTCTGTTGATGAGCGGCACTTGAAGTGAAGTCT 2340
Db 2326 CCTCTCTGATTTCCCGAGCTCATCTCTGTTGATGAGCGGCACTTGAAGTGAAGTCT 2385
Qy 2341 CATACAGAGATATTTGAGAGTGAAGATGTCGCGGCAATCTTGTCTCCCTGCGCCCAACCT 2400
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Qy 2401 TTACCGGATATCTTGACAACTCTCCAAATTTTCTAAATGATATGAGAGCTCTGAAGGCA 2460
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Qy 2581 GACTTCATTTGAGCTGCAAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Db 2626 GACTTCATTTGAGCTGCAAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2685
Qy 2641 TTTGTGAAAAAAGGCACTTTTAAACATATAGCAGCAAGAAATCAAGTCCAGTCTAATCTG 2700
Db 2686 TTTGTGAAAAAAGGCACTTTTAAACATATAGCAGCAAGAAATCAAGTCCAGTCTAATCTG 2745
Qy 2701 AATTCATGTTGATTTGCAAGATATGTTCTCATTTATTTTGG 2741
Db 2746 AATTCATGTTGATTTGCAAGATATGTTCTCATTTATTTTGG 2786

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RESULT 8
 ADM76619
 ID ADM76619 standard; DNA; 4508 BP.
 XX
 AC ADM76619;

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XX 24-MAR-2005 (first entry)
DT Human interleukin-17 (IL-17) receptor DNA.
XX
DE Interleukin-17 receptor; IL-17 receptor; ds; gene.
XX
KW Homo sapiens.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 553..2340
FT /product= "Human interleukin-17 (IL-17) receptor protein"
PN CN1465592-A.
XX
PD 07-JAN-2004.
XX
PF 01-JUL-2002; 2002CN-00123540.
XX
PR 01-JUL-2002; 2002CN-00123540.
XX
PA (U901) UNIV QINGHUA.
XX
PI Xiong S, Chang Z, Fu X;
XX
DR WPI: 2004-248799/24.
XX
DR P-PSDB; ADM76620.
XX
PT Human Interleukin-17 receptor sample protein, coding gene and its uses.
XX
PS Claim 3; SEQ ID NO 1; 14bp; Chinese.
XX
CC The invention relates to a novel human interleukin-17 (IL-17) receptor
CC protein, the coding gene and application. The current sequence is that of
CC the human interleukin-17 receptor DNA of the invention.
XX
SQ Sequence 4508 BP; 1175 A; 1061 C; 1141 G; 1131 T; 0 U; 0 Other;

Query Match 87.1%; Score 2684.6; DB 13; Length 4508;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2690; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 134 CCGTGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 193
Db 233 CCGTGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 292
Qy 194 TCAAAATATGACAAATTTGATCACTTGAATCAAGTGGAGAGATGATGCTGAGC 253
Db 293 TCAAAATATGACAAATTTGATCACTTGAATCAAGTGGAGAGATGATGCTGAGC 352
Qy 254 CCCAAGATATCACTTCAAGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313
Db 353 CCCAAGATATCACTTCAAGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 412
Qy 314 GGTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 373
Db 413 GGTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 472
Qy 374 TGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 433
Db 473 TGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 532
Qy 434 GTAGCTTCAAAAGAACTGGAATGGAATCAACCTTCTGTAATATGAAATTTGAAAGCG 493
Db 533 GTAGCTTCAAAAGAACTGGAATGGAATCAACCTTCTGTAATATGAAATTTGAAAGCG 592
Qy 494 ATTATTTGTAAGGATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 553
Db 593 ATTATTTGTAAGGATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 652
Qy 554 TCTTCTTTAGAACCGAGCTGAGCTGTTGTTTACAGCCGAGCAATGAGCTTGAAC 613

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Db 653 TCTTCTTAGAACCCGAGCCTGTGACCTGTGTTTACAGCCGAGCAATTAAGCTTGTAAAC 712
Qy 614 CCTTCTGGAAGCTCGGAACCTGGAATCAAGCCAGATGGCTCGGACATGCAAGTGTCTT 673
Db 713 CCTTCTGGAAGCTCGGAACCTGGAATCAAGCCAGATGGCTCGGACATGCAAGTGTCTT 772
Qy 674 TCGACACGACCGGACCACTTCGAGCTTCGCTTCCTTATCTTCACTTCAAGCTCAAGC 733
Db 773 TCGACACGACCGGACCACTTCGAGCTTCGCTTCCTTATCTTCACTTCAAGCTCAAGC 832
Qy 734 ACGAAGACCTTTCAGACGAAAGACCTGTAAAGCAGAGCAAACTACAGAGACGACAGCT 793
Db 833 ACGAAGACCTTTCAGACGAAAGACCTGTAAAGCAGAGCAAACTACAGAGACGACAGCT 892
Qy 794 GCTCTCTTCAAAATGTTTCTCCAGGGATTTATTAATTGAAGCTGTGATGACATTAACA 853
Db 893 GCTCTCTTCAAAATGTTTCTCCAGGGATTTATTAATTGAAGCTGTGATGACATTAACA 952
Qy 854 CAACAAGAAAGTATGATTAATGCTTAAAGCAGATGACCTCCCGGTGGCCGGGCCCA 913
Db 953 CAACAAGAAAGTATGATTAATGCTTAAAGCAGATGACCTCCCGGTGGCCGGGCCCA 1012
Qy 914 TCGAGACCATGAGCATCAGATGACCTGTAGTCAATCGGCAATTCGGACGCTTTCA 973
Db 1013 TCGAGACCATGAGCATCAGATGACCTGTAGTCAATCGGCAATTCGGACGCTTTCA 1072
Qy 974 CTGTATGTGCGGCAAGAACCAAGAAATATATATTTACATTTAATGAAGAGCT 1033
Db 1073 CTGTATGTGCGGCAAGAACCAAGAAATATATATTTACATTTAATGAAGAGCT 1132
Qy 1034 CTGAGCTTTCCATATCACTGAGACCTCCCAAGAGAGCTCCGGCCGGCCGCAAG 1093
Db 1133 CTGAGCTTTCCATATCACTGAGACCTCCCAAGAGAGCTCCGGCCGGCCGCAAG 1192
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Db 1193 TCTTCTCTGCTATTCAGATTAAGATGCGCAGATCACTGAATGTCTCCAGTGTTCG 1252
Qy 1154 CCTACTTCTCCAGACCTTCTGTGCTGTGAGGTGCTCTGACCTGTGGAAGACTTCA 1213
Db 1253 CCTACTTCTCCAGACCTTCTGTGCTGTGAGGTGCTCTGACCTGTGGAAGACTTCA 1312
Qy 1214 GCTCTGTGAGAAAGGAGGAGAGAAATGGCTATCCAGAAATCCAGATCCCAATTCA 1273
Db 1313 GCTCTGTGAGAAAGGAGGAGAGAAATGGCTATCCAGAAATCCAGATCCCAATTCA 1372
Qy 1274 TCATTGTGTTTGTTCCAAAAGTATGAAGTACTTGTGCAAGAAACTCAAAACACA 1333
Db 1373 TCATTGTGTTTGTTCCAAAAGTATGAAGTACTTGTGCAAGAAACTCAAAACACA 1432
Qy 1334 AAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTTTCCTGTGCGGTGTGAGCCATTG 1393
Db 1433 AAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTTTCCTGTGCGGTGTGAGCCATTG 1492
Qy 1394 CCGAAAAGCTCCGCCAGGACCAAGCAGATTTCTCCGGCGGCTCAGAGATTATGCGG 1453
Db 1493 CCGAAAAGCTCCGCCAGGACCAAGCAGATTTCTCCGGCGGCTCAGAGATTATGCGG 1552
Qy 1454 TCTACTTTGATTAATTCCTGCGAGGGAGAGCTCCCGGTATCTTGAAGCTGAAGCAAGT 1513
Db 1553 TCTACTTTGATTAATTCCTGCGAGGGAGAGCTCCCGGTATCTTGAAGCTGAAGCAAGT 1612
Qy 1514 ACAGACTCATGACATCTTCTCAGCTGTGTTCCACCTGCACTCCCGAGACAGAGGCC 1573
Db 1613 ACAGACTCATGACATCTTCTCAGCTGTGTTCCACCTGCACTCCCGAGACAGAGGCC 1672
Qy 1574 TCGAAGAGCGCGGGGCGAGCAAGCGGACAGGGCAGAGAACTTCTCCGAGCAAGT 1633
Db 1673 TCGAAGAGCGCGGGGCGAGCAAGCGGACAGGGCAGAGAACTTCTCCGAGCAAGT 1732
Qy 1634 CAGGCGGCTCCCTATATCTGCGCATTTGCAACATGACAGATTATTTGAAGAGAGCCCG 1693
Db 1733 CAGGCGGCTCCCTATATCTGCGCATTTGCAACATGACAGATTATTTGAAGAGAGCCCG 1792

Qy 1694 ACTGTTGAAAAAGAGTTCGTTCCCTTCATCTCTCCACTAGGGCTACCGGGAGCCAG 1753
Db 1793 ACTGTTGAAAAAGAGTTCGTTCCCTTCATCTCTCCACTAGGGCTACCGGGAGCCAG 1852
Qy 1754 TCTTGAAGAAATTTTATTCGGGCTTGTGTTTAAATGATGATGTGCAAAACGAGGCTG 1813
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Qy 1814 AGAGTGAATTCGCTTAAAGGTAGAGGCGCTGTTCTTGAGGCAACCGGACAGCCGACT 1873
Db 1913 AGAGTGAATTCGCTTAAAGGTAGAGGCGGCTGTTCTTGAGGCAACCGGACAGCCGACT 1972
Qy 1874 CCCAGACGAGAGTCAAGCATGAGGAGGCTGTAGACCAAGACGGGAGGCGGCTGCTTGG 1933
Db 1973 CCCAGACGAGAGTCAAGCATGAGGAGGCTGTAGACCAAGACGGGAGGCGGCTGCTTGG 2032
Qy 1934 ACGGTAGCGCGCCCTGCAACCCCTGTGCAACGAGTGAAGCCGGGACCCCTCGGACA 1993
Db 2033 ACGGTAGCGCGCCCTGCAACCCCTGTGCAACGAGTGAAGCCGGGACCCCTCGGACA 2092
Qy 1994 TCCCGCGGAGCTCAGGCAATCTATGACTGCTGTGCTGCTCATCCGAGCTGTCTGCAAC 2053
Db 2093 TCCCGCGGAGCTCAGGCAATCTATGACTGCTGTGCTGCTCATCCGAGCTGTCTGCAAC 2152
Qy 2054 TGAATGAAGACTCTCGACGAGCAAGACAGAAAGCTTTCCCTGACGAGAGCGTCTT 2113
Db 2153 TGAATGAAGACTCTCGACGAGCAAGACAGAAAGCTTTCCCTGACGAGAGCGTCTT 2212
Qy 2114 CCTCTTACGGCCTGAGGTAGAGAGAACTCTGAGCCCTTCCAGAGCTCTCTCTG 2173
Db 2213 CCTCTTACGGCCTGAGGTAGAGAGAACTCTGAGCCCTTCCAGAGCTCTCTCTG 2272
Qy 2174 GGTCAATGCAAAAGCAGATCTTGTGTCGCGAGCTTACATGATGAACTCCAGCGGTCGCC 2233
Db 2273 GGTCAATGCAAAAGCAGATCTTGTGTCGCGAGCTTACATGATGAACTCCAGCGGTCGCC 2332
Qy 2234 CTTTGTAAACAAAAGAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 2293
Db 2333 CTTTGTAAACAAAAGAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 2392
Qy 2294 CCCAGCTCATCTCCCTGTTGATGAGGCGCACTTGAAGCTGAGGTCTCATAGAGATAT 2353
Db 2393 CCCAGCTCATCTCCCTGTTGATGAGGCGCACTTGAAGCTGAGGTCTCATAGAGATAT 2452
Qy 2354 TTGAGTGAATGCTGGCAGACTGTTCTCTCCCTTGGCCCAACCCCTTACCGGATATCT 2413
Db 2453 TTGAGTGAATGCTGGCAGACTGTTCTCTCCCTTGGCCCAACCCCTTACCGGATATCT 2512
Qy 2414 TGACAAACTTCCAAATTTTCTAAATATGATGAGCTTGAAGGCAATGCTCAATAGGTC 2473
Db 2513 TGACAAACTTCCAAATTTTCTAAATATGATGAGCTTGAAGGCAATGCTCAATAGGTC 2572
Qy 2474 TGAACAAGCTTCCAAATTTTGTGATGCTTGAATCAAGGCTTGTGGAAGGATGAGG 2533
Db 2573 TGAACAAGCTTCCAAATTTGTTGATGCTTGAATCAAGGCTTGTGGAAGGATGAGG 2632
Qy 2534 AGGAATATGTAAGAAAAAGAAAGCAAGAAATCACTGACATATCACTTCACTTGAAGC 2593
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Qy 2594 TCTGCAAACTTGTCTGTTTGTGATGCTATCTTGAATGTAATGCTTGTGAAAAAG 2653
Db 2693 TCTGCAAACTTGTCTGTTTGTGATGCTATCTTGAATGTAATGCTTGTGAAAAAG 2752
Qy 2654 GCACTTTTAACTCAATTAAGCAAGAAATCAAGTGCAGCTATCTGGAATCAATGTGTA 2713
Db 2753 GCACTTTTAACTCAATTAAGCAAGAAATCAAGTGCAGCTATCTGGAATCAATGTGTA 2812
Qy 2714 TTGAGATTAATGTTCTCAATTTATTTTGAATGATGAAATTTTACATGAGGCTGTTAAT 2773
Db 2813 TTGAGATTAATGTTCTCAATTTATTTTGAATGATGAAATTTTACATGAGGCTGTTAAT 2872
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QY 2774 AACGTTTGAGTCAAAAGTCAAGAAAGTCACTGATATATACAGTCACTTTTATGAATGA 2832
 |||||
 CC 2873 AAGCTTTGAGTCAAAAGTCAAGAAAGTCACTGATATATACAGTCACTTTTATGAATGA 2931
 |||||

RESULT 9
 ADB63275
 ID ADB63275 standard; cDNA; 2894 BP.
 XX

AC ADB63275;

DT 04-DEC-2003 (first entry)

DE Human cDNA encoding clone TESTI20046540.

XX Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
 KM tissue regeneration; cell regeneration; membrane protein;
 KW signal transduction-related protein; transcription-related protein;
 KM osteoporosis; neurological disease; cancer; tumour.
 XX

OS Homo sapiens.

Key Location/Qualifiers
 FT CDS 123..2309
 FT /tag= a
 FT /product= "Clone TESTI20046540 protein"

EP1308459-A2.

PD 07-MAY-2003.

PF 28-MAR-2002; 2002EP-00007401.

PR 05-NOV-2001; 2001JP-00378298.
 PR 25-JAN-2002; 2002US-00350978.

PA (HELI-) HELIX RES INST.
 (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
 XX MPI: 2003-450961/43.
 DR P-PSDB; ADB65245.

PT New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX

PS Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesizing the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a cDNA of the invention. Note: Some of the sequence

CC data for this patent is not represented in the printed specification, but
 CC is based on sequence information supplied by the European Patent Office.
 CC
 XX
 SQ Sequence 2894 BP; 735 A; 751 C; 730 G; 678 T; 0 U; 0 Other;

Query Match 86.9%; Score 2678.6; DB 10; Length 2894;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2684; Conservative 9; Indels 0; Gaps 0;

QY 134 CCTGTGCTGAGGGAGTGGGGCCAGACAGAGAAAGTGGGCTGTAACATCACT 193
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 DB 202 CCTGGCCTTGGAGGAGTGGGGCCAGACAGAGAAAGTGGGCTGTAACATCACT 261
 |||||
 QY 194 TCAATATGACAAATTGTACCACTTGTGAATCCAGTGGGAGGATGTGCTGACG 253
 |||||
 DB 262 TCAATATGACAAATTGTACCACTTGTGAATCCAGTGGGAGGATGTGCTGACG 321
 |||||
 QY 254 CCCAGAAATATCAACATCAACGCCAGTATGCTTGCATGACCAAGTGGCAGTCACTTT 313
 |||||
 DB 322 CCCAGAAATATCAACATCAACGCCAGTATGCTTGCATGACCAAGTGGCAGTCACTTT 381
 |||||
 QY 314 GGTCCCGAGGGGCTCTGGCATTCGAATTCCTGAAGAATTTGGGTATATCTGAGGAGC 373
 |||||
 DB 382 GGTCCCGAGGGGCTCTGGCATTCGAATTCCTGAAGAATTTGGGTATATCTGAGGAGC 441
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 QY 374 TGAAGTCGAGGAGGAGAGACAGTGGCAACATGATCTGAAGGATTCGAAAGCAGTCAACA 433
 |||||
 DB 442 TGAAGTCGAGGAGGAGAGACAGTGGCAACATGATCTGAAGGATTCGAAAGCAGTCAACA 501
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 QY 434 GTAGCTTCAAAAGAACTGGAATGGAATCTCAACTCTTCTGTAATGAATTTGAAACGG 493
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 DB 502 GTAGCTTCAAAAGAACTGGAATGGAATCTCAACTCTTCTGTAATGAATTTGAAACGG 561
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 QY 494 ATTATTTTGTAAAGTGTGCTTTTCTTCTTCAATTAAAAAGAAAGCAATTACCACTT 553
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 DB 562 ATTATTTTGTAAAGTGTGCTTTTCTTCTTCAATTAAAAAGAAAGCAATTACCACTT 621
 |||||
 QY 554 TCTTCTTTAGAAACCCGAGCTGTGACCTGTGTGTAAGCCGAGCAATCTAGCTTTGAAC 613
 |||||
 DB 622 TCTTCTTTAGAAACCCGAGCTGTGACCTGTGTGTAAGCCGAGCAATCTAGCTTTGAAC 681
 |||||
 QY 614 CCTTCTGGAAGCTCTGGAACCTGGAACATCAAGCAGACATGCTGAGATGCTGCT 673
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 DB 682 CCTTCTGGAAGCTCTGGAACCTGGAACATCAAGCAGACATGCTGAGATGCTGCT 741
 |||||
 QY 674 TCGACGACGACCGCAACATCTTGGCTTCCGTTTCTTCTATTTCACTCAAGCTCAACG 733
 |||||
 DB 742 TCGACGACGACCGCAACATCTTGGCTTCCGTTTCTTCTATCTTCACTCAAGCTCAACG 801
 |||||
 QY 734 ACGAAGACCTTTCAAGCGAAAGACCTGTAAAGCAGAGCAACTACAGAGCAACAGCT 793
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 DB 802 ACGAAGACCTTTCAAGCGAAAGACCTGTAAAGCAGAGCAACTACAGAGCAACAGCT 861
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 QY 794 GCGTCTTCAAAATGTTTCTCCAGGGGATTAATTAATTAATTAATTAATTAATTAATTA 853
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 DB 862 GCGTCTTCAAAATGTTTCTCCAGGGGATTAATTAATTAATTAATTAATTAATTAATTA 921
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 QY 914 TCAGAGCAATGGCCATCAAGTGCACATGATGATTAATTAATTAATTAATTAATTAATTA 973
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 DB 982 TCAGAGCAATGGCCATCAAGTGCACATGATGATTAATTAATTAATTAATTAATTAATTA 1041
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 QY 1034 CTGAGTCTTTCACATCACTGACAGCACTTCCAGAGAGAGCTCCGCGCGCGCGAGAG 1093
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 DB 1102 CTGAGTCTTTCACATCACTGACAGCACTTCCAGAGAGAGCTCCGCGCGCGCGAGAG 1161
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1094 TCTTCTCTGCTATTCAGTAAAGATGGCCAGATCATGATGTGTCAGTGTTCG 1153
1162 TTTTCTCTGCTATTCAGTAAAGATGGCCAGATCATGATGTGTCAGTGTTCG 1221
1154 CCTACTTCTCTGCTATTCAGTAAAGATGGCCAGATCATGATGTGTCAGTGTTCG 1213
1222 CCTACTTCTCTGCTATTCAGTAAAGATGGCCAGATCATGATGTGTCAGTGTTCG 1281
1214 GGCTCTGTAGAGAGAGAGAGAGATGGTGTCTCCAGAAATCCAGATGCCAGTTCA 1273
1282 GGCTCTGTAGAGAGAGAGAGATGGTGTCTCCAGAAATCCAGATGCCAGTTCA 1341
1274 TCAATGTGTGTGTTCCTCAAGGATATGATCTTTGTGACAAAGAACTACAAACAA 1333
1342 TCAATGTGTGTGTTCCTCAAGGATATGATCTTTGTGACAAAGAACTACAAACAA 1401
1334 AAGAGATGGCCGAGGCTCGGAGAAAGAGAGCTCTTCTGTGGGCTGTCCAGTTG 1393
1402 AAGAGATGGCCGAGGCTCGGAGAAAGAGAGCTCTTCTGTGGGCTGTCCAGTTG 1461
1394 CCGAAAAGCTCCGCGCCAGAGCAGAGATGTCCTCCGCGGCTCAGCAAGTTATGCGG 1453
1462 CCGAAAAGCTCCGCGCCAGAGCAGAGATGTCCTCCGCGGCTCAGCAAGTTATGCGG 1521
1454 TCTACTTGTATTAATTCGCGAGAGAGAGTCCCGGATTCCTAGACTGATGACAGT 1513
1522 TCTACTTGTATTAATTCGCGAGAGAGAGTCCCGGATTCCTAGACTGATGACAGT 1581
1514 ACAGACTCATGACATCTTCTCAGCTGTGTCCAGCTGCACTCCGAGACAGAGGCT 1573
1582 ACAGACTCATGACATCTTCTCAGCTGTGTCCAGCTGCACTCCGAGACAGAGGCT 1641
1574 TCCAGAGACCCGCGGCGAGCAGCAGAGGCGAGCAGAGAACTACTTCCGAGCAAGT 1633
1642 TCCAGAGACCCGCGGCGAGCAGCAGAGGCGAGCAGAGAACTACTTCCGAGCAAGT 1701
1634 CAGGCGCGCTCCGATAGTCCGATTTGCAACATGACAGTTATTTGACAGAGACCGG 1693
1702 CAGGCGCGCTCCGATAGTCCGATTTGCAACATGACAGTTATTTGACAGAGACCGG 1761
1694 ACTGTTTCGAAAAGAGCTGTCCTTCCTCATCTCTCCACTGCGCTACCGGAGACCA 1753
1762 ACTGTTTCGAAAAGAGCTGTCCTTCCTCATCTCTCCACTGCGCTACCGGAGACCA 1821
1754 TCTTGTAGAAATTTGATTCGGGCTTGTGTTAAATGATGTCATGCAACCGAGGCTTG 1813
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1814 AAGATGACTTTCGCTTAAGATGAGAGCCCTGTTTGGGGGCAACCGGACCGAGCT 1873
1882 AAGATGACTTTCGCTTAAGATGAGAGCCCTGTTTGGGGGCAACCGGACCGAGCT 1941
1874 CCGAGACGAGATGAGATGAGAGCCCTGTAACCAAGAGCGGAGCCCGGCTGACCTTG 1933
1942 CCGAGACGAGATGAGATGAGAGCCCTGTAACCAAGAGCGGAGCCCGGCTGACCTTG 2001
1934 ACGGATGAGCCGCGCTGCAACCCCTGCTGACACGGTGAAGCCGCGAGCCCTCGGACA 1993
2002 ACGGATGAGCCGCGCTGCAACCCCTGCTGACACGGTGAAGCCGCGAGCCCTCGGACA 2061
1994 TGGCGCGGAGCTCAGGATCTATGATCTGCTGTGCTTCATCCGAGCTGTCTGTGCAAC 2053
2062 TGGCGCGGAGCTCAGGATCTATGATCTGCTGTGCTTCATCCGAGCTGTCTGTGCAAC 2121
2054 TGAATGAGAGATCTGAGACGAGCAGACAGAAAGCTTTCCCTGAGAGAGAGGCTGCT 2113
2122 TGAATGAGAGATCTGAGACGAGCAGACAGAAAGCTTTCCCTGAGAGAGAGGCTGCT 2181
2114 CCTCTTTCAGGCTCGGCTGAGAGAGAACTCTCTGCTCTTCCCTTCAAGCTCTCTTCTG 2173
2182 CCTCTTTCAGGCTCGGCTGAGAGAGAACTCTCTGCTCTTCCCTTCAAGCTCTCTTCTG 2241
2174 GGTGATGCAAGAGATCTTGTGCTGCGGAGCTACACTGATGAATCTCAAGCGGCTGCCC 2233

2242 GGTGATGCAAGAGATCTTGTGCTGCGGAGCTACCTGATGAATCTCAAGCGGCTGCCC 2301
2234 CTTTGTAAACAAACGAAAGAGCTAAGCATTTGACCTTTAGCTGCTGCTCTCTGAT 2293
2302 CTTTGTAAACAAACGAAAGAGCTAAGCATTTGACCTTTAGCTGCTGCTCTCTGAT 2361
2294 CCCAGCTCATCTCCCTGCTGATGAGCCCACTTGGAGCTGAGTCTCATACAGATAT 2353
2362 CCCAGCTCATCTCCCTGCTGATGAGCCCACTTGGAGCTGAGTCTCATACAGATAT 2421
2354 TTGAGTGAATGCTGCGCAGTACTTGTCTCTGCCCCCAACCTTTACCGGATATCT 2413
2422 TTGAGTGAATGCTGCGCAGTACTTGTCTCTGCCCCCAACCTTTACCGGATATCT 2481
2414 TGAACAACCTCTCAATTTCTTAAATGATGATGAGCTGGAAGAGATCCATAGCTC 2473
2482 TGAACAACCTCTCAATTTCTTAAATGATGATGAGCTGGAAGAGATCCATAGCTC 2541
2474 TGAACAACCTCTCAATTTGATGCTGATCAGAGCTGTGTGAGAGGTAAGG 2533
2542 TGAACAACCTCTCAATTTGATGCTGATCAGAGCTGTGTGAGAGGTAAGG 2601
2534 AGAAATATGTAAGAAAGAAACAGAAATACCTGCACTATCATTCAGACTTATGAGC 2593
2602 AGAAATATGTAAGAAAGAAACAGAAATACCTGCACTATCATTCAGACTTATGAGC 2661
2594 TCTGCAACTTTCCTGCTTGTGCTATTTGCTACCTGATTTGAATCTTTGAAAAAG 2653
2662 TCTGCAACTTTCCTGCTTGTGCTATTTGCTACCTGATTTGAATCTTTGAAAAAG 2721
2654 GCACCTTTAATCATATGCAAGAAATCAAGTCCAGCTCATGAGATCCATGTTGTA 2713
2722 GCACCTTTAATCATATGCAAGAAATCAAGTCCAGCTCATGAGATCCATGTTGTA 2781
2714 TTGACATATATGCTCATTTATTTTGTGATGATTAATTTACATTCGATGAGTGTAAAT 2773
2782 TTGACATATATGCTCATTTATTTTGTGATGATTAATTTACATTCGATGAGTGTAAAT 2841
2774 AAGCTTGTAGTCAAAAGTCAAGAAAGTGAATGATATACATGACCTTTATG 2826
2842 AAGCTTGTAGTCAAAAGTCAAGAAAGTGAATGATATACATGACCTTTATG 2894

RESULT 10
AADS1235
ID AADS1235 standard; cDNA; 4450 BP.
XX
AC AADS1235;
XX
DT 02-APR-2003 (first entry)
XX
DE Human REMAP-16 cDNA.
XX
KW Human; receptor and membrane-associated protein; REMAP; arteriosclerosis;
cell proliferative disorder; atherosclerosis; polycythemia vera; cancer;
cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;
primary thrombocytopaenia; developmental disorder; mental retardation;
renal tubular acidosis; neurological disorder; Alzheimer's disease;
Parkinson's disease; anaemia; reproductive disorder; autoimmune disorder;
infertility; inflammatory disorder; acquired immune deficiency syndrome;
AIDS; epilepsy; allergy; asthma; autoimmune thyroiditis; Crohn's disease;
contact dermatitis; diabetes mellitus; glomerulonephritis; osteoporosis;
Goodpasture's syndrome; gout; Graves' disease; Hashimoto's thyroiditis;
irritable bowel syndrome; multiple sclerosis; Reiter's syndrome; uveitis;
osteoarthritis; pancreatitis; rheumatoid arthritis; Sjogren's syndrome;
gene therapy; viricide; protozoacide; fungicide; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 512..2299
CDS /*tag= a

/product= "Human REMAP-16 protein"

WT 0020294990-A2.

28-NOV-2002.

16-MAY-2002; 2002WO-US015899.

18-MAY-2001; 2001US-0292197P.

08-JUN-2001; 2001US-0297012P.

21-JUN-2001; 2001US-0300582P.

22-JUN-2001; 2001US-0300495P.

28-JUN-2001; 2001US-0301922P.

14-DEC-2001; 2001US-0340542P.

(INCYTE GENOMICS INC.

Lal PG, Warren BA, Xu Y, Duggan BM, Honchell CD, Kallick DA; Baughn MR, Tang YT, Yue H, Bandman O, Jones KA, Becha SD, Tran UK; Au-Young JK, Griffin JA, Zebardjian Y, Lee EA, Elliott VS; Thangavelu K, Raskumar J, Lu Y, Hafalla AJA, Walla NK, Ison CH; Thornton M, Swarnakar A, Yang J, Richardson TW, Emerling BM, Yao MG; Cooke BG, Sanjanwala B, Mason PM, Gandhi AR, Li JK, Forsythe JD; Gururajan R, Gietzen KU;

WPI: 2003-129423/12.

P-PSDB; AAE33485.

New human receptors and membrane-associated proteins and nucleic acids, useful for diagnosing, treating or preventing inflammatory disorder, e.g. hepatitis.

Claim 97; Col 232-233; 243pp; English.

The present invention relates to human receptor and membrane-associated proteins (REMP) and polynucleotides encoding such proteins. Sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of REMAP, particularly cell proliferation disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis), primary thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle) or autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis) or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. They are also useful in gene therapy. The present sequence is human REMAP-16 cDNA

Sequence 4450 BP; 1151 A; 1046 C; 1086 G; 1167 T; 0 U; 0 Other;

Query Match 85.1%; Score 2672.2; DB 8; Length 4450;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2624; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

206 ATTGACCACTTGAATTCAGTGGGGAAGCATGTGTTGCTGACGGCCGGAATATCA 265

264 ATTGACCACTTGAATTCAGTGGGGAAGCATGTGTTGCTGACGGCCGGAATATCA 323

266 CCATGACCACTGATCTTGCATGACCAAGTGACATCCATCTTTGGTCCCAAGGG 325

324 CCATGACCACTGATCTTGCATGACCAAGTGACATCCATCTTTGGTCCCAAGGG 383

326 CCCTGGCATGCAATCTCTGAAAGATTTGGGTAATATCTGAGAGAGCTGAAGTGGAG 385

384 CCCTGGCATGCAATCTCTGAAAGATTTGGGTAATATCTGAGAGAGCTGAAGTGGAG 443

386 GAAAGACAGTCCCACTGATTTCTAAGATCCGAGAGAGCTCAACAGTACTTCAAA 445

444 GAAAGACAGTCCCACTGATTTCTAAGATCCGAGAGAGCTCAACAGTACTTCAAA 503

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624 CCCGAGCTTGACCTGTTGTTACAGCCGAGCAATCTGATCTGTAACCTTTCTGAAAG 683

626 CTGGACCTGAAACATCAAGCCAGATGCTGACATGAGGTGCTTTCAGCACGCAAC 685

684 CTGGACCTGAAACATCAAGCCAGATGCTGACATGAGGTGCTTTCAGCACGCAAC 743

686 CGCAACTTGGGCTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 745

744 CGCAACTTGGGCTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 803

746 TCAAGCAAGAAAGCTGTAAAGCAGAGCAAACTACAGAGACAGCTGCTCTTCAAA 805

804 TCAAGCAAGAAAGCTGTAAAGCAGAGCAAACTACAGAGACAGCTGCTCTTCAAA 863

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864 ATGTTTCTCAGGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 923

866 TGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 925

924 TGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 983

926 CCATGACAGTGCACCTGATGATCATATGCGCATTCGACAGCTCTTCACTGATGATGCC 985

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1164 ATTCAAGTAAGATGAGCCAGATCATGAAATGTCGACATGTTTGGCTTACTTCTTCC 1223

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1284 AAGGCAAGAGAAATGGTCAATCCAGAGATCCAGAGTCCAGTTCATCATTTGGTGT 1343

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1344 GTTCCAAAGTATGAAGTATTTTGTGACAAAGAACTTCAACAAACAAAGAGGTGGCC 1403

1346 GAGGCTGGGGAAGAGAGCTTTCTGTGGCGGTGTGACCAATGCGGAAAGCTTCC 1405

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1466 ATTCTGAGAGAGAGAGCTCCCGGTATCTTGAAGCTGATACCAAGTACAGACTCATGG 1525


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Qy 2546 AAGAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2605

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RESULT 11
ABZ11243
ID ABZ11243 standard; cDNA; 3948 BP.
XX
AC ABZ11243;
XX
DT 20-JUN-2003 (first entry)
XX
DE Human polynucleotide SEQ ID NO 125.
XX
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
XX haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
XX antirheumatic; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002MO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F,
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
XX
DR P-PDB; ABP69026.
XX
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 1; SEQ ID NO 125; 1012bp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ1119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's

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or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, amyloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences

Sequence 3948 BP; 1013 A; 938 C; 975 G; 1022 T; 0 U; 0 Other;

Query Match 78.7%; Score 2426.4; DB 6; Length 3948;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2430; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 397 CAACAACGATGCTTAAAGGATCCGAAGACGCTCAACAGTAGCTTCAAAAGAACTGGAATG 456
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DB 63 GAATCTCAACCTTCTCGAATATGAAATTGAAACGGAATTAATTCGTAAGGTTGTCCT 122
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QY 577 GACCTGTGTTACAGCCGGAACAATCTAGCTGTGAACCCCTTCTGGAAGCTCGGAACCTG 636
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QY 817 GGGGATTAATATTAATGAGCTGTGATGACACTAACAACAAGAAATGATGACTAT 876
DB 423 GGGGATTAATATTAATGAGCTGTGATGACACTAACAACAAGAAATGATGACTAT 482
QY 877 GCGTTAAAGCAGTGACTCCCGTGCGCCGCGCCATCAAGCCATGCGCATCAGTG 936
DB 483 GCGTTAAAGCAGTGACTCCCGTGCGCCGCGCCATCAAGCCATGCGCATCAGTG 542
QY 937 CCACTGTATGATTAATCGGCATTGCGAGGCTCTTCACTGTGATGTCGCGGAAGAA 996
DB 543 CCACTGTATGATTAATCGGCATTGCGAGGCTCTTCACTGTGATGTCGCGGAAGAA 602
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DB 603 CAAGAAATATATTAATTAATTAATGATGAAGAGCTGTGAGCTTCACTAATCTGCA 662
QY 1057 GCACTCCCAAGAGAGGCTCCGCGCCGCGCGGAAGGCTTTTCTGTCTATTCAGTAA 1116
DB 663 GCACTCCCAAGAGAGGCTCCGCGCCGCGCGGAAGGCTTTTCTGTCTATTCAGTAA 722
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QY 1237 GAATGGGTATCCAGAAAGATCCAGAGTCCAGTTCATCATTTGTGTTTCCAAAGGT 1296
DB 843 GAATGGGTATCCAGAAAGATCCAGAGTCCAGTTCATCATTTGTGTTTCCAAAGGT 902
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DB 1923 ATGGCCCACTTGGAGCTGAGTCTCATACAGAGATATTTGAGTAAATGCTGGCAGTA 1982
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QY 2377 CTGTGTCCTCCCTGCCCCCAACCTTTACGGATATCTGACAAACCTCCAAATTTTCTAA 2436
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 DB 2403 AAGTGACTGAATATACATGTCATGCTTTTATGAATGA 2438

RESULT 12

ID ADM43761 standard; cDNA; 3948 BP.

XX ADM43761;

XX 03-JUN-2004 (first entry)

XX Novel human arginine-rich protein cDNA #125.

XX ss; gene; human; arginine-rich protein; cancer; inflammation;

XX genetic disorder.

XX Homo sapiens.

XX US2004053250-A1.

XX 18-MAR-2004.

XX 21-NOV-2002; 2002US-00302172.

XX 05-MAR-2001; 2001US-00799451.

XX 05-MAR-2002; 2002WO-US005095.

XX 20-AUG-2002; 2002US-00225251.

XX (TANG/) TANG Y T.

XX (XUEA/) XUE A.

XX (DRMA/) DRMANAC R T.

XX Tang YT, Xue A, Drmanac RT;

XX WPI: 2004-238579/22.

XX New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and inflammation.

XX Disclosure; SEQ ID NO 125; 51bp; English.

CC The invention relates to an isolated polynucleotide. The methods and
 CC compositions of the present invention are useful for the diagnosis and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the arginine-rich protein-like polypeptides, such as
 CC cancer and inflammation. They can also be used in forensics, gene
 CC mapping, identification of mutations responsible for genetic disorders,
 CC and in assessing biodiversity. The present sequence represents a novel
 CC human arginine-rich protein cDNA.

XX Sequence 3948 BP; 1013 A; 938 C; 975 G; 1022 T; 0 U; 0 Other;

Query Match 78.7%; Score 2426.4; DB 12; Length 3948;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2430; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 397 CAACAACGATTTCTAAAGATCCGAGACGCTCAACAGTACTTCAAAAGAACTGGAATG 456
 DB 3 CCACAACGATTTCTAAAGATCCGAGACGCTCAACAGTACTTCAAAAGAACTGGAATG 62
 QY 457 GAATCTCAACCTTCTGTAATGAAATTTGAAAGGATTAATTTGTAAGGTTGCCCT 516
 DB 63 GAATCTCAACCTTCTGTAATGAAATTTGAAAGGATTAATTTGTAAGGTTGCCCT 122
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 QY 577 GACCTGTGTTTACAGCCGAGCAATCTAGCTTGAACCCCTTGAAGGCTGGAACCTG 636
 DB 183 GACCTGTGTTTACAGCCGAGCAATCTAGCTTGAACCCCTTGAAGGCTGGAACCTG 242
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 Db 1083 GGAGAGTCCCGGGTATCTTAGACCTGAGTACCAATGAGACTCATGAGCAATCTTCTCT 1142
 Qy 1537 CAGCTCTGTTCCCACTGCACTCCGAGACCAAGGCTCCAGAGGCGGGGAGCAACAG 1596
 Db 1143 CAGCTCTGTTCCCACTGCACTCCGAGACCAAGGCTCCAGAGGCGGGGAGCAACAG 1202
 Qy 1597 CGACAGGAGCAGCAAGAAAGAACTA CTTCCGAGCAAGTCAAGGCGGTCCCTATACGTGCC 1656
 Db 1203 CGACAGGAGCAGCAAGAAAGAACTA CTTCCGAGCAAGTCAAGGCGGTCCCTATACGTGCC 1262
 Qy 1657 AATTGGAATGCAACAGTTTATTTGACGAGAGCCGACCTGGTTGAAAAGAGCTTCGTT 1716
 Db 1263 AATTGGAATGCAACAGTTTATTTGACGAGAGCCGACCTGGTTGAAAAGAGCTTCGTT 1322
 Qy 1717 CCCTTCATCTCTCTCACTGCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGC 1776
 Db 1323 CCCTTCATCTCTCTCACTGCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGC 1382
 Qy 1777 TTGGTTTAAATGATGATCATGTGCAAA CCAAGGCTCGAGAGTGACTTTGCTTAAAGTGA 1836
 Db 1383 TTGGTTTAAATGATGATCATGTGCAAA CCAAGGCTCGAGAGTGACTTTGCTTAAAGTGA 1442
 Qy 1837 GAGGCGGCTGTTCTTGGGGCAACCGGACCGAATCCAGACCAAGAGTCAAGATGAGG 1896
 Db 1443 GAGGCGGCTGTTCTTGGGGCAACCGGACCGAATCCAGACCAAGAGTCAAGATGAGG 1502
 Qy 1897 GGCCTGACCAAGACGGGAGGCGCGGCTG CTTGACGTTAGCGGTAGCCGCCCTGCAACCC 1956
 Db 1503 GGCCTGACCAAGACGGGAGGCGCGGCTG CTTGACGTTAGCGGTAGCCGCCCTGCAACCC 1562
 Qy 1957 CTGCTGCACACGGGTGAAGACCGGCA GCGCTCGGACATGCGCGGAGCTTCAGGCATCTAT 2016
 Db 1563 CTGCTGCACACGGGTGAAGACCGGCA GCGCTCGGACATGCGCGGAGCTTCAGGCATCTAT 1622
 Qy 2017 GACTGCTGTGTGCTCTCATCTCCAGCT GTCCTCTGCTGCTGATGGAAGAGCTTCGAGAGGAC 2076
 Db 1623 GACTGCTGTGTGCTCTCATCTCCAGCT GTCCTCTGCTGCTGATGGAAGAGCTTCGAGAGGAC 1682
 Qy 2077 CAGACGAAACGTCCTCCCTGACGAGAG GGTGTCCTCTTCAGGCTCGGGTGAAGAG 2136
 Db 1683 CAGACGAAACGTCCTCCCTGACGAGAG GGTGTCCTCTTCAGGCTCGGGTGAAGAG 1742
 Qy 2137 GAACCTCTGCTCCCTCTTCCAAGCTCT CTTCTTCTGAGGTCAAGAGAGATCTTGGT 2196
 Db 1743 GAACCTCTGCTCCCTCTTCCAAGCTCT CTTCTTCTGAGGTCAAGAGAGATCTTGGT 1802
 Qy 2197 TGGCCGAGCTACACTGATGAATCTCA CAGCGGGTGGCCCTTTGTAACAAAAGAGATC 2256
 Db 1803 TGGCCGAGCTACACTGATGAATCTCA CAGCGGGTGGCCCTTTGTAACAAAAGAGATC 1862
 Qy 2257 TAAGCAATGCACTTAGCGTGCCTCCCT CAGATTCGCCAGCTCATGCTCCCTGATTCG 2316
 Db 1863 TAAGCAATGCACTTAGCGTGCCTCCCT CAGATTCGCCAGCTCATGCTCCCTGATTCG 1922
 Qy 2317 ATGGCCCACTTGGAGCTGAGGTCTCAT ACAAAGATATTTGAGTGAATGCTGGCCAGTA 2376
 Db 1923 ATGGCCCACTTGGAGCTGAGGTCTCAT ACAAAGATATTTGAGTGAATGCTGGCCAGTA 1982

Qy 2377 CTGTGTTCTCCCTTGGCCCAACCCCTT TACCGGATATCTTGACAAACCTCTCCAAATTTCTAA 2436
 Db 1983 CTGTGTTCTCCCTTGGCCCAACCCCTT TACCGGATATCTTGACAAACCTCTCCAAATTTCTAA 2042
 Qy 2437 AATGATATGAGCTCTGAAGAGCATGT CCAATAGGTTCTGACAAACAGCTTGGCCAAATTTGG 2496
 Db 2043 AATGATATGAGCTCTGAAGAGCATGT CCAATAGGTTCTGACAAACAGCTTGGCCAAATTTGG 2102
 Qy 2497 TTAGTCCCTTGAATCAAGACCTGTTGT GGGAGGTAGGGAGAAATGTGTAAGAAAACAG 2556
 Db 2103 TTAGTCCCTTGAATCAAGACCTGTTGT GGGAGGTAGGGAGAAATGTGTAAGAAAACAG 2162
 Qy 2557 GAAGTATACCTGCACTAATCATTTCA GACTTCATTGAGCTCTGCAAACTTTGCTGTTGGCT 2616
 Db 2163 GAAGTATACCTGCACTAATCATTTCA GACTTCATTGAGCTCTGCAAACTTTGCTGTTGGCT 2222
 Qy 2617 ATTGCTACCTTGATTTGAAATGCTTT GTGAAAAAAGCACTTTTAACTCATACCA 2676
 Db 2223 ATTGCTACCTTGATTTGAAATGCTTT GTGAAAAAAGCACTTTTAACTCATACCA 2282
 Qy 2677 GAAATCAAGTGCAGTCTATCTGGAAT CCAATGTTATTTGAGATATGTTCTCAATTA 2736
 Db 2283 GAAATCAAGTGCAGTCTATCTGGAAT CCAATGTTATTTGAGATATGTTCTCAATTA 2342
 Qy 2737 TTTGATGTGAATTTTACATTCATG GGTGTTAATAAGCTTGAATCAAAAGTCAAGA 2796
 Db 2343 TTTGATGTGAATTTTACATTCATG GGTGTTAATAAGCTTGAATCAAAAGTCAAGA 2402
 Qy 2797 AAGTGACTGAATATACAGTCACTT TATGAAATGA 2832
 Db 2403 AAGTGACTGAATATACAGTCACTT TATGAAATGA 2438

RESULT 13
 ABX71363
 ID ABX71363 standard; cDNA; 2406 BP.
 XX
 AC ABX71363;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Human transmembrane protein cDNA from clone DKZphes3_2013.
 XX
 KW Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
 OS Homo sapiens.
 XX
 PN WO200112659-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000MO-IB001496.
 XX
 PR 18-AUG-1999; 99US-0149499P.
 XX
 PR 28-SEP-1999; 99US-0156503P.
 XX
 PA (GENU-) GERMAN HUMAN GENOME PROJECT.
 XX
 PI Wiemann S;
 XX
 DR WPI: 2001-327840/34.
 XX
 DR P-PSDB; ABUS3091.
 XX
 PT Nucleic acids having the sequences of clones isolated from libraries of
 XX different human tissues, useful in recombinant DNA methodologies.
 XX
 PS Claim 1; Page 698; 1095pp; English.
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases

associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence encodes a polypeptide described in the disclosure of the invention

Sequence 2406 BP; 633 A; 650 C; 589 G; 534 T; 0 U; 0 Other;

Query Match 74.8%; Score 2307.6; DB 5; Length 2406;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2113; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 135 CTGTGGCTGAGGGAGTGGGGCCAGCCAGAGAAACATGGGGCTTACAACTACCTT 194
DB 27 CAGTGAAGACAGGAGTGGGGCCAGCCAGAGAAACATGGGGCTTACAACTACCTT 86
QY 195 CAATATGACAAATTTGACCACTTCTGATCCAGTGGGGAGAGCATGTGATGCTGACGC 254
DB 87 CAATATGACAAATTTGACCACTTCTGATCCAGTGGGGAGAGCATGTGATGCTGACGC 146
QY 255 CCAGAAATATCACCATGACCAAGTATGCTTGCATGACCAAGTGGCAGTCACTTTTGG 314
DB 147 CCAGAAATATCACCATGACCAAGTATGCTTGCATGACCAAGTGGCAGTCACTTTTGG 206
QY 315 GTCCCCAGGGGCTCTGGCATGGAATCTTGAAAGATTTGGGTAAATCTGAGAGAGCT 374
DB 207 GTCCCCAGGGGCTCTGGCATGGAATCTTGAAAGATTTGGGTAAATCTGAGAGAGCT 266
QY 375 GAAGTCGAGGAGAGACAGTGCACCACTGATCTTAAAGATCCGAGAGAGCTCAACAG 434
DB 267 GAAGTCGAGGAGAGACAGTGCACCACTGATCTTAAAGATCCGAGAGAGCTCAACAG 326
QY 435 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTCTGAAATATGAAATTTGAAACGA 494
DB 327 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTCTGAAATATGAAATTTGAAACGA 386
QY 495 TTATTTCTGAAAGTGTGCTCTTCTTCTTCAATTAAGAAAGAAAGCAATTCACCTTT 554
DB 387 TTATTTCTGAAAGTGTGCTCTTCTTCTTCAATTAAGAAAGAAAGCAATTCACCTTT 446
QY 555 CTCTTTTGAACCCGAGCTGTGACCTGTGTTTAAAGCGGGAACAATCTGACTTGTAAACC 614
DB 447 CTCTTTTGAACCCGAGCTGTGACCTGTGTTTAAAGCGGGAACAATCTGACTTGTAAACC 506
QY 615 CTCTGGAAGCTCTGGAACCTGAACATCAAGCAGTGGCTCGACATGCAAGTGTCTT 674
DB 507 CTCTGGAAGCTCTGGAACCTGAACATCAAGCAGTGGCTCGACATGCAAGTGTCTT 566
QY 675 CGACCAAGCAGCAGCACTTGGGCTTCCGTTTCTTCTATCTTCACTAAGCTCAAGCA 734
DB 567 CGACCAAGCAGCAGCACTTGGGCTTCCGTTTCTTCTATCTTCACTAAGCTCAAGCA 626
QY 735 CGAAGGACCTTTCAAGCGGAAAGACCTGTAAAGCAGGAGCAAACTACAGAAATGACGCTG 794
DB 627 CGAAGGACCTTTCAAGCGGAAAGACCTGTAAAGCAGGAGCAAACTACAGAAATGACGCTG 686
QY 795 CCTCTTCAAAATGTTTCTCAAGGGATTAATATTAATGAGCTGTGATGACACTAAAC 854
DB 687 CCTCTTCAAAATGTTTCTCAAGGGATTAATATTAATGAGCTGTGATGACACTAAAC 746
QY 855 AACAAAGAAAGTATGATGATTAATGCTTAAAGCAGTGCCTCCGCTGGGCGGGCCCAT 914
DB 747 AACAAAGAAAGTATGATGATTAATGCTTAAAGCAGTGCCTCCGCTGGGCGGGCCCAT 806
QY 915 CAGAGCAGTGGCATCAAGTGCACCTGTAAGTCAATGCGCATTTGGCGACGCTCTTCAAC 974
DB 807 CAGAGCAGTGGCATCAAGTGCACCTGTAAGTCAATGCGCATTTGGCGACGCTCTTCAAC 866
QY 975 TGTGATGTCCCGCAAGAGCAACAAAGAAATATATATTTCACTTTAGATGAAGAGCTC 1034
DB 867 TGTGATGTCCCGCAAGAGCAACAAAGAAATATATATTTCACTTTAGATGAAGAGCTC 926

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QY 1035 TGAATCTTCCACATACATGACGACATCCCAAGAGAGAGGCTCCGGCCGCGCCAGAGGT 1094
DB 927 TGAATCTTCCACATACATGACGACATCCCAAGAGAGAGGCTCCGGCCGCGCCAGAGGT 986
QY 1095 CTTTCTGTCTATTTCCAGTAAAGATGCGCAGATATCAATGAATGTCTCACTGTTTGGC 1154
DB 987 CTTTCTGTCTATTTCCAGTAAAGATGCGCAGATATCAATGAATGTCTCACTGTTTGGC 1046
QY 1155 CTACTTCTCCAGGACTTCTGTGCTGTGAGAGTGTCTGACACTGTGAGGAAGACTTCCG 1214
DB 1047 CTACTTCTCCAGGACTTCTGTGCTGTGAGAGTGTCTGACACTGTGAGGAAGACTTCCG 1106
QY 1215 CCTGTGAGAGAGGCGAGAGAAATGGGTCACTCCAGAAAGATCCAGAGTCCAGTTCAT 1274
DB 1107 CCTGTGAGAGAGGCGAGAGAAATGGGTCACTCCAGAAAGATCCAGAGTCCAGTTCAT 1166
QY 1275 CATTTGTGTTTGTTCCAAGGTATGAAATCTTTGTGACAAAGAACTACAAACAA 1334
DB 1167 CATTTGTGTTTGTTCCAAGGTATGAAATCTTTGTGACAAAGAACTACAAACAA 1226
QY 1335 AGAGGTGGCCGAGGCTGGGGGAAAGAGAGCTTTCTGTGTGGCGGTCTAGCCATTGC 1394
DB 1227 AGAGGTGGCCGAGGCTGGGGGAAAGAGAGCTTTCTGTGTGGCGGTCTAGCCATTGC 1286
QY 1395 CGAAAGGCTCGGCGCAAGGCAAGTTCGTCGGGGGCTCAGCAAGTTATGCGCGT 1454
DB 1287 CGAAAGGCTCGGCGCAAGGCAAGTTCGTCGGGGGCTCAGCAAGTTATGCGCGT 1346
QY 1455 CTACTTGTATTTCTCTGAGAGGAGAGAGTCCCGGTATCTTACAGCTTGAATCAAGTA 1514
DB 1347 CTACTTGTATTTCTCTGAGAGGAGAGAGTCCCGGTATCTTACAGCTTGAATCAAGTA 1406
QY 1515 CAGACTCATGACAAATCTTCTCACTCTGTTCCACTGCACTCCCGAGACAGGCTT 1574
DB 1407 CAGACTCATGACAAATCTTCTCACTCTGTTCCACTGCACTCCCGAGACAGGCTT 1466
QY 1575 CCAGAGCCGGGGCGAGCAAGCGGCAAGGGCGAGAGAAAGAACTACTCCGAGCAAGTC 1634
DB 1467 CCAGAGCCGGGGCGAGCAAGCGGCAAGGGCGAGAGAAAGAACTACTCCGAGCAAGTC 1526
QY 1635 AGGCGGTCCTCATATAGTGCAGTATTGCAACATGACAGAGTAAATGAGAGAGCCGA 1694
DB 1527 AGGCGGTCCTCATATAGTGCAGTATTGCAACATGACAGAGTAAATGAGAGAGCCGA 1586
QY 1695 CTGTTTGAAGAAAGCAATTCCTTCCATCTCTTCACATGCTGCTACCGGAGCCAGT 1754
DB 1587 CTGTTTGAAGAAAGCAATTCCTTCCATCTCTTCACATGCTGCTACCGGAGCCAGT 1646
QY 1755 CTGGAAGAAATTTGATGCGGCTTGTGTTTAAATGATGATGTCGAAACAGAGGCTTGA 1814
DB 1647 CTGGAAGAAATTTGATGCGGCTTGTGTTTAAATGATGATGTCGAAACAGAGGCTTGA 1706
QY 1815 GAGTGACTTCTGCTTAAAGGTGAGAGGCTGTTCTTGGGGGCAACGGAACGAGCACTC 1874
DB 1707 GAGTGACTTCTGCTTAAAGGTGAGAGGCTGTTCTTGGGGGCAACGGAACGAGCACTC 1766
QY 1875 CCAGCAGCAGAGTCAAGATGAGGAGGCTTGAACCAAGACGAGGAGCCCGGCTTGA 1934
DB 1767 CCAGCAGCAGAGTCAAGATGAGGAGGCTTGAACCAAGACGAGGAGCCCGGCTTGA 1826
QY 1935 CCGTACGCGCGGCTGCAACCTCTGTGCAACGCTGAAAGCGGCGAGCTCTTGGACAT 1994
DB 1827 CCGTACGCGCGGCTGCAACCTCTGTGCAACGCTGAAAGCGGCGAGCTCTTGGACAT 1886
QY 1995 GCGGCGGGACTCAGGACATCTATGACTCGTGTGCGCTCATCCAGAGCTGTCTGCACT 2054
DB 1887 GCGGCGGGACTCAGGACATCTATGACTCGTGTGCGCTCATCCAGAGCTGTCTGCACT 1946
QY 2055 GATGGAAGACTCTGACGAGCAGACAGAAAGCTTTCTCTGACGAGAGCGGTCTTC 2114
DB 1947 GATGGAAGACTCTGACGAGCAGACAGAAAGCTTTCTCTGACGAGAGCGGTCTTC 2006
QY 2115 CTCTTCAAGGCTGGGTGAGAGGAACCTCTGCGCTTCTTCAAGCTCTCTCTTCTGG 2174

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QY 901 TGGGCGGCGCCATCAGAGCCATGAGGCTGAGTGCATATGCGCATTC 960
 DB 965 TGGGCGGCGCCATCAGAGCCATGAGGCTGAGTGCATATGCGCATTC 1024
 QY 961 GCGAGCTCTTCACTGATGATGCGCGAGAGAGCAAGAAAATATATTCATTTA 1020
 DB 1025 GCGAGCTCTTCACTGATGATGCGCGAGAGAGCAAGAAAATATATTCATTTA 1084
 QY 1021 GATGAAGAGAGCTCTGATGCTTCCATACATCAGCACTCTCCAGAGAGAGGCTCCG 1080
 DB 1085 GATGAAGAGAGCTCTGATGCTTCCATACATCAGCACTCTCCAGAGAGAGGCTCCG 1144
 QY 1081 CCGCGGCGGAGGCTCTTCTGCTATTCAGATGAAGAGAGAGAGAGAGAGAGAGAG 1140
 DB 1145 CCGCGGCGGAGGCTCTTCTGCTATTCAGATGAAGAGAGAGAGAGAGAGAGAGAG 1204
 QY 1141 GTCAGTGTTCGCTACTTCTCTCAGAGACTCTGAGGCTGAGAGGCTCTGAGCTG 1200
 DB 1205 GTCAGTGTTCGCTACTTCTCTCAGAGACTCTGAGGCTGAGAGGCTCTGAGCTG 1264
 QY 1201 TGGGAAAGCTTCAAGCTCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1265 TGGGAAAGCTTCAAGCTCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1324
 QY 1261 GAGTCCAGCTTCACTATGCTGCTTCCAGAGAGATGAAGTATCTTGTGACAGAG 1320
 DB 1325 GAGTCCAGCTTCACTATGCTGCTTCCAGAGAGATGAAGTATCTTGTGACAGAG 1384
 QY 1321 AACTACAAACAAAGAGAGGTCGAGGCTCGGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 DB 1385 AACTACAAACAAAGAGAGGTCGAGGCTCGGAGAGAGAGAGAGAGAGAGAGAGAG 1444
 QY 1381 GTGTGAGCCATTCGAG 1440
 DB 1445 GTGTGAGCCATTCGAG 1504
 QY 1441 AAGTTATTCGCTCTTCACTTGTATTTCTGCGAGAGAGAGAGAGAGAGAGAGAG 1500
 DB 1505 AAGTTATTCGCTCTTCACTTGTATTTCTGCGAGAGAGAGAGAGAGAGAGAGAG 1564
 QY 1501 CTGAGTACCAAGTACAGACTCATGAGCAATCTTCTGAGCTCTGAGCTCTGAGCTCC 1560
 DB 1565 CTGAGTACCAAGTACAGACTCATGAGCAATCTTCTGAGCTCTGAGCTCTGAGCTCC 1624
 QY 1561 CGAGACCAAGGCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 DB 1625 CGAGACCAAGGCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1684
 QY 1621 TTCGAGAGAGTCAAGGCTCGCTTATACATGCTGCTTCAATGCAATGCAAGTTATT 1680
 DB 1685 TTCGAGAGAGTCAAGGCTCGCTTATACATGCTGCTTCAATGCAATGCAAGTTATT 1744
 QY 1681 GAGGAG 1740
 DB 1745 GAGGAG 1804
 QY 1741 TACCGGAG 1800
 DB 1805 TACCGGAG 1864
 QY 1801 AAGCAAGAGCTTGAAGAGTCTTCTGCTTAAAGTGAAGAGAGAGAGAGAGAGAGAG 1860
 DB 1865 AAGCAAGAGCTTGAAGAGTCTTCTGCTTAAAGTGAAGAGAGAGAGAGAGAGAGAG 1924
 QY 1861 GAGCAAG 1920
 DB 1925 GAGCAAG 1984
 QY 1921 GAGCAAG 1980
 DB 1985 GAGCAAG 2044

QY 1981 AGCCCTCGGACATGCGCGGAGACTCAGGACATATGACTGCTGAGCCCTGATCCGAG 2040
 DB 2045 AGCCCTCGGACATGCGCGGAGACTCAGGACATATGACTGCTGAGCCCTGATCCGAG 2104
 QY 2041 CTGCTCTGCACTGATGAGAGAGACTCTGACGAGACAGACAGAGAGAGAGAGAGAG 2100
 DB 2105 CTGCTCTGCACTGATGAGAGAGACTCTGACGAGACAGACAGAGAGAGAGAGAGAG 2164
 QY 2101 GAGAGGCTGCTCTCTCTTCAAGGCTGCGGTGAGAGAGAGAGAGAGAGAGAGAGAG 2160
 DB 2165 GAGAGGCTGCTCTCTCTTCAAGGCTGCGGTGAGAGAGAGAGAGAGAGAGAGAGAG 2224
 QY 2161 CTGCTCTCTTCTGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
 DB 2225 CTGCTCTCTTCTGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2284
 QY 2221 CAGCGGCTGCGCCCTTGTGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2277
 DB 2285 CAGCGGCTGCGCCCTTGTGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2341

RESULT 15
 ABA95031
 ID ABA95031 standard; DNA; 2383 BP.
 XX
 AC ABA95031;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE Human cytokine receptor, Zcytor18 nucleotide sequence.
 XX
 KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
 KM pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 XX erythroid leukemia; chromosome 3p14.3; gene therapy; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 86..2347
 FT /tag= a
 FT /product= "Zcytor18"
 XX
 PN WO200208259-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US023253.
 XX
 PR 26-JUL-2000; 2000US-0220747P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Kuestner RE, Gao Z;
 XX
 DR WPI; 2002-217048/27.
 DR P-SDB; ABB07626.
 XX
 PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor growth,
 PT and modulating immune system by binding to endogenous zcytor18 ligand.
 XX
 PS Claim 5; Page 85-90; 119pp; English.
 XX
 CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
 CC and localize Zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in

CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 nucleotide sequence
XX

Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;

Query Match 71.9%; Score 2215.4; DB 6; Length 2383;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2271; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

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QY 1 TGGCTGGGCGAGCGCAGCGCCATGAGCCCGTGGCTGCAAGCTGCTCCGCTTCTTTAGG 60
DB 65 TGGCTGGGCGAGCGCAGCGCCATGAGCCCGTGGCTGCAAGCTGCTCCGCTTCTTTAGG 124
QY 61 GTCAAGCGCTGCTCAACGGCTGCGAGCTGCTGCTGCGCGCTGCGCGGCTCGCGCGG 120
DB 125 GTCAAGCGCTGCTCAACGGCTGCGAGCTGCTGCTGCGCGCTGCGCGGCTCGCGCGG 184
QY 121 TGGGCGGTGAGACCTGTGGCTGGAG----- 146
DB 185 CGGCGCGCGGACCTGTGGCTGGAGAGTGAAGCGGCTGCCGACCCGCGCTTGTGTT 244
QY 147 -----GGAGTGGGCGCAGCCAGCAGAAACAGTGGCTGTACAACTCACTTCAAA 198
DB 245 GCTAATAGAGGAGTGGGGCCAGCCAGCAAGAAACAGTGGCTGTACAACTCACTTCAAA 304
QY 199 TATGACATTTGTAACCACTTCTTGAATCCAGTGGGGAAGCATGTGATTTGTGACGCCG 258
DB 305 TATGACATTTGTAACCACTTCTTGAATCCAGTGGGGAAGCATGTGATTTGTGACGCCG 364
QY 259 AATATCACCATCAGCAGCATGTGCTTGCATGACCAAGTGGCAGTCACTTCTTGTGTC 318
DB 365 AATATCACCATCAGCAGCATGTGCTTGCATGACCAAGTGGCAGTCACTTCTTGTGTC 424
QY 319 CAGGGGCGCTCGGCACTGCAATTCCTGAAAGATTTGGGTAACTAGTGAAGAGCTGAAG 378
DB 425 CAGGGGCGCTCGGCACTGCAATTCCTGAAAGATTTGGGTAACTAGTGAAGAGCTGAAG 484
QY 379 TGGAGGGAAGACAGTGGCAACATGATTTCTAAGAGATCCGAAGCAGTCAACAGTAGC 438
DB 485 TGGAGGGAAGACAGTGGCAACATGATTTCTAAGAGATCCGAAGCAGTCAACAGTAGC 544
QY 439 TTCAAAAGAACTGGAATGGAATCTCAACCTTCTGAAATGGAATTTGAAAGGATAT 498
DB 545 TTCAAAAGAACTGGAATGGAATCTCAACCTTCTGAAATGGAATTTGAAAGGATAT 604
QY 499 TTCTAAAGGTGTCCCTTTCTTCCATTTAAAGAAAGCAATTACACCTTTCTTC 558
DB 605 TTCTAAAGGTGTCCCTTTCTTCCATTTAAAGAAAGCAATTACACCTTTCTTC 664
QY 559 TTTAGAACCCGAGCGCTGTGACTGCTGTTGTTACAGCCGAGCAATTAGCTGTTAAACCTTC 618
DB 665 TTTAGAACCCGAGCGCTGTGACTGCTGTTGTTACAGCCGAGCAATTAGCTGTTAAACCTTC 724
QY 619 TGGAAAGCCTCGAAGCTGAACATCAGCCAGCATGAGCTCGGACATGAGGTCCTTCGAC 678
DB 725 TGGAAAGCCTCGAAGCTGAACATCAGCCAGCATGAGCTCGGACATGAGGTCCTTCGAC 784
QY 679 CAGGCAACCCGACAACTTGGCTTCCGTTTCTTCTATCTTCACTCAAGAGCTCAAGACGAA 738
DB 785 CAGGCAACCCGACAACTTGGCTTCCGTTTCTTCTATCTTCACTCAAGAGCTCAAGACGAA 844
QY 739 GGAACCTTTAAGGGAAGAACTGTAAAGCAGAGCAAACTACAGAGACGACAGCTGCTTC 798
DB 845 GGAACCTTTAAGGGAAGAACTGTAAAGCAGAGCAAACTACAGAGACGACAGCTGCTTC 904
QY 799 CTTCAAAAGTGTTCCTCAAGGGAATTAATTAATTGACTGTGATGACATTAACAAGA 858
DB 905 CTTCAAAAGTGTTCCTCAAGGGAATTAATTAATTGACTGTGATGACATTAACAAGA 964
QY 859 AGAAAAGTATGATATGATCTTTAAAGCAGTGCATCCCGTGGCGCGGACCATCAGA 918
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DB 965 AGAAAAGTATGATATGATCTTTAAAGCAGTGCATCCCGTGGCGCGGACCATCAGA 1024
QY 919 GCCATGCGCATCAGTGCATGTGAGTCAATGCGGATTCGCGAGCGCTTCTGCTG 978
DB 1025 GCCGTGGCCATCAGTGCATGTGAGTCAATGCGGATTCGCGAGCGCTTCTGCTG 1084
QY 979 ATGTGCGCGAAGACAAACAAATAATATATTTCACTTTAGATGAGAGAGCTGTAG 1038
DB 1085 ATGTGCGCGAAGACAAACAAATAATATATTTCACTTTAGATGAGAGAGCTGTAG 1144
QY 1039 TCTTCAATACATGACGACATCCCAAGAGAGAGCTTCGCGCGCGGACGATCTTT 1098
DB 1145 TCTTCAATACATGACGACATCCCAAGAGAGAGCTTCGCGCGCGGACGATCTTT 1204
QY 1099 CTTGCTATTTCAAGTAAAGTGGCAGATCAATGAATGTGTCAGTGTTCGCTAC 1158
DB 1205 CTTGCTATTTCAAGTAAAGTGGCAGATCAATGAATGTGTCAGTGTTCGCTAC 1264
QY 1159 TTCTTCAGGACCTTCTGTGGCTGTGAGGTGCTGACCTGTGGGAAGACTTCAGCTC 1218
DB 1265 TTCTTCAGGACCTTCTGTGGCTGTGAGGTGCTGACCTGTGGGAAGACTTCAGCTC 1324
QY 1219 TGTAGAAAGGCAAGAGAAATGGGTCAATCAAGAAATCAAGATCCCATGTTCAAT 1278
DB 1325 TGTAGAAAGGCAAGAGAAATGGGTCAATCAAGAAATCAAGATCCCATGTTCAAT 1384
QY 1279 GTGTGTTGTTCCAAAGTATGAAATCTTGTGGAACAAGAAACTACAAACAAGGA 1338
DB 1385 GTGTGTTGTTCCAAAGTATGAAATCTTGTGGAACAAGAAACTACAAACAAGGA 1444
QY 1339 GGTGCGCAGAGCTCGGGGAAGAGAGCTCTCTGTGGCGGTGACAGCTTCGCGAA 1398
DB 1445 GGTGCGCAGAGCTCGGGGAAGAGAGCTCTCTGTGGCGGTGACAGCTTCGCGAA 1504
QY 1399 AAGCTCCGCAAGCCAGACAGAGTTCGTCGCGGCTCAGCAAGTTATGCCCGTAC 1458
DB 1505 AAGCTCCGCAAGCCAGACAGAGTTCGTCGCGGCTCAGCAAGTTATGCCCGTAC 1564
QY 1459 TTTGATTTTCTGTGAGGGAAGACGTCCCGGTATCTAGACTAGTACCAAGTACGA 1518
DB 1565 TTTGATTTTCTGTGAGGGAAGACGTCCCGGTATCTAGACTAGTACCAAGTACGA 1624
QY 1519 CTCAATGACAAATCTTCTCAAGCTCTGTTCCACTGCACTCCGAGACCAAGCGCTCAG 1578
DB 1625 CTCAATGACAAATCTTCTCAAGCTCTGTTCCACTGCACTCCGAGACCAAGCGCTCAG 1684
QY 1579 GAGCGGCGGCAAGCAAGCGGACAGGAGCAAGAGAACTACTTCGAGCAAGTAGGC 1638
DB 1685 GAGCGGCGGCAAGCAAGCGGACAGGAGCAAGAGAACTACTTCGAGCAAGTAGGC 1744
QY 1639 CGGTCCCTATATGTCGCTTTGGCAACATGCAACAGTTTATGAGAGAGCCGACGTG 1698
DB 1745 CGGTCCCTATATGTCGCTTTGGCAACATGCAACAGTTTATGAGAGAGCCGACGTG 1804
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RESULT 4
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 LOCUS
 DEFINITION Sequence 15 from Patent WO0214358.
 ACCESSION AX392973
 VERSION AX392973.1 GI:19701020
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Homnidae; Homo.
 REFERENCE
 1 Edmonde, B. T., Micanovic, R., Ou, W., Su, B. W., Tschang, S. H. and
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LOCUS Sequence 13 from Patent WO0190358.
DEFINITION AX350979
ACCESSION AX350979
VERSION AX350979.1 GI:18616355
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Gorman, D.M.
AUTHORS Mammalian receptor proteins; related reagents and methods
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JOURNAL SCHERING CORPORATION (US)
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ORIGIN
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Query Match	87.1%; Score 2684.6; DB 8; Length 4478;
Best Local Similarity	99.7%; Pred. No. 0;
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 VERSION AX747904.1 GI:32132292
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 SOURCE Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE
 1
 Isozaki, T., Sugiyama, T., Otsuki, T., Makematsu, A., Sato, H., Ishii, S.,
 Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
 Tamehika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
 Masuno, Y.
 TITLE Full-length cDNA sequences
 JOURNAL Patent: EP 1308459-A 1429 07-MAY-2003;
 Helix Research Institute (JP) ; Research Association for
 Biotechnology (JP)
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 Best Local Similarity 99.7%; Pired. No. 0;
 Matches 2684; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Qy	2654	GCACCTTTTAACATCATATGACCCACAGAAATCAAGTGCACAGTCTATCTGGAATCCAGTTGTA	2713
Db	2722	GCACCTTTTAACATCATATGACCCACAGAAATCAAGTGCACAGTCTATCTGGAATCCAGTTGTA	2781
Qy	2714	TTGCAGATTAATGTTCTCATTTATTTTGTGATGATGAGATTTTACATTTGCCATGGGTGTAAAT	2773
Db	2782	TTGCAGATTAATGTTCTCATTTATTTTGTGATGAGATTTTACATTTGCCATGGGTGTAAAT	2841
Qy	2774	AAGCTTTGAGTCGCAAAAGTCGAGAAAGTACGATGATATTCACATCACCTTTATG	2826
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
<p>BC038369 4490 bp mRNA linear PRI 30-MAR-2005</p> <p>Hom sapiens interleukin 17 receptor D, mRNA (CDNA clone MGC:42862</p> <p>IMAG:4830807), complete cds.</p> <p>BC038369</p> <p>BC038369.1 GI:23512250</p> <p>MGC.</p> <p>Homo sapiens (human)</p> <p>Hom sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.</p> <p>1 (bases 1 to 4490)</p> <p>Straussberg, R. L., Felting, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hele, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Schaefer, T. E., Brownstein, M. J., Udell, T. B., Tothyluk, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullany, S. J., Bosak, S. A., McEwan, P. J., Mockerman, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalón, D. M., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bonfield, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butlerfield, Y. S., Krzywinski, M. I., Skalska, U., Smalins, D. E., Schmech, A., Schein, J. E., Jones, S. J. and Marra, M. A.</p>			

CONSRMT TITLE JOURNAL PUBMED REFERENCE AUTHORS CONSRMT TITLE JOURNAL	<p>Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 4490)</p>
REMARK COMMENT	<p>NIH MGC Project Direct Submission Submitted (01-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: ggaabs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki Toshiyuki and Piero Carninci (RIKEN) cDNA library Arrayed by: The I.M.A.G.E. Consortium (LIND) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amebcm.tmc.edu Guaratine, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.</p>
FEATURES SOURCE	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIND at: http://image.lnl.gov Series: IRAC Plate: 72 Row: h Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24308146. Location/Qualifiers 1..4490 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:42862 IMAGE:4830807" /tissue_type="Testis" /clone_lib="NIH MGC_97" /lab_host="DH10B" /note="Vector: pBluescript"</p>
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CD5	
ORIGIN	

86.84; Score 2675.2; DB 8; Length 4490.

Best Local Similarity 99.7%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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DEFINITION	Sequence 125 from patent US 6783969.				
ACCESSION	AR577949				
VERSION	AR577949.1	GI:56580745			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 3948)				
AUTHORS	Tang Y.T., Goodrich, R.W., Asundi, V. and Drmanac, R.T.				
TITLE	Cathepsin V-like polypeptides				
JOURNAL	Patent: US 6783969-A 125 31-AUG-2004;				
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location/Qualifiers	1..3948				
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O	y	817	GGGATATATATATTAATTGAGCTGTGGATGACCTTAACAACAAGAAATGATGCAATTAT	876
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D	b	483	GCCTTAAAGCAGTGCACCTCCCGTGGGCGGGGCCATCAAGAGCATGGCATCAAGT	542
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D	b	1023	CAGAGTTCGTCCGGGGGCTCAGGAATTTATGCGCGTCACTTTGATTTATTCCTGAG	1082
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D	b	1083	GGAGACGTCCCGGGTATCTTAGACTGTAGATCCAAAGTACAGACTATGAGCAATCTTCT	1142
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 Direct Submision
 Submitted (15-NOV-1999) MIPS, Am Klopferspitze 18a, D-82152
 Martinsried, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the CDNA sequencing consortium of the
 German Genome Project.
 This clone (DKFZp434N1928) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

FEATURES

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REFERENCE
1 Presnell, S.R., Kuestner, R.E. and Gao, Z.
AUTHORS
TITLE Human cytokine receptor
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ZymoGenetics, Inc. (US)
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Location/Qualifiers

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Db      1030 ACGCGACAGGAGCAGCAAGAGAACTACTTCCGAGCAAGTCAAGCGCGTCTCTAAGTGC 1089
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Qy      1654 GCGATTGCAACATGACCAAGTATTTAGAGAGAGCCGACCTGCTTCAAAAAGCACTTC 1713
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Db      1090 GCGATTGCAACATGACCAAGTATTTAGAGAGAGCCGACCTGCTTCAAAAAGCACTTC 1149
      |||
Qy      1714 GTTCCCTTCATCTCTCTCACTGCGCTACCGGAGCAGTCTTGGAGAAATTGATTGC 1773
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Db      1150 GTTCCCTTCATCTCTCTCACTGCGCTACCGGAGCAGTCTTGGAGAAATTGATTGC 1209
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Qy      1774 GCGTTGGTTTAAATGATGTCATGTCAAACAGGCGCTGAGATGACTTCTGCTTAAAG 1833
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Db      1210 GCGTTGGTTTAAATGATGTCATGTCAAACAGGCGCTGAGATGACTTCTGCTTAAAG 1269
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Qy      1834 GTAGAGGCGGCTGTTCTTGGGGGCAACCGGACAGCGGACCTCCAGCAGCAGAGATCAGCAT 1893
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Db      1270 GTAGAGGCGGCTGTTCTTGGGGGCAACCGGACAGCGGACCTCCAGCAGCAGAGATCAGCAT 1329
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Qy      1894 GGGGAGCTGAGACCAAGACGCGGAGAGCCGCGCTGCGCTTGAACGTTAGCGCGCTGCAA 1953
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Qy      1954 CCCCTGCTGACACGCGTGAAGGCGGAGCCCTCGGACATGCGCGGAGCTCAGGACATC 2013
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Qy      2014 TATGACTCGTCTGTCCTCTCATCCGAGCTGTCCTGCACTGATGAGAGACTCTGAGAG 2073
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Qy      2074 GACCAAGAGAAAGCTCTTCCCTGAGGAGAGGCTGCTCTTCAAGGCTGAGGAG 2133
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Db      1510 GACCAAGAGAAAGCTCTTCCCTGAGGAGAGGCTGCTCTTCAAGGCTGAGGAG 1569
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Qy      2134 GAGGAACTTCTGCTGCTTCTTCAAGCTCTCTTCTGAGTCAAGAGAGATCTT 2193
      |||
Db      1570 GAGGAACTTCTGCTGCTTCTTCAAGCTCTCTTCTGAGTCAAGAGAGATCTT 1629
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Qy      2194 GCTTGGCGGACGTCACACTGATGAATCCCAAGCGGCTGCGCTTGTGA 2241
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Db      1630 GCTTGGCGGACGTCACACTGATGAATCCCAAGCGGCTGCGCTTGTGA 1677
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RESULT 3
AY408490      1677 bp      DNA      linear      GSS 12-DEC-2003
LOCUS      AY408490
DEFINITION      Pan troglodytes HCM3241 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION      AY408490
VERSION      AY408490.1 GI:39764461
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
BUTRYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
1 (bases 1 to 1677)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarlwal,A.,
Todd,M.A., Tannenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,

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TITLE      Adame,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE      2 (bases 1 to 1677)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarlwal,A.,
            Todd,M.A., Tannenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
            Adame,M.D. and Cargill,M.
TITLE      Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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Best Local Similarity 92.4%; Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 25; Indels 111; Gaps 2;
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Qy      514 CTTTTTCTTCATTAATAAGAAAGCAATTACACCCCTTCTCTTGAACCCGAGCC 573
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Qy      574 TGTGACCTGTGTTACAGCGGACCAATCTAGCTGTGAACCTTCTGGAAGCTCGGAC 633
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Qy      634 CTGAACATCAGCAGCAGTGGCTCGGACATGACAGTGTCTTGCACACGACCGACAC 693
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Db      136 CTGAACATCAGCAGCAGTGGCTCGGACATGACAGTGTCTTGCACATCAGCAGAC 195
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Qy      694 TTGGGCTTCCGTTCTTCTCATCTTCACTCAAGCTCAAGCAAGAGACCTTCAAGCA 753
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Db      256 AAGACCTGTAGC----- 268
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Qy      814 CAGGGGATTATATTAATGAGCTGTGATGACACTTAACAACAAGAAAGTATGAT 873
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Qy      1054 GCGAGACTCCCAAGAGAGAGGCTCGGCGCGCGCGGAGAGCTTCTGCTATTCAGCT 1113
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Db      490 GCGAGACTCCCAAGAGAGAGGCTCGGCGCGCGCGGAGAGCTTCTGCTATTCAGCT 549
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Qy      1114 AAAGATGGCCAGAAATCACTAGATGTGTCAGTGTTCGCTACTTCTCCAGGACTTC 1173
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Db      610 TGTGCTGTAGAGTGGCTCTGACCTGTGGAGACTTCAGCTCTGTAGAGAGGGCAG
Qy      1234 AGGAATAGGTCATCCGAGAGATCCAGAGTCCAGTTCATGTCGTTGTTCCAAA
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Qy      1294 GGTATGAGTACTTGTGACAAGAAAGACTAACAAACAAGAGAGTGGCCGAGCTCG
Db      730 GGTATGAGTACTTGTGACAAGAAAGACTAACAAACAAGAGAGTGGCCGAGCTCG
Qy      1354 GAGAAAGAGAGCTCTTCTGTGGTGGTGTCAAGCTTCGCGAAAGCTCCGCAAGCC
Db      790 GAGAAAGAGAGCTCTTCTGTGGTGGTGTCAAGCTTCGCGAAAGCTCCGCAAGCC
Qy      1414 AAGCAGAGTTCGTCGGGGGCTCAGCAAGTTATCCCGCTTCTTGAATTTCTCTGC
Db      850 AAGCAGAGTTCGTCGGGGGCTCAGCAAGTTATCCCGCTTCTTGAATTTCTCTGC
Qy      1474 GAGGAGAGCTCCCGGATCTAGACTGTAGTCAAGTCAAGTCAAGTCAAGTCAATCTT
Db      910 GAGGAGAGCTCCCGGATCTAGACTGTAGTCAAGTCAAGTCAAGTCAAGTCAATCTT
Qy      1534 CCTCAGCTGTATCCCACTGCACTCCGAGACCAAGGCTCCGAGAGCCGAGGACAC
Db      970 CCCAGCTGTATCCCACTGCACTCCGAGACCAAGGCTCCGAGAGCCGAGGACAC
Qy      1594 ACCGACAGGCGCAGAGAGAACTACTTCCGAGCAAGTCAAGGCTCCGAGGCTTACGTC
Db      1030 ACCGACAGGCGCAGAGAGAACTACTTCCGAGCAAGTCAAGGCTCCGAGGCTTACGTC
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Qy      1714 GTTCCCTTCATCTCTCCATGCTGCTACCGGAGGCACTTGTGAAGAAATTTGATTCG
Db      1150 GTTCCCTTCATCTCTCCATGCTGCTACCGGAGGCACTTGTGAAGAAATTTGATTCG
Qy      1774 GGTGCTGTTTAAATGATGATGTCATGTCAAACAGAGGCTTGAAGTCTTCTGCTTAAG
Db      1210 GGTGCTGTTTAAATGATGATGTCATGTCAAACAGAGGCTTGAAGTCTTCTGCTTAAG
Qy      1834 GTAGAGGCGGCTGTTTGGGGGCAACGGACAGGCGGCTCCAGACAGAGTCAAGCAT
Db      1270 GTAGAGGCGGCTGTTTGGGGGCAACGGACAGGCGGCTCCAGACAGAGTCAAGCAT
Qy      1894 GGGGGCTGAGCAAGAGAGGGGAGGCGGCGCTGCTTGAAGGTAAGCGGCTTCAAG
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Qy      1954 CCCCTGCTGCAACAGTGAAGCGGAGGCGGCTTGAAGTCCGAGGAGCTCAAGCATC
Db      1390 CCCCTGCTGCAACAGTGAAGCGGAGGCGGCTTGAAGTCCGAGGAGCTCAAGCATC
Qy      2014 TATGACTGCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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Qy      2074 GACCAAGCAAGAAAGTCTTCCCTGAGAGAGGCTCTCTTCAAGGCTTGGAGTGA
Db      1510 GACCAAGCAAGAAAGTCTTCCCTGAGAGAGGCTCTCTTCAAGGCTTGGAGTGA
Qy      2134 GAGGAACCTCTGCTTCTTCTTCAAGCTCTCTCTTCTGAGTCAAGCAAGCATCTT
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Qy      2194 GGTGCGGAGCTTACATGATGAATCAGGCGGTGCGCCCTTTGTTAA 2241

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Db      1630 GGTGCGGAGCTTACATGATGAATCTCAAGCGGCTGCGCCCTTTGTTAA 1677
RESULT 4
AY408491
LOCUS
DEFINITION
Mus musculus HCM3241 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY408491
VERSION
AY408491.1 GI:39764462
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1674)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1674)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/locus_tag="HCM3241"
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Best Local Similarity 75.8%; Pred. No. 3,3e-259;
Matches 1360; Conservative 0; Mismatches 308; Indels 126; Gaps 5;
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Db      1 ATGAATCTCAACCTTCTCGAATATGAATTTGAACGATTTATTCGTAAGTTGTC
Qy      514 CTTTTCCTTCACTTAAAGCAAGCAATTAACACCTTTCTTCTTGAACCGAGCC
Db      61 CTTTTCCTTCACTTAAAGCAAGCAATTAACACCTTTCTTCTTGAACCGAGCC
Qy      574 TGTGACTGTTGTTACGCGGACCAATCTGTTGAACCTTCTGGAAGCTCTGGAAC
Db      119 -----TTGGAAGCTCTGGAAC 135
Qy      634 CTGAACATGACGACATGCTGAGCATGTCAGAGTGTCTTTCGACACGACGACAC
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Qy      754 AAGACCTGTAAGCAGAGCAACTACAGACGACAGCTGCTCTTCAAAAATGTTTCT
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Db	1384	TTGCAAGCCCCCTGTATCAAGCAGATGAAGACCTGGCAGTCCCTCAGAGATGCCAGGGACCTCA	1443
Qy	2008	GGCATCTATGACTGTCTGTGCGCCCTCATTCGAGCTGTCTCTGCACATGATGAAGACTC	2067
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Qy	2128	GGTAGAGAGAACTCTGCGCTTCTCTTCCAAAGCTCTCTCTTCTGAGTCAATGCAAGCA	2187
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Qy	2188	GATTTGATGGCGGACGCTACACTGATGAATCTCAGCGGCGGCGGCGCCCTTTGTAA	2241
Db	1621	GACATGATTTGCCACAGCCACACTGAGAACTGAAAGCGCTTGTCTCTTTGTAA	1674

RESULT	5
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LOCUS	CJ025168
DEFINITION	908 bp mRNA linear EST 22-Oct-2004
ACCESSION	CJ025168 full-length enriched swine cDNA library, adult crachea Sus
VERSION	CJ025168
KEYWORDS	scrofa clone TCHO1B080037 5', mRNA sequence.
SOURCE	CJ025168.1 GI:54533576
ORGANISM	EST.
	Sus scrofa (pig)
	Sus scrofa

REFERENCE	1 (pages 1 to 908)
AUTHORS	Uemzshi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,

TITLE
PEDS (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
JOURNAL
Nucleic Acids Res. 32 (1), D484-D488 (2004)

COMMENT Contact: Hirohide Uenishi

Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Fax: +81-29-838-8627

EST project with full-length enriched cDNA libraries carried out in

Animal Genome Research Program (Japan) by National Institute of

Single pass sequencing of clones derived from oligo-capped cDNA

Vector sequences were eliminated by RepeatMasker version 2002/07/13

Low quality bases were trimmed based on the quality values.

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INTRODUCTION

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Matches 816; Conservative 0; Mismatches 87; Indels 0; Gaps 0;


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DB 121 CACCTGTGGCTGGAGGGAGTGGGGCCAGCCAGCAGAAACAGTGGCTGTGACCAATCAC 180
QY 192 CTTCAAAATATGACAAATGTAACCACTGTAATTCAGTGGGGAGACATGTGTTGCTGA 251
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DB 241 CCCCCAGAAATATCAGCATGAGCCAGTATGATGCTGTCAGCAGCAAGTGGCAGTCAATTC 300
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QY 912 CAT 914
DB 901 CAT 903

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RESULT 6
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LOCUS DN282586 118679 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
DEFINITION DN282586
ACCESSION DN282586
VERSION DN282586.1 GI:60451196
KEYWORDS EST.

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SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 856)
AUTHORS Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RIK015 row: B column: 19
Seq primer: TAGAAGCAGCTGAGG.
Location/Qualifiers
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Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."
ORIGIN
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Best Local Similarity 91.1%; Pred. No. 4.7e-181;
Matches 780; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
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DB 736 AGAATATCAACATCAAGTATGCTGTCAGACCAAGTGGCAGTCACTTCTTGGT 677
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DB 676 CCCCAGGGCCCTCGGCATCGAATTCCTGAAAGATTTGCGGTAAATCTGAGAGAGCTGA 617
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DB 496 ACTTGTAAAGATGCTCCCTTCTTCTTCAATTAAGAAAGCAATTCAGCTTGAACCT 437
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DB 436 TCTTCAAGAACCCGAGCTGTGACCTGTGTTACAGCCGAGCAATTCAGCTTGAACCT 377
QY 617 TCTGAGAGCTTGGAACTGGAACATCAGCAGCAGTGGCTGGACATGACAGGTGCTTGG 676

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 Db 677 ACCAGCAGCCGAGCAACTTCGCTTCGTTCTTATCTTCACTCAAGCTCAAGCAGC 736
 Db 316 ACCATGCGCCGAGCAACTTCGCTTCGTTCTTATCTTCACTCAAGCTCAAGCAGC 257
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 Db 737 AAGAACCTTTCAAGCAGAAAGACCTGTAAAGCAGAGCAAACTACAGAGCAGCAGCTGCG 796
 Db 256 AAGAACCTTTCAAGCAGAAAGACCTGTAAAGCAGAGCAAACTACAGAGCAGCAGCTGCG 197
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 Db 196 TCTTCAAAATGTTTCTCCAGGGGATTATTAATTGAGCTGTGATGACATTAACA 137
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 QY 136 CAGAAAGATGATGATTAATGATTAAGCAGTGCATCCCGTGGGCGGGCCCATCA 77
 Db 917 GAGCCATGCGCATCAAGTGCATCTGTAGTCAATTCGAGCATTCGAGCAGCTCTTCACTG 976
 QY 76 GAGCTGTGCGCATCACTGTGCGCATTTGTGTCTCATATCGGATTCGAGCAGCTCTTCACTG 17
 Db 977 TGATGTGCGCGAAGAA 992
 QY 16 TGATGTGCGCGAAGAA 1

RESULT 7
 DN283973 851 bp mRNA linear EST 02-MAR-2005
 LOCUS 1184215 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION
 ACCESSION DN283973
 VERSION DN283973.1 GI:60452583
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 851)
 Smith,T.P., Roberts,A.J., Echerkamp,S.E., Chitko-Mckown,C.G.,
 Wray,J.E. and Keeler,J.W.
 A second set of bovine ESTs from pooled-tissue normalized libraries
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: RLK8015 row: E column: 19
 Seq primer: GTAATACGACTCACTATAGGG.
 Location/Qualifiers
 1..851
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_id="MARC 7BOV"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with RNA pooled from multiple tissues
 including ovary, hindbrain, uterus, and day-30 whole
 embryos."

ORIGIN
 Query Match 23.7%; Score 730; DB 8; Length 851;
 Best Local Similarity 91.1%; Pred. No. 6,7e-180;
 Matches 775; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

FEATURES
 source
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 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_id="MARC 7BOV"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with RNA pooled from multiple tissues
 including ovary, hindbrain, uterus, and day-30 whole
 embryos."

QY 137 GTGGCTGAGAGGAGTGGGGCCAGCCAGAGAAACAGTGGGCTGTACAACTACCTTCA 196
 Db 1 GTGGCTGAGAGGAGTGGGGCTGGCCAGAGAAACAGGGGCTGTACAACTACCTTCA 60
 QY 197 AATATGACAAATTGTATACACTTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCC 256
 Db 61 GATATGACAACTGACACACTTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCC 120
 QY 257 AATATGACAACTGACACACTTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCC 316
 Db 121 AATATGACAACTGACACACTTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCC 180
 QY 317 CCCAGAGGGCCCTCGGCATCGAATTCCTGAAGAATTCCTGGTAAATCTGAGAGCTGA 376
 Db 181 CCCAGAGGGCCCTCGGCATCGAATTCCTGAAGAATTCCTGGTAAATCTGAGAGCTGA 240
 QY 377 AGTCGAGAGGAGAGACAGTGCACAACTGATTTCTAAAGATTCGAGACAGCTCAACATGA 436
 Db 241 AGTCGAGAGGAGAGACAGTGCACAACTGATTTCTAAAGATTCGAGACAGCTCAACATGA 300
 QY 437 GCTTCAAAAGAACTGGAATGGAATCTCAACCTTCTGAAATGAAATTTGAAAGGATTT 496
 Db 301 GCTTCAAAAGAACTGGAATGGAATCTCAACCTTCTGAAATGAAATTTGAAAGGATTT 360
 QY 497 ATTTGCTAAAGGTTGTCTCTTCTTCTTCCATTAAAAACGAAAGCAATTACCACTTTCT 556
 Db 361 ACTTTGTAAGATGATGATCTCTTCTTCTTCCATTAAAAAGAAAGCAATTATCACCTTTCT 420
 QY 557 TCTTTTGAACCCGAGCCTGTGACCTGTGTTTACAGCCGAGCAATGCTTGTAAACCTT 616
 Db 421 TCTTCAAGAACCCGAGCCTGTGACCTGTGTTTACAGCCGAGCAATGCTTGTAAACCTT 480
 QY 617 TCTGGAAGCCTGGAACCTGGAACATCAGCAGCAGTGGCTGGACATGAGGTGCTTGG 676
 Db 481 TCTGGAAGCCTGGAACCTGGAACATCAGCAGCAGTGGCTGGACATGAGGTGCTTGG 540
 QY 677 ACCAGCAGCCGAGCAACTTCGCTTCGTTCTTATCTTCACTCAAGCTCAAGCAGC 736
 Db 541 ACCAGCAGCCGAGCAACTTCGCTTCGTTCTTATCTTCACTCAAGCTCAAGCAGC 600
 QY 737 AAGAACCTTTCAAGCAGAAAGACCTGTAAAGCAGAGCAAACTACAGAGCAGCAGCTGCC 796
 Db 601 AAGAACCTTTCAAGCAGAAAGACCTGTAAAGCAGAGCAAACTACAGAGCAGCAGCTGCC 660
 QY 797 TCCCTCAAAATGTTTCTCCAGGGGATTATTAATTGAGCTGTGATGACATTAACA 856
 Db 661 TCTTCAAAATGTTTCTCCAGGGGATTATTAATTGAGCTGTGATGACATTAACA 720
 QY 857 CAGAAAGATGATGATTAATGATTAAGCAGTGCATCCCGTGGGCGGGCCCATCA 916
 Db 721 CAGAAAGATGATGATTAATGATTAAGCAGTGCATCCCGTGGGCGGGCCCATCA 780
 QY 917 GAGCCATGCGCATCAAGTGCATCTGTAGTCAATTCGAGCATTCGAGCAGCTCTTCACTG 976
 Db 781 GAGCTGTGCGCATCACTGTGCGCATTTGTGTCTCATATCGGATTCGAGCAGCTCTTCACTG 840
 QY 977 TGATGTGCGCG 987
 Db 841 TGATGTGCGCG 851

RESULT 8
 BP154750 724 bp mRNA linear EST 30-DEC-2003
 LOCUS BP154750 full-length enriched swine cDNA library, adult ovary Sus
 DEFINITION
 ACCESSION BP154750
 VERSION BP154750.1 GI:40404223
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	COMMENT
1 (bases 1 to 724)	Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasim, N., and Awata, T.	PD8E (pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries	Nucleic Acids Res. 32 (1), D484-D486 (2004)	14681463	
	Contact: Hirohide Uenishi				
	Animal Genome Laboratory, Genome Research Department				
	National Institute of Agrobiological Sciences				
	2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan				
	Tel: +81-29-838-8627				
	Fax: +81-29-838-8627				
	Email: huenishi@afc.go.jp				
	EST project with full-length enriched cDNA libraries carried out in				
	Animal Genome Research Program (Japan) by National Institute of				
	Agrobiological Sciences and STAFF-Institute				
	Single pass sequencing of clones derived from oligo-capped cDNA				
	library				
	Vector sequences were eliminated by RepeatMasker version 2002/07/13				
	and crossmatch version 0.990319				
	Low quality bases were trimmed based on the quality values.				
FEATURES	location/Qualifiers				
source	1..724				
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	/db_xref="taxon:9823"				
	/clone="OVRM10115H10"				
	/tissue_type="ovary"				
	/dev_stage="adult"				
	/clone_lib="full-length enriched swine cDNA library, adult				
	ovary"				
ORIGIN					
Query Match	19.7%: Score 608.4; DB 3; Length 724;				
Best Local Similarity	91.2%: Pred. No. 5.6e-148;				
Matches	645; Conservative 0; Mismatches 62; Indels 0; Gaps 0;				
Dy	2 GGGTGGGCGAGCGACGGCCATGCGCCCGTGGCTGACGCTGCTCTTCTTTACG 61				
Db	18 GGGTGGGCGAGCGACGGCCATGCGCCCGTGGCTGACGCTGCTCTTCTTTACG 77				
Dy	62 TCAACGCTGCTTCAACGGCTGCGAGCTGCTGCTGCGCGCGGCTCCGCGCGCT 121				
Db	78 TCAACGCTGCTTCAACGGCTGCGAGCTGCTGCTGCGCGCGGCTCCGCGCGCT 137				
Dy	122 GGGGCGTGGACACCTGCTGGCGAGAGGAGAGTGGGCGCGACGACGAAACAGTGGCTGT 181				
Db	138 GGGGCGGCGACCGCTGGCGAGAGGAGAGTGGGCGCGCGACGACGAAACAGTGGCTGT 197				
Dy	182 ACAACATCACCTTCAAAATATGACATTTTACCACTTGAATTCAGTGGGAAAGCAT 241				
Db	198 ACAACATCACCTTCAAAATATGACATTCACCACTTGAATTCAGTGGGAAAGCAT 257				
Dy	242 TGAATGTCGACGCCCGAGAAATACACATCAGCCAGTATGCTTGCATGACCAAGTGG 301				
Db	258 TGAATGTCGACGCCCGAGAAATACACATCAGTCAATGAGCTGCGACGACCAAGTGG 317				
Dy	302 TCACCATCTTTTGTGTCGCCAGGGGCGCTCGGATGGAATTTCTGAAAGAAATTTGGGCTGA 361				
Db	318 TCACCATCTCTGTGTCGCCAGGGGCGCTCGGATGGAATTTCTGAAAGAAATTTGGGCTGA 377				
Dy	362 TACTGAGAGAGCTGAAGTCGAGGGAGACAGTGCACCACTGATTTCTAAAGAGATCCGA 421				
Db	378 TACTGAGAGAGCTGAAGTCAGAGAGAAACAGTGCACCACTGATTTCTGAAGAGACCCGA 437				
Dy	422 AGCAGCTCAACAGTATGCTTCAAAAGAACTGAATGAATCTTCAACTTCTCTGAATATGA 481				
Db	438 AGCAGCTCAACAGTATGCTTCAAAAGAACTGAATGAATCTTCAACTTCTCTGAATATGA 497				
Dy	482 AATTGAAACGAGTATTTTGTAAAGTTTGTCCCTTCTTCCATTTAAACGAAAGCA 541				

Db	498	AATTGAAACAGATTACTTGTCTGCAAGATGTCCCTTTTCCTTCATTTAAAAAGCAAGCA	557
Qy	542	ATPACACCCTTTCTCTCTTTGAACCCGAGCCTGACCTGTCTTTCACGCGGACATC	601
Db	558	ATTATCACCCCTTTCTCTTTGAACCCGACCTGTGACCTGTATTAAGCCGGAACCC	617
Qy	602	TAGCTTGAACCCCTTCTGAAAGCCTGGAACCTGAAACATGACGACAGATGGCTCGACA	661
Db	618	TGGCTGTAAACCTTTCTGAAAGCCTGGAACCTTCACATACCAACATGGCTTCAGACA	677
Qy	662	TGCAGGTCTCCTTCGACACGCGACCGACCACTTCGCGCTTCGTTTC	708
Db	678	TGCANGTGTCTTCGACACGCGCACATATCTTCGCGCTTCGTTTC	724
RESULT 9			
BP275741		583 bp	mRNA
LOCUS	BP275741		linear
DEFINITION	BP275741 Sugano cDNA library, kidney Homo sapiens cDNA clone		EST 16-SEP-2004
ACCESSION	KDND04362, mRNA sequence.		
VERSION	BP275741		
KEYWORDS	BP275741.1 GI:52189473		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
	1 (bases 1 to 583)		
REFERENCE	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chida,J.,		
AUTHORS	Mizushima-Sugano,J., Nakai,K. and Sugano,S.		
TITLE	Sequence comparison of human and mouse genes reveals a homologous		
JOURNAL	block structure in the promoter regions		
PUBMED	Genome Res. 14 (9), 1711-1718 (2004)		
COMMENT	Contact: Yutaka Suzuki		
	Department of Virology		
	Institute of Medical Science, University of Tokyo		
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan		
	Email: yusuzuki@ims.u-tokyo.ac.jp.		
FEATURES	Location/Qualifiers		
source	1..583		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="KDND04362"		
	/tissue_type="kidney"		
	/clone_lib="Sugano cDNA library, kidney"		
ORIGIN			
Query Match	18.8%;	Score 578.8;	DB 3; Length 583;
Best Local Similarity	99.5%;	Pred. No. 3,2e-140;	
Matches 580;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
Qy	1512	GTACAGACTACGACGACATCTTCTCAGCTGTGTTCCGACTCGACCTCCGAGACACAGG	1571
Db	1	GTACAGACTACGACGACATCTTCTCAGCTGTGTTCCGACTCGACCTCCGAGACACAGG	60
Qy	1572	CCTCAGAGAGCGGGGAGCAGACGAGCGACAGGGGAGAGGAAGAACTACTTCGGAGCA	1631
Db	61	CCTCAGAGAGCGGGGAGCAGACGAGCGACAGGGGAGAGGAAGAACTACTTCGGAGCA	120
Qy	1632	GTCAGAGCGGCTCCTATACGTGCGCATTTGGCAATGACCACTTTATTAACGAGAGCC	1691
Db	121	GTCAGAGCGGCTCCTATACGTGCGCATTTGGCAATGACCACTTTATTAACGAGAGCC	180
Qy	1692	CGACTGTTGCAAAAGCAGTTGTTCCCTTCGATCTTCGACTGCGGCTACCGGAGCC	1751
Db	181	CGACTGTTGCAAAAGCAGTTGTTCCCTTCGATCTTCGACTGCGGCTACCGGAGCC	240
Qy	1752	AGCTGTGGAAGAAATTTGATTCGGGCTGGTTTAAATGATGTCATGTGCAAAACGAGGC	1811
Db	241	AGCTGTGGAAGAAATTTGATTCGGGCTGGTTTAAATGATGTCATGTGCAAAACGAGGC	300

QY 1812 TGAGAGTGAATCTTCTGCTAAAGTAGAGCGCCTGTCTTGGGGCAACCGSACAGCCGA 1871
 DB 301 TGAAGATGACTTCTGCTTAAAGGTAGAGCGCGCTGTCTTGGGGCAACCGSACAGCCGA 360
 QY 1872 CTCGCCAGCAGAGTGTACGATGAGGGGCTTGACCAAGACGGGAGGCCCTGCTCCCT 1931
 DB 361 CTCGCCAGCAGAGTGTACGATGAGGGGCTTGACCAAGACGGGAGGCCCTGCTCCCT 420
 QY 1932 TGACCGTACGGCGCCCTGCAACCCCTGTGCAACAGGTGAAGCGCGGAGGCCCTGCGGA 1991
 DB 421 TGACCGTACGGCGCCCTGCAACCCCTGTGCAACAGGTGAAGCGCGGAGGCCCTGCGGA 480
 QY 1992 CATGCCGCGGACTCAGGCACTATGACTGTCTGTGCTCATCCGAGCTGTCTGCTCC 2051
 DB 481 CATGCCGCGGACTCAGGCACTATGACTGTCTGTGCTCATCCGAGCTGTCTGCTCC 540
 QY 2052 ACTGATGAGGAGCTCTGCAACGAGCAGACAGAAAGCTCTTCC 2094
 DB 541 ACTGATGAGGAGCTCTGCAACGAGCAGACAGAAAGCTTTC 583

RESULT 10
 BM965550 679 bp mRNA linear EST 08-AUG-2005
 LOCUS BM965550 full-length enriched swine cDNA library, adult ovary Sus
 DEFINITION scrofa cDNA clone OVR010067A07 5', mRNA sequence.
 ACCESSION BM965550
 VERSION BM965550.1 GI:71964881
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 679)
 Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.
 PEDR (pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 14681463
 JOURNAL Contact: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 PubMed EST project with full-length enriched cDNA libraries carried out in Agrobiological Sciences and STAPF-Institute of Animal Genome Research Program (Japan) by National Institute of Single pass sequencing of clones derived from oligo-capped cDNA library

FEATURES
 source Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
 low quality bases were trimmed based on the quality values.
 Location/Qualifiers
 1..679

ORIGIN
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="OVR010067A07"
 /issue_type="ovary"
 /dev_stage="adult"
 /clone_1b="full-length enriched swine cDNA library, adult ovary"

Query Match 18.5%; Score 570.4; DB 5; Length 679;
 Best Local Similarity 90.9%; Pred. No. 5.3e-138;
 Matches 607; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 2 GGCTGGCGAGGCGCAGCGGCATGCCCCCGTGGCTGCACTGCTCCCTCTTCTTACG 61
 DB 12 GGCTGGCGAGGCGCAGCGGCATGCCCCCGTGGCTGCACTGCTCCCTCTTCTTACG 71
 QY 62 TCAGAGCTGCTCTCAACGGCTTGGAGCTGCTGTGTGGCCGCTGGCGGCTCCGCGCT 121
 DB 72 TCAGAGCTGCTCTCAACGGCTTGGAGCTGCTGTGTGGCCGCTGGCGGCTCCGCGCT 131
 QY 122 GGGGCGTGCACACTGTGTGCTGAGAGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGT 181
 DB 132 GGGGCGGCGCACACTGCGGCTGAGAGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGT 191
 QY 182 ACAACATCACTTCAATATGCAATATGCAATATGCAATATGCAATATGCAATATGCAATATG 241
 DB 192 ACAACATCACTTCAATATGCAATATGCAATATGCAATATGCAATATGCAATATGCAATATG 251
 QY 242 TGATTGCTGAGCGCCGCAATATCAGCATCAGCAGTATGCTTCCATGACCAAGTGGCAG 301
 DB 252 TGATTGCTGAGCGCCGCAATATCAGCATCAGCAGTATGCTTCCATGACCAAGTGGCAG 311
 QY 302 TCACCATCTTGTGTCCCGAGGGGCTCGGCAATGCAATTCCTGAAAGATTTCCGGGTAA 361
 DB 312 TCACCATCTTGTGTCCCGAGGGGCTCGGCAATGCAATTCCTGAAAGATTTCCGGGTAA 371
 QY 362 TACTGAGAGAGCTGAGTGCAGAGGAGAGCAGTGCACCACTGATTTCTTAAAGATTCGA 421
 DB 372 TACTGAGAGAGCTGAGTGCAGAGGAGAGCAGTGCACCACTGATTTCTTAAAGATTCGA 431
 QY 422 AGCAGCTCAACAGTACGCTTCAAAAAGACTGGAATGGAATCTTACCTTCTGAAATATGA 481
 DB 432 AGCAGCTCAACAGTACGCTTCAAAAAGACTGGAATGGAATCTTACCTTCTGAAATATGA 491
 QY 482 AATTGGAACGGATATTTGTAAGGTGTCCTTTCTTCCATTAATAAGAAAGCA 541
 DB 492 AATTGGAACGGATATTTGTAAGGTGTCCTTTCTTCCATTAATAAGAAAGCA 551
 QY 542 ATTACACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 601
 DB 552 ATTACACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 611
 QY 602 TAGCTTGTAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 661
 DB 612 CGGCTGTAAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 671
 QY 662 TGCAGGTG 669
 DB 672 TGCAGGTG 679

RESULT 11
 DN391145 609 bp mRNA linear EST 07-MAR-2005
 LOCUS LTB3925-001-Q1-B10 LTB3925 Canis familiaris cDNA clone
 DEFINITION LTB3925-001-Q1-B10 LTB3925 Canis familiaris cDNA clone
 ACCESSION DN391145
 VERSION DN391145.1 GI:60572366
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 609)
 Staten,N.R.
 Direct Submission (Staten,N.R.)
 JOURNAL Unpublished (2005)
 COMMENT Contact: Nick Staten
 Tel: 636 247 6855
 Email: nicholas.r.staten@fizer.com.

FEATURES
 source Location/Qualifiers
 1..609
 /organism="Canis familiaris"
 /mol_type="mRNA"

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
C0204557	GI:54532279	EST.	Sub scrofa (pig)	Sub scrofa (pig)	1 (bases 1 to 803)	Unishih, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., . . .	Okumura, N., Hamasima, N. and Awata, T.	PERE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries	Nucleic Acids Res. 32 (1), D484-D488 (2004)	14681463
					Contact: Hirohide Unishih	Animal Genome Laboratory, Genome Research Department	National Institute of Agrobiological Sciences	2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan	Tel: +81-29-838-8627	Fax: +81-29-838-8627
					Email: huenishih@affrc.go.jp	EST project with full-length enriched cDNA libraries carried out in	Agri Genome Research Program (Japan) by National Institute of	Agrobiological Sciences and STRP-Institute	Single pass sequencing of clones derived from oligo-capped cDNA library	Vector sequences were eliminated by RepeatMasker version 2002/07/13/
					and crossmatch version 0.990319	Low quality bases were trimmed based on the quality values.	Location/Qualifiers	1..803	/organism="Sus scrofa"	/mol_type="mRNA"
					/db_xref="taxon:3823"	/clone="TCH01A100029"	/issue_type="trachea"	/dev_stage="adult"	/clone_id="full-length enriched swine cDNA library, adult trachea"	
ORIGIN										
Query Match	16.1%	Score 496;	DB 7;	Length 803;						
Best Local Similarity	92.1%;	Pred. No. 2e-118;								
Matches 523;	Conservative	0;	Mismatches 45;	Indels 0;	Gaps 0;					
QY	2	GGCTGGGGAAGGACGAGCGGCAGTGGCCCGTGGAGCTGACCTCGCTCTTTTACGG	61							
DB	56	GCGTGGGGAAGGACGAGCGGCAGTGGCCCGTGGAGCTGACCTCGCTCTTTTACGG	115							
QY	62	TCAAGCGCTGCTCAAGCGCTCGAGCTGAGCTGGCCGCTGGCGGCTCGGCGCGCT	121							
DB	116	TCAAGCGCTGCTCAAGCGCTCGAGCTGAGCTGGCCGCTGGCGGCTCGGCGCGCT	175							
QY	122	GGGGCGTGCACACTGTGGCTGGAGGGGAGTGGGGCCAGCCAGAAACAGTGGCTGT	181							
DB	176	GGGGCGTGCACACTGTGGCTGGAGGGGAGTGGGGCCAGCCAGAAACAGTGGCTGT	235							
QY	182	ACAACATCACCTTCAATATATAGCAATTGACACCTACTTGAATTCAGTGGGAAAGCATG	241							
DB	236	ACAACATCACCTTCAATATATAGCAATTGACACCTACTTGAATTCAGTGGGAAAGCATG	295							
QY	242	TGATTGTGACGCCAGAAATATCAACATCAGCCAGTATGCTTGGCATGACCAAGTGGCAG	301							
DB	296	TGATTGTGACGCCAGAAATATCAACATCAGTATGAGCTGTGCACAGCAAGTGGCAG	355							
QY	302	TCACCAATTCCTTGGTCCCGAGGGGCGCTGGCATCGAATTCCTGAAAGGATTTGGGTAA	361							
DB	356	TCACCAATTCCTTGGTCCCGAGGGGCGCTGGCATCGAATTCCTGAAAGGATTTGGGTAA	415							
QY	362	TACTGGAGAGCTGAAGTGGAGGGAAGACAGTGCACAACTGATTTCTTAAGATCCGGA	421							
DB	416	TACTGGAGAGCTGAAGTGGAGGGAAGACAGTGCACAACTGATTTCTTAAGATCCGGA	475							

QY	422	AGCAGCTCAACAGACGCTTGAAAGAACTGGAAGAAATCTCAACCTTTCTGAAATATGA	481
Db	476	AGCAGCTCAACAGATGCTTCAAAAAGCTGGAATGAATCTCACCTTTCTGAAATATGA	535
QY	482	AATTTGAACGAAATATTTCTGTAAGGTGTCTCTTTCTTCATTAAAAACGAAGA	541
Db	536	AATTTGAACGAAATATTCTTTGTCAAGATGTGTCCCTTTCTTCATTAAAAACGAAGA	595
QY	542	ATTACCAACCTTTCTTTCTTTGAACCG	569
Db	596	ATTATCAACCTTTCTTTCTTTGAACCG	623
RESULT 14			
LOCUS	DR003317		
DEFINITION	DR003317	494 bp	mRNA
ACCESSION	DR003317		linear
VERSION	DR003317.1		EST 17-MAY-2005
KEYWORDS	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 494) Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,M.		
TITLE	High-throughput cloning of full-length human cdnas directly from cDNA libraries optimized for large and rare transcripts		
JOURNAL	Unpublished (2005)		
COMMENT	Contact: Kovacs, KR High Throughput cDNA Cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: cDNA@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access. Origene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188 http://www.origene.com Seq primer: PCMV6 Sprieme forward vector primer, Origene Technologies Inc.		
FEATURES			
source	Location/Qualifiers		
	1..494		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="TC100455"		
	/tissue_type="Fetal Brain"		
	/clone_lib="Human fetal brain, large insert, pcMV expression library"		
	/note="Organ: Fetal Brain; Vector: pCMV6-XL4; Site 1: ECoR1; Site 2: Xho1/SalI compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"		
ORIGIN			
Query Match	15.9%;	Score 490;	DB 8; Length 494;
Best Local Similarity	100.0%;	Pred. NO. 6.4e-117;	Indels 0;
Matches 490;	Conservative 0;	Mismatches 0;	Gaps 0;

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